

Tue Apr 20 10:02:30 2004

us-09-508-377-12.rst

Page 1

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 17, 2004, 19:51:10 ; Search time 3340 Seconds

(without alignments)
6866.513 Million cell updates/sec

Title: US-09-508-377-12
Perfect score: 4169
Sequence: 1 MATFAVSATGVAVRPAA.....PSFSYTPSRVAVVATLE 768

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 27513289 segs, 14931090276 residues
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame_plus_p2n.model -DEV=xlh
-O=/cgn2.1/USPTO-US09508377/runat.150422004.084306.2316/app_query.fasta.1.967
-DB=EST -QFMT=fastap -SUFFIX=rest -MINMATCH=0.1 -LOOPEXT=0 -LIST=45
-UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi -ALIGN=LOCAL
-OCALIGN=200 -THR SCORE=Pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=Pct -NCM=Ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-NO_WMAP -LANG=QUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-GAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
EST :
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2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estrov:*
6: em_estrpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
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16: em_estom:*
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19: em_gss_pln:*
20: em_gss_vit:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_phg:*
27: em_gss_vit:*
28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Match	Query Length	DB ID	Description
1	3379.5	81.1	2766	11 AY109521	AY109521 Zea mays
2	3150.5	75.6	2732	11 AY109532	AY109532 Zea mays
3	2128	51.0	2738	11 AK009815	AK009815 Mus muscu
4	2127	51.0	2862	11 AK050365	AK050365 Mus muscu
5	2121	50.9	3012	11 AY105679	AY105679 Zea mays
6	2054	49.3	2044	29 AY413117	AY413117 Homo sapi
7	2047	48.1	2109	29 AY413115	AY413115 Homo sapi
8	2002	48.0	3305	11 AK050423	AK050423 Mus muscu
9	1995	47.9	2109	29 AY413116	AY413116 Pan trogl
10	1412	33.9	852	14 CD438018	CD438018 EL01N0508
11	1404	33.7	881	14 CD440241	CD440241 EL01N0552
12	1352.5	32.4	871	14 CD444875	CD444875 EL01N0445
13	1340	32.1	796	14 CD445867	CD445867 EL01T0204
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15	1255	30.1	752	10 CD423046	CD423046 SAI_29_CO
16	1241	29.8	705	14 CD897929	CD897929 G174.1071
17	1234	29.6	756	14 CA400276	CA400276 EL01N0402
18	1233	29.6	825	10 BF065047	BF065047 HV_CEB002
19	1219	29.2	690	13 CA083722	CA083722 SCFPM205
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21	1197	28.7	678	9 AV939010	AV939010 AV939010
22	1197	28.7	1161	14 CD505751	CD505751 CDA75-D10
23	1195	28.3	736	14 CD444184	CD444184 EL01N0436
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25	1159.5	27.8	695	13 BQ240494	BQ240494 TA05016F
26	1141	27.4	728	10 BQ008463	BQ008463 QGR7K17.Y
27	1138	27.3	650	10 BE427534	BE427534 PSR7153.I
28	1129	27.1	698	14 CD827444	CD827444 BN25.067H
29	1128	27.1	623	13 BU986646	BU986646 HF12102r
30	1124	27.0	713	13 CA202517	CA202517 SCRFLL102
31	1110.5	26.6	650	10 BE602517	BE602517 HYSMBH009
32	1094.5	26.3	731	10 BE602527	BE602527 OS1EB051
33	1093.5	26.2	831	14 CB629365	CB629365 C81EB051
34	1093	26.2	621	14 CD890409	CD890409 G118.114J
35	1090	26.1	926	14 CD446615	CD446615 EL01T0204
C 36	1080	25.9	1482	28 BH770747	BH770747 LLMGrag49
C 37	1070	25.7	594	6 AL812505	AL812505 Trilicium
38	1066	25.6	592	10 BE402623	BE402623 CSB009H05
39	1066	25.6	592	13 BQ608128	BQ608128 BRY_4030
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41	1057	25.4	590	14 CD899778	CD899778 G174.1131
C 42	1055	25.3	644	14 CF039312	CF039312 OCH34b03.
43	1052	25.2	659	13 BQ589993	BQ589993 E012840-0
44	1051	25.2	592	12 BQ268430	BQ268430 BQ268430
45	1051	25.2	623	14 CD977851	CD977851 QAF35d03.

ALIGNMENTS

RESULT 1
AY109521
LOCUS AY109521
DEFINITION Zea mays CU1245_1 mRNA sequence.
ACCESSION AY109521
VERSION AY109521.1 GI:21213273
KEYWORDS
SOURCE
ORGANISM
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
1 (bases 1 to 2766)

AUTHORS	JOURNAL REFERENCE	TITLE
Hainey, C. F., Dolan, M., Mao, G. H., Vogel, J. M., Whitsett, M. S., Athur, L. W., Hanafey, M., Morcote, M., and Tinney, S. V.	Unpublished (2002)	Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes
Coe, E. H.	2 (bases 1 to 2766)	
Submitted (25-APR-2002)	Direct Submission	Maize Mapping Project, University of

ORIGIN

Alignment Scores:

Pred. No.:	0	Length:	631
Score:	3379.50	Matches:	276
Percent Similarity:	84.658	Conservative:	31
Best Local Similarity:	80.694	Mismatches:	81
Query Match:	81.068	Indels:	39
BB:	11	Gaps:	4

US-09-508-377-12 (1-768) X AY109521 (1-2766)

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QY	31	IleGIuGIuInThraIaGIuValaIaIaMetThrGIyGIYThraIaGIuIuIeGIuIeSer	50
Db	170	-----GCAGACTG-----ACTGTGGAGAG--ACATCC	199
QY	51	SerGIuProThrGIu-----	55
Db	197	TCCTCACCACACTCAACAACATCAGCAGTGGCTGGAAGCAAGTCAGGAGTTGAGGCTGAG	256
QY	56	-----GIYIleValGIuThrIleThrAsp	63
Db	257	GAGAGCCCTGAGCTCTCAGAAAGTATTGAGATTGAGAGTTACTGGTGGACCAAAATTGAT	316
QY	64	GIYValThrIuIeGIYValIuIeGIuIeValIaGIYGIuIuIeProAArgValIaIaProIuIe	83
Db	317	GGTGACAGGCATCAAAAGCCAAAGACACACTGTGGAGAGAAACCAACAGATTATCCACCA	376
QY	84	ProGIaAspGIYGIuIeIleIeTYrGIuIeAspProThrIeIuIeAspPheArgSerHis	103
Db	377	CCAGAGAGTGGCCAAACGAAATATATGTGATTGACCCCAATGTTGGAAAGGGTTTCGGGGCTCAC	436
QY	104	LeuAspTYrArgTYrSerGIuTYrArgArgIleArgIaIaIaIeAspGIuInIeGIuGIY	123
Db	437	CTTGACTACCGATACGTGAATATTAAGAGATTACGTCCGGCTATTGATCAACAGAAAGGT	496
QY	124	GIYIeGIuIaIaPheSerArgGIYTYrGIuIuIeGIYpHeThrArgSerIaIaGIuGIY	143

[illegible]

[illegible]

JOURNAL	Overgo Probes
REFERENCE	Unpublished (2002)
AUTHORS	2 (bases 1 to 2732)
TITLE	Coe, E. H.
JOURNAL	Direct Submission
COMMENT	Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSU, maizemap.org ; ZmDB, www.zmdb.iastate.edu ; TIGR, www.tigr.org ; or NCBI, www.ncbi.nlm.nih.gov . When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu .
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	/db_xref="taxon:4577"
	/clone_id="Maize Mapping Project/DuPont Cornsensus Library"
	/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"
ORIGIN	
Alignment Scores:	
Pred. No.:	0
Scores:	3150.50
Percent Similarity:	82.96%
Best Local Similarity:	75.55%
Query Match:	75.57%
DB:	11 Gaps: 4
US-09-508-377-12 (1-768) x AY109532 (1-2732)	
Qy 2 AlAtThrPheAlaValSerGlyAlaThrLeuGlyValAlaArgProProAlaAlaAla---	20
Db 278 GCGGTCATGTTCTCGAGAGGCGAGATGATGCGCTCGATCAAGGGCTGACTCGCTCAA	337
Qy 21 ---GlnProGluGluLeuGlnLeuProGluAspIleGluGlnThrAlaGluValAsn	39
Db 338 TTCAGTCGGATGAACCTGAGATCA---GACATTTCGAAGAGACA-----	362
Qy 40 MetThrGlyGlyThrAlaGluLeuGluSerSerGluProThrGlnGlyIleValGlu	59
Db 382 -----	362
Qy 60 ThrIleThrAspGlyValThrLysGlyValLysGluLeuValAlaGlyGluLysProArg	79
Db 383 -----ACGTGCGGTGCT-----GGTGTGGCTGATGCTCAAGCCTTGAACAGAGTTGCA	430
Qy 80 ValValAlaProLysProGlyAspGlyGlnLysIleTyrgluIleAspProThrLeuLysAsp	99
Db 431 GTGGTNNNNNNNACCAAGCGATGACNNNNNNNTATTCAGATTGACCCCATGTTCACAGGC	490
Qy 100 PheArgSerHisLeuAspTyrglyArgTyrSerGluTyrglyArgIleArgAlaAlaLeuAsp	119
Db 491 TATAAGTACCATCTTGAATATCGGTACAGCCCTCTATGAAGATCCGTTCCAGACATTGAT	550
Qy 120 GlnHisGluGlyGlyLeuGluAlaPheSerArgGlyTyrgluLysLeuGlyPheThrArg	139
Db 551 GAACATAGAGAGGCTTGGAAGCCCTTCCCGGTATGAGAAAGTTTGATTAATCCG	610
Qy 140 SerIleGluGlyIleThrTyrglyArgGluTyrglyAlaHisSerAlaAlaLeuVal	159
Db 611 AGCGCGAAGTATCACATATCGAAGATGGGCTCTGAGACATTTTCTCGACAGATTGGTG	670
Qy 160 GlyAspPheAsnAsnTPAsnProAsnAlaAspThrMetThrArgAspAspTyrglyVal	179

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DB 731 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 790
QY 200 Vallyleleargmetaphrproserqlyvallyleaspsertileseraltrileys 219
DB 791 GFAAGGTAGATGATGATCTCATGAGGATTAAGATTCATTCAGCGTGGATCAAG 850
QY 220 pheSerValGlnAlaProqlygluilepropheserqlyleTytrpProProqly 239
DB 851 TACTAGTCCAGGCCCGAGGAATAATGCAATGATGAGATTTATATGATCCTCTGA 910
QY 240 GluGluValTyValPheGlnHleProGlnProLyArProGlnUserleuArgileTy 259
DB 911 GAGGTAAAGTATGTTGTTACGCGATGCGCAACCTAAACGCAAAATCATTCGCGATAT 970
QY 260 GluSerHleileglymetserProGluProLyArleasnsertYrAlaasnPhearq 279
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QY 280 AspGluValleuProargilelysarqleuglyTyAsnAlaValGlnleleAlaile 299
DB 1031 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1090
QY 300 GlnGluHleSerTyTyraIleSerPheqlyTyHleValThrasPhehealaproser 319
DB 1091 CAAGAGCACTCATATATGAGAGCTTGGATACATGATTAANNNNNNNNNNNNNNNN 1150
QY 320 SerArgPheqlyThProGluaspLeuLyserleileaspArgAlailegylueugly 339
DB 1151 ATCTGTTTGGTACCCCAAGATTTGAAGCTTTGATGATGAGCAATAGAGCTGTGT 1210
QY 340 LeuleuValleuMetAspIleValHleSerHleSerSerAsnAsnthreuspsqlyleu 359
DB 1211 TTGCTAGTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1270
QY 360 AsnglyPheaspqlyThrasPthrHleTyPheHleGlyProArglyHleShleTP 379
DB 1271 AATGTTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1330
QY 380 MetTPasSerArgleuPheasnthreusTyserTPGluValleuArgheleuenser 399
DB 1331 ATGCGGATTCCTCGCTATTAACTHAGGAACTGGGAAGTTTAAAGATTTCTCTCC 1390
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DB 1451 TCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1510
QY 440 PheqlyPhealThrasPValaspAlaValTyTyPheMetleuValasnsPheulle 459
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QY 460 HleGlyleuHlePheaspAlaValserleileGlyaspValSerqlymetProThre 479
DB 1571 CATGACATTTATCTCGAGCTGATGATGATGATGATGATGATGATGATGATG 1630
QY 480 CysIleProValProaspqlyGlyValGlyPheaspTyArgleuHleMetAlaVala 499
DB 1631 GCCCTTCCTGTCAGATGATGATGATGATGATGATGATGATGATGATGATG 1690
QY 500 AspylTPTrleGluLeuLeuLyserAspGluSerTPTrlyMetGlyaspIleVal 519
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QY 560 PheMetAlaLeuAspArgProserThProArgIleAspArgIlyleAlaLeuHlelys 579
DB 1871 TTCATGCGCCCTGATPAGACTTCACTCTACATGATGATGATGATGATGATG 1930
QY 580 MetIleArgleuValThreGlyleuglygluGlyTyTyPheAsnthreMetGlyasn 599
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QY 620 LysValleuProGlyAsnAsnsertTyAspIlyCysArgArgArgPheaspLeugly 639
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QY 700 AsnsertPheaspTyTyraValGlyCysSerArgProGlyLysTyTyValAlaLeu 719
DB 2291 AACAGCTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2350
QY 720 AspSerAspAspAlaLeuPheqlyGlyPheSerArgleuAspHleAspValleTPhe 739
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QY 760 ThraAlaValTyTyraLeuThrglu 768
DB 2471 ACATGTGTCGTATGATGATGATGATGATGATGATGATGATGATGATG 2497

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RESULT 3
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 LOCUS Mus musculus adult male tongue cDNA, RIKEN full-length enriched
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 enzyme 1, full insert sequence.
 ACCESSION AK009815.1 GI:1284841
 VERSION AK009815
 KEYWORDS HTC; CAP trapper
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)
 MEDLINE 99279253
 PUBMED 10349636
 2
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Kono, H., Okazaki, Y., Muramatsu, N. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to

Db	444	CTGAAGGAGTATTATTACTAGTAAGAGTGGCCAGATCACTGTATCCGATTTTCCCATGGGGCA	503
Qy	219	LysPheSerValGlnAlaProGlyGluLeuProPheAsnGlyIleTyrTyrAspProPro	238
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Qy	339	GlyLeuLeuValLeuMetAspIleValHisSerHisSerSerAsnAsnThrLeuAspGly	358
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Qy	379	TyrMetTPAspSerArgLeuPheAsnTyrGlySerTPGluValLeuArgPheLeuLeu	398
Db	978	GATCTTGGGACAGTAATTTATTTATTCATTCACAGCTGGAAAGTTTAAGATTCCTTCTG	1037
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Db	1458	CATGATCAGGCAATGTGGTGTGACAAAGACACTGGGCTTTGGTGTATGACCGCTGAGATG	1517
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Oy		638	IeuuliyasprlaaaprrheleuargTYHhisgLYmetcInglupheaspglnalameGlIn	657
Db		1725	TTAACCGACGATGACTCTTTCGGTATTAAGCTCTTAATAATACTTTGACAGGATATGAAT	1784
Oy		658	HisteugluglulystyrglyPheMetThrsSercluhisglnlyrValserArgLYshis	677
Db		1785	AGACTGGAAGAAABAATGTGTGCTTCCTTCAGCTCCAAAGCCATACGTGATGAAAAACAT	1844
Oy		678	GUUgluasplysVallleilepheguarGlyAspleuValPhevalPheasnPhehis	697
Db		1845	GAAACCAATAGAACAATACACTTGGAGAGACAGAGACTTCTTTATTTTCAACTTCCAC	1904
Oy		698	TrpserasenserPheprieaseryTYrArgValIGLYcyseerArgProgllystyrylVal	717
Db		1905	CCAAAGCAAGAGCTTACGCACTCCCGAGTGGGACACACACACGGAAGTCCAAAATT	1964
Oy		718	AlaleuaspsesarspaBpalaleuPheglVgLYPheSerArgLeuasPHisasPvalasp	737
Db		1965	GTTACTAGATTCTGACGCAAGCGAGTATGAGAGTATAGAGACTGACCCACACACCAAC	2024
Oy		738	TyrPheThrThrgluHisProHisaspAsnarProArgrSerPheSerValTYrTh-Pro	757
Db		2025	TACTTTGGTAGCGCTTTGAAACATAATAGGGGGCCCCCTATCTCTTGTGTGATCAATCCA	2084
Oy		758	SearThralaValval 763 :::::	
Db		2085	AGCCAGAGTGCCTCTCATC 2102	
RESULT 4				
AKO50365		2862 bp	mRNA	linear HTC 20-SEP-2003
LOCUS				
DEFINITION	Mus musculus adult male liver tumor cDNA, RIKEN full-length			
	enriched library, clone:C730040P17 product:glucan (1,4-alpha)-,			
	branching enzyme 1, full insert sequence.			
AKO50365				
ACCESSION	AKO50365.1 GI:26341095			
VERSION				
KEYWORDS	HTC; CAP trapper.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
REFERENCE				
AUTHORS	Carninci,P. and Hayashizaki,Y.			
TITLE	High-efficiency full-length cDNA-cloning			
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)			
MEDLINE	99279253			
PUBMED	10349636			
REFERENCE				
AUTHORS	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,			
TITLE	Itoh,M., Kono,H., Okazaki,Y., Muraitsu,M. and Hayashizaki,Y.			
	Normalization and subtraction of cap-trapper-selected cDNAs to			
	prepare full-length cDNA libraries for rapid discovery of new genes			
	Genome Res. 10 (10), 1617-1630 (2000)			
JOURNAL				
MEDLINE	20499374			
PUBMED	11042159			
REFERENCE				
AUTHORS	Shibata,K., Itoh,M., Aizawa,K., Nagoka,S., Sasaki,N., Carninci,P.,			
	Kono,H., Akiyama,T., Nishi,K., Kitanishi,T., Tashiro,H., Itoh,M.,			
	Sunai,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,			

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DEFINITION        Zea mays AY105679
ACCESSION          AY105679
VERSION            AY105679.1 GI:21208757
KEYWORDS           HTC
SOURCE             Zea mays
ORGANISM           Zea mays
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REFERENCE          1 (bases 1 to 3012)
                   Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitesitt,M.S.,
                   Arthur,L.W., Hanafey,M., Morante,M. and Tingey,S.V.
                   Maize Mapping Project/Dupont Consensus Sequences for Design of
                   Overgo Probes
                   Unpublished (2002)
TITLE              2 (bases 1 to 3012)
JOURNAL            Coe,E.H.
REFERENCE          Submitted (25-APR-2002) Maize Mapping Project, University of
AUTHORS            Missouri, Columbia, MO 65211, USA
COMMENT            If you are interested in getting corresponding physical clones,
                   these are publicly available from ZmDB and may be found by BLAST
                   searching at MSU, maizegap.org; ZmDB, www.zmdb.iastate.edu; TIGR,
                   www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the
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                   /note="this sequence is part of a project of EST
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                   Mapping Project"

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ORIGIN

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Alignment Scores:
Pred. No.:      3,71e-226      Length:      3012
Score:          2121.00      Matches:      393
Percent Similarity: 71.18%      Conservative: 101
Best Local Similarity: 56.63%      Mismatches:  173
Query Match:    50.86%      Indels:      27

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DB: 11 Gaps: 6

US-09-508-377-12 (1-768) x AY105679 (1-3012)

QY 86 AspglylnlyslleTyrgluileaspProthrleuLysaspPheargSerHisleuasp 105
 DB 395 GACATCTCCCATACGACCTGGACCCCAAGCTGGAGATATTCAGAACCATTTCCAG 454
 QY 106 TyrargTysergluTyrgargrglleargAlaAlaIleaspGlnHisgluylglyLeu 125
 DB 455 TACCGAGTAAAGATTCCTTAGACGAAAGATCATTTGAAGAAATAGGGAACTTT 514
 QY 126 GluIleAspSerArgglyTyrgluLysleuglyPheThrArgSerAlaagluyllethr 145
 DB 515 GAATCTTTTCTAAAGGCTATTGAAATTTGGGATTAATACAAATGAGATGGAAGCTGA 574
 QY 146 TyrarggluTPAlaProgluValHisSerAlaAlaLeuValGlyaspPheAsnMetP 165
 DB 575 TATCGTGAATGGGACCTGCTGCCAGAGGACGACCTTATGTGACTTCAATGACTGG 634
 QY 166 AsnProAsnAlaaspThrMetThrArgAspAspTyrglyValTPgluilePheleuPro 185
 DB 635 AATGTCGCAACCATTAAGATGAGAAAGATTAATTTGGTGTGGTCGATCAAAATT--- 691
 QY 186 AsnAsnAlaaspGlySerProAlaIleProHisglYSerArgValLysIleArgMetAsp 205
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 DB 1232 GTTGGACAAAGACCCCAAGAGTCTTATTTTCATGCGGAGATAGAGGTTATCAATAACT 1291
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 DB 1292 TGGGATAGTCGGGTGTTTCAACTATGCTAATCGGAAGTATATACGTTTCTTCTTCTTA 1351
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 DB 1472 CAGTTTGGACACAGCTGTGATGATGAGTTGTTTATCATGATGTGTGAAACCATTTATGCA 1531
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 DB 1532 CAAACTCTTCCAGAAACCACTGTGTGTGCTGAAGATCTTTCAGGACATGCCGCTCTTGG 1591
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 AT413117

[illegible]

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Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@cc.riken.go.jp, URL: <http://genome.gsc.riken.go.jp/>, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to

prepare mouse tissues.

Tissue was provided by William A. Held, Roswell Park Cancer Institute, Department of Molecular and Cellular Biology, Elm and Carlton Streets, Buffalo, NY 14263, whose assistance we gratefully

acknowledge.

Please visit our web site for further details.
URL: <http://genome.gsc.riken.go.jp/>
URL: <http://fantom.gsc.riken.go.jp/>.

Location/Qualifiers

source
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CDS

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Best Local Similarity: 58.10% Mismatches: 151
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US-09-508-377-12 (1-768) x AK050423 (1-3305)

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Db 358 GATGGGCCCCAGAGACCAAGAGAGATTCTTCTACGGAGATTCAAGTGTGGATTCCA 417
QY 168 AsnAlaAspThrMetThrArgAspAspTYrGlyValITrPGluILEpheLeuProASn 187
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 REFERENCE 1 (bases 1 to 2109)
 AUTHOR Clark, A.G., Gnanowsky, S., Nielson, R., Thomas, P., Kejarival, A.,
 Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B.,
 Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.O.,
 Adams, M.D. and Cargill, M.
 TITLE Interfering nonneutral evolution from human-chimp-mouse orthologous
 gene trices
 JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 REFERENCE 2 (bases 1 to 2109)
 AUTHOR Clark, A.G., Gnanowsky, S., Nielson, R., Thomas, P., Kejarival, A.,
 Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B.,
 Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.O.,
 Adams, M.D. and Cargill, M.
 DIRECT SUBMISSION

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 COMMENT This sequence was made by sequencing genomic exons and ordering
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      1969 TATGAGGGCATCAGACAGCTGACACAGACTGACTTTTCTTCTAGGCTTTGAACAT 2028
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ACCESSION      CD438018
VERSION      CD438018.1 GI:31353661
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clade; Panicoideae; Andropogoneae; Zea.
REFERENCE      1 (bases 1 to 852)
AUTHORS      Lai,J., Dey,N., Kim,C.S., Becraft,P., Larkins,B., Linton,E. and
              Messing,J.
TITLE      Sequencing of the maize endosperm ESTs
JOURNAL      Unpublished (2002)
COMMENT      Contact: lai, jinsheng
              Dr. Joachim Messing, 6 lab
              Wakeman Institute, Rutgers University
              190 Frelinghuysen Rd., Piscataway, NJ 08854, USA
              Tel: 732-445-3801
              Fax: 732-445-5735
              Email: jlai@wakeman.rutgers.edu
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 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 881)
 Authors Lai, J., Dey, N., Kim, C.S., Becraft, P., Larkins, B., Linton, E. and
 Messing, J.

TITLE Sequencing of the maize endospERM ESTs
 JOURNAL Unpublished (2002)
 COMMENT Contact: Lai, Jinsheng
 Dr. Joachim Messing's Lab
 Makeman Institute, Rutgers University
 190 Freilighuysen Rd., Piscataway, NJ 08854, USA
 Tel: 732-445-3801
 Fax: 732-445-5735
 Email: jlai@makeman.rutgers.edu
 Seq primer: T3.

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ORIGIN Choi"

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QY 558 TyrAspPheMetAlaLeuAspArgProSerThrProArgIleAspArgGlyIleAlaLeu 577
Db 429 TATGATTTTCATGCGCTTCATGACCTTCAACCTTCAACCTTCAACCTTCAACCTTCA 488
QY 578 HisIleuMetIleArgLeuValThrMetGlyLeuGlyGlyGlyTyrLeuAsnAspMet 597
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QY 618 ThrGlyValValLeuProGlyAsnAsnAsnSerTyrAspIleCysArgAspPheAsp 637
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QY 638 LeuGlyAspAlaAspPheLeuArgTyrHisGlyMetGlnGluPheAspGlnAlaMetGln 657
Db 669 CTGGGTGATGACACTTATCTTACGATGATGATGATGATGATGATGATGATGATGATGAT 728
QY 658 HisLeuGlnGluTyrGlyPheMetThrSerGlnHisGlnTyrValSerArgGlyHis 677
Db 729 CATCTTGACCAAAATATATGATTCATGACATCTGATCACCAGTATATTTCCCGGAAACAT 788
QY 678 GlnGlu 679
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ORIGIN

Alignment Scores:

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Percent Similarity:	93.68%	Conservative:	6
Best Local Similarity:	91.45%	Mismatches:	11
Query Match:	30.39%	Indels:	6

FEATURES

source

HVCDNA0009 (5 to 45 DAP) Hordeum vulgare subsp. vulgare cDNA clone
 HVSMEN0089P20F, mRNA sequence.
 BE195628
 BE195628.2 GI:13188305
 EST.
 Hordeum vulgare subsp. vulgare
 Hordeum vulgare subsp. vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Hordeum.
 1 (bases 1 to 801)
 Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Fritsch,D.,
 Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W.,
 Fenton,R.D., Close,S.J., Oates,R. and Main,D.
 Development of a genetically and physically anchored EST resource
 for barley genomics: Morex 5-45 DAP spike cDNA library
 Unpublished (2001)
 On Jun 26, 2000 this sequence version replaced gi:8707823.
 Contact: Ming RA
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Tel: 864 656 7288
 Fax: 864 656 4293
 Email: rwing@clemson.edu
 Total hg bases = 408
 Seq primer: AATTACCTCCTCAATGAGG
 High quality sequence stop: 611.
 Location/Qualifiers
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 /rname="5-45 DAP spike"
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 HVCDNA0009 (5 to 45 DAP)"
 /note="Vector: lambdaZAP, Site 1: EcoRI, Site 2: XhoI;
 plants were grown in the greenhouse at the University of
 California, Riverside (Penton, SJ Close, TJ Close). Whole
 spikes with awns trimmed were collected at 5, 10, 15, 20,
 30 and 45 DAP (Penton). Total RNA was prepared from each
 pool, equal quantities of all six RNA pools were combined,
 poly(A) RNA was purified from the mixture, one primary
 unamplified cDNA library was made, and 1 million plv were
 in vivo excised to give pluescript SK(-) cDNA phagemids
 (Choi) in the TJ Close lab at the University of California,
 Riverside. Phagemids were plated and picked at the Clemson
 University Genomics Institute (CUGI) (Begum, Palmer,
 Fritsch, Atkins and Wing). Plasmid DNA preparations, DNA
 sequencing and sequence analysis were performed at CUGI
 (Wing, Yu, Fritsch, Henry, Simmons, Oates, Rambo, Main).
 The sequence has been trimmed to remove vector sequence
 and contains a minimum of 100 bases of phred value 20 or
 above. For more details, on library preparation and
 sequence analysis see
 http://www.genome.clemson.edu/projects/barley. To order
 this clone see http://www.genome.clemson.edu/orders Also
 see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
 Genetically and physically anchored EST resources for
 barley genomics. Barley Genetics Newsletter 31:29-30.
 (http://wheat.pw.usda.gov/g99pages/bgn/31/cover.html)"


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QY 212 AspSerIleSerAlaTppIleIysPheSerValGlnIleProGlyGlnIleProPheAsn 231
DB 363 GATTCATTCTCTGAGTGGTCAAGTTTCTGTACAAAGCTCCAGGTGAAATACCATCAAT 422
QY 232 GlyIleTyrTyrAspProProGluGluGluIleTyrValPheGlnHisProGlnProIys 251
DB 423 GGTATATATATGATCCACCTGAAGAGAGAAATATGTATCAAAACACCTCAACTAAG 482
QY 252 ArgProGluSerLeuArgIleTyrGluSerHisIleGlyMetSerSerProGluProIys 271
DB 483 CGGCCAAGTCACCTGCGGATATACGAATCACATATTGGATGAGTAGTCCGGAAACCAAG 542
QY 272 IleAsnSerTyrAlaAsnPheArgAspGluValLeuProArgIleIysArgLeuGlyTyr 291
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QY 332 IleAspArgAlaHisGluLeuGlyLeuLeu 341
DB 723 ATTGACAAAGCGCAATGAGCTTGCTGCTA 752
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Search completed: April 17, 2004, 22:35:08
Job time : 3388 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 17, 2004, 21:39:56 ; Search time 579 Seconds

(without alignments)
5935.195 Million cell updates/sec

Title: US-09-508-377-12

Perfect score: 4169
Sequence: 1 MATRAVSAGTIGVAPPPAA.....PASFVYTPSRNAVYALRE 768

Scoring table:

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Ygapop 10.0 , Ygapext 0.5
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Delop 6.0 , Delext 7.0

Searched: 2890132 seqs, 2237290429 residues

Total number of hits satisfying chosen parameters: 5780264

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Command line parameters:

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Database : Published Applications NA:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	3938	94.5	2554	12	US-10-434-893A-1	Sequence 1, Appl
2	3363	80.7	3039	9	US-09-792-127-3	Sequence 3, Appl
3	3348.5	80.3	2780	12	US-10-434-893A-2	Sequence 2, Appl
4	3342	80.2	2640	12	US-10-336-753-55	Sequence 55, Appl
5	3329	79.9	2559	9	US-09-792-127-1	Sequence 1, Appl
6	3305.5	79.3	5164	12	US-10-424-599-130849	Sequence 130849,
7	3258	78.1	2418	9	US-09-938-842A-872	Sequence 872, App
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11	3189	76.5	2578	14	US-10-056-454A-19	Sequence 19, Appl
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13	3164.5	75.9	2576	14	US-10-056-454A-16	Sequence 16, Appl
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15	3155	75.7	2577	9	US-09-938-842A-337	Sequence 337, App
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33	1978	47.4	2324	12	US-10-425-114-22172	Sequence 32172, A
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39	1656	39.7	1941	15	US-10-359-493-13970	Sequence 33970, A
40	1520.5	36.5	5402	12	US-10-194-163-194	Sequence 194, App
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42	1428.5	34.3	2551	15	US-10-397-954A-2	Sequence 2, Appl
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ALIGNMENTS

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Sequence 1, Application US/10434893A
Publication No. US2004060083A1
GENERAL INFORMATION:
APPLICANT: Ahmed Regina
APPLICANT: Matthew Kennedy Morell
APPLICANT: Sategur Rahman
TITLE OF INVENTION: Baitly with altered branching enzyme activity and starch and sta
FILE REFERENCE: 69425
CURRENT APPLICATION NUMBER: US/10/434.893A
CURRENT FILING DATE: 2003-05-09
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 2.1
SEQ ID NO 1
LENGTH: 2554
TYPE: DNA
ORGANISM: Hordeum vulgare
FEATURE:
OTHER INFORMATION: SSBETA cDNA
US-10-434-893A-1

Alignment Scores:

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 Score: 3938.00 Matches: 722
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 Best Local Similarity: 98.23% Mismatches: 7
 Query Match: 94.46% Indels: 0
 DB: 12 Gaps: 0

US-09-508-377-12 (1-768) x US-10-434-893A-1 (1-2554)

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 QY 694 PheAsnPheHisTyrSerAsnSerPhePheAspTyrArgValGlyCysSerArgProGly 713
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Db      2104 CATGATGTCGACTACTTCCAAACCGAATCCGCAATGACAGCAACGGCCACGCTCTTCTCG 2163
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; Patent No. US2002002713A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Beckles, Diane M.
; APPLICANT: Butler, Karla
; APPLICANT: Pearlstein, Rich
; TITLE OF INVENTION: Search Branching Enzyme Iib
; FILE REFERENCE: B81439 US NA
; CURRENT APPLICATION NUMBER: US/09/792,127
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/186098
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 3
; LENGTH: 3039
; TYPE: DNA
; ORGANISM: Triticum aestivum
; US-09-792-127-3

Alignment Scores:
Pred. No.: 0 Length: 3039
Score: 3363.00 Matches: 607
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Query Match: 80.67% Indels: 14
Gaps: 4
DB: 9

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Db      339 TCTGATGATCTGAAGGTTCCA---TTCATGATGATGAACA-----AGCTTACAG 386
Qy      42  GlyGlyThrAlaGluLeuGluLeuSerSerGluProThrGluGluIleValGluThrIle 61
Db      387 GATGGAGGTGAAGATAGTATTGGTCTTCAGAGCAAAATCAGGTACTGAAGAAATTGAT 446
Qy      62  ThrAspGlyValThrIysGlyValIysGluLeuValAlaGlyGluIysProArgValVal 81
Db      447 GGTGAAGACACGACGACAAATGACAAAGATCATCTCGAGGAGGAATTAACGATTCTG 506
Qy      82  ProIysProGlyAspGlyGluIysIleTyrGluIleAspProThrLeuIysAspPheArg 101
Db      507 CCAACCAACCGGAAATGACACGAAATATACAGATTGACCCACGCTCCGAGACTTTAAG 566
Qy      102  SerHisLeuAspIysArgTyrSerGluTyrArgArgIleArgAlaIleAspGluHis 121
Db      567 TACCACTCTGAGATGATAGCTATACAGGAGAAATACGTTAGACATTGATGAACAC 626
Qy      122  GluGlyGlyLeuGluAlaPheSerArgGlyTyrGluIysLeuGlyPheThrArgSerAla 141
Db      627 GAAAGGAGCATGATGATTTTCCCGCGGTTTACGAGAAGTTTGAATTTATGCGCAGCGCT 686
Qy      142  GluGlyIleThrTyrArgGluTyrAlaProGlyAlaHisSerAlaAlaLeuValGlyAsp 161

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Db	Seq ID	Accession	Length	Type
Db	1767	TGATGTGAACCTTCGAAGAAACAGATGAAGCTTGGAGATGGGTAAATATTGTGCACACA	1826	DNA
QY	522	LeuthAsnaArxArgTrrPLeugIuYsCyvValThrTyraIaGIuSerHisAspGlnA	541	Protein
Db	1887	CTAACAAACAGAAAGGTGGCTGGAAAAAGTGTACTTAATGTGTGAAGATCAGATCAAGCA	1886	DNA
QY	542	LeuValGIyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyrAspPheMet	561	Protein
Db	1887	CTTGTGGAGACAAAGCTATTGGCAATCTGGTGAATGCAGAAAGATAGTAAGATTTCATG	1946	DNA
QY	562	AlaLeuAspArgProSerThrProArgIleAspArgGlyIleAlaLeuHisLysMetIle	581	Protein
Db	1947	GCGCTGAAGACGACCTTCGACGCGCTAATATTGATCGTGAAATAGCACTCAATAATGATTT	2006	DNA
QY	582	ArgLeuValThrMetGlyLeuGIyGlyLeuGIyTyrIleuAsnPheMetGlyAsnGluPhe	601	Protein
Db	2007	AGACTTAATACAAATGGGTCTTAAGAGAGAGAGAGAGAGATTTTAACTTAATAGGAATAGTTC	2066	DNA
QY	602	GlyHisProGlnTrpIleAspPheProArgGlyProGlnThrLeuProThrGlyLysVal	621	Protein
Db	2067	GGGCAATCTCGAATGGATGAATGACTTTCACAGAGGCCCAAGATCTTCCAAAGTGGTAAGTTC	2126	DNA
QY	622	LeuProGlyAsnAsnAsnSerTyrAspLysCyAspArgArgPheAspLeuGIyAspAla	641	Protein
Db	2127	ATCCACAGAAACAAACAACAGATTAAGCAAAATGCCGTGAAATTTGAACCTGGGTATGCA	2186	DNA
QY	642	AspPheLeuArgTyrHisGlyMetGlnGluPheAspGlnAlaMetGlnHisGluGlnGlu	661	Protein
Db	2187	GAATTTCTTAAGGATGATCATGGTATGACACAGCTTGAATGATGACCAATGCACTTGAAGAA	2246	DNA
QY	662	LysTyrGlyPheMetThrSerGlnHisGlnTyrValSerArgLysHisGlnGluAspLys	681	Protein
Db	2247	AAATATGCTTTTATGACATCAGACCAACCAAGTACGTATCTCCGAACATGAGGAATAG	2306	DNA
QY	682	ValIleIlePheGlnArgGlyAspLeuValPheValPheAsnPheHisTrpSerAsnSer	701	Protein
Db	2307	GTGATCGTGTGTTGAAAAAAGGGGCACTTGGTATTGTGTCAACTTCCAGTGGAGTGTAGC	2366	DNA
QY	702	PhePheAspTyrArgValGIyCyvSerArgProGlyLysTyrLysValAlaLeuAspSer	721	Protein
Db	2367	TATTTTGCATTAACCGGTGGCTGTTTAAAGCTCGGAAAGTACAAAGTGGCTTAAGCTCG	2426	DNA
QY	722	AspAspAlaLeuPheGlyGlyPheSerArgPheAspHisAspValAspTyrPheThrThr	741	Protein
Db	2427	GACGCTGGACTCTTTGGTGGATTTGGTAGATTCATCCATCGACGAGAGACGCTCACTCT	2486	DNA
QY	742	GluHisProHisAspAsnArgProArgSerPheSerValTyrThrProSerArgThrAla	761	Protein
Db	2487	GACTGCCAATGATGACACAGGCCCCATTCATTCAGGTGACACTCTTAAGCAAGAACTGTG	2546	DNA
QY	762	ValValIleTyrAla 765		Protein
Db	2547	GTTGTCTATGCT 2558		DNA
RESULT 3				
US-10-434-893A-2				
Sequence 2, Application US/10434893A				
Publication No. US20040060083A1				
GENERAL INFORMATION:				
APPLICANT: Ahmed Regina				
APPLICANT: Matthew Kennedy				
APPLICANT: Sadeeq Rahman				
TITLE OF INVENTION: Barley with altered branching enzyme activity and starch and				
TITLE OF INVENTION: containing products with an increased amylose content				
FILE REFERENCE: 69425				
CURRENT APPLICATION NUMBER: US/10/434, 893A				
CURRENT FILING DATE: 2003-05-09				
NUMBER OF SEQ ID NOS: 11				
SOFTWARE: PatentIn version 2.1				
SEQ ID NO 2				
LENGTH: 2780				
TYPE: DNA				

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FEATURE: OTHER INFORMATION: SSBElb CDNA
US-10-434-893A-2

Alignment Scores:
Pred. No.: 0 Length: 2780
Score: 3348.50 Matches: 605
Percent Similarity: 88.50% Conservative: 72
Best Local Similarity: 79.08% Mismatches: 75
Query Match: 60.32% Indels: 13
DB: 12 Gaps: 3

US-09-508-377-12 (1-768) x US-10-434-893A-2 (1-2780)

QY      8 GLVLAthrLeuGLyValAlaArgProProAlaAlaAla-----GlnPro 22
Db      208 GGGCGTATGGCGGAGAAAGCGAACACCGCTTCCATCCAGGGTCCGTTCAAGTGAAGCT 267
QY      23 GluGluLeuGlnIlePro-----GluAspIleGluGlnIthrAlaGluValAsnMet 40
Db      268 GATGATCTGAGAGGTTCATCTCATGACAGAT-----GAACCAAGCTTG 309
QY      41 ThrGlyGlyThrAlaGluLysLeuGlnSerGluProThrGlnGlyIleValGlnThr 60
Db      310 CACGATGAGGTGAGATATCTATTCCGCTTCCAGACATATCGAGTTACTGAGAAATT 369
QY      61 IleThrAspGlyValAlaThrIleGlyValIleGluLeuValAlaGlyLysProArgVal 80
Db      370 CATGCTGAAGCGCTGACGACAGATGACAAAGATCATCCAGGTGAGAAATAATACGACT 429
QY      81 ValProLysProGlyAspGlyGlnLysIleTyrgIuIleAspProThrLeuLysAspHe 100
Db      430 GGGCCACAACCGCGAAATGGAACAGCAAAATATACGACATTGACCCCATGCTCGAGACTTT 489
QY      101 ArgSerHisLeuAspTyrgTyrgSerGluTyrgArgGlyIleArgAlaAlaIleAspGln 120
Db      490 AAGTACCACTTGAATATCGATTACAGCTTATTTAGAGAAATACGTTCAGACATTGATGA 549
QY      121 HisGluGlyGlyLeuGlnAlaAspHisSerArgGlyTyrgIuLysLeuGlyPheThrArgSer 140
Db      550 TACGATGAGAGATGATGATGATTTTCCCGCGGCTACGAGAGTTGATTTGTTGGCAGC 609
QY      141 AlaGluGlyIleThrTyrgArgIuThrAlaProGlyAlaHisSerAlaAlaLeuValGly 160
Db      610 GGTGAGAGTATCATCTTACCGGAAGAGGGCTCCTGAGCAGATTCGCGACATTACTGTGC 669
QY      161 AspPheAsnAspThrAsnProAsnAlaAspThrMetTrpArgAspAspTyrgIleValTrp 180
Db      670 GACTTCAACAAATGGATGATCCAACTGCAAGCCATATGAGCAAAATGACTGGGTATTGG 729
QY      181 GluIlePheLeuProAsnAsnAlaAspGlySerProAlaIleProHisGlySerArgVal 200
Db      730 GAGATTTTTCGCCAAACATGCAATGATGTTGGCGCCCAATCTCATGGCTCACGGGPG 789
QY      201 LysIleIleArgMetAspThrProSerGlyValLysAspSerIleSerAlaTrpIleLysPhe 220
Db      790 AAGGTGCGGATGATGATCTCCATCTGGGCAAAAGATTCATTCCTGCTGGATCAAGTAC 849
QY      221 SerValGlnAlaProGlyGluIleProPheAsnGlyIleTyrgTyrgAspProGluGln 240
Db      850 TCCGTCGACAGCTCCGAGACATATACATACATGATGATATATATGACCCCTCGTAGAG 909
QY      241 GluLysTyrgValPheGlnHisProGlnProLysArgProGluSerLeuArgIleTyrgIu 260
Db      910 GAGAAGTATGATTCAAAGCATCTCAACTTAACACCAAAATCATTTGGGATATATGAA 969
QY      261 SerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrgAlaAsnPheArgAsp 280
Db      970 AACACAGTTGGGATGATGAGCCCGGAAACCAAAAGATCAACATATGCAAACTTCAGAGAT 102
QY      281 GluValLeuProArgIleLysArgLeuGlyTyrgAsnAlaValGlnIleMetAlaIleGln 300
Db      1030 GAGCTCTCTTCCATCAATTAATTAAGACTTGGATCAATGAGCTCAATATATGCAATCCCA 108

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QY 301 GIuHsSerTyxTyZAlaSerPhegiTyxHsValThraSnPhepealAProSerSer 320
DB 1090 GAGCATCTACTATGAGAGCTTTGGGTACCACTTTCATTCCTTGACCAAGAGC 1149
QY 321 ArgPhegiTyHProGluSpleuLySerLeuLlLeaSpArgAlahSgiUleuGlyLeu 340
DB 1150 CATTGGGTCCCAAGATTAAATCCTTATATAGAGCTCAGAGCTTGTTG 1209
QY 341 LeuValLeuMerAspLleValHsSerHsSerSerSerSerSerSerSerSerSer 360
DB 1210 CTTCCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1289
QY 361 GlyPheAspGlyThraSpThraHsTyxPheHsGlyGlyProArgGlyHsHsTrpMet 380
DB 1270 GATTGATGCGACGAGTACATTAATCTTCATGCGCGCTCAGCGGCGCATCTGAGATG 1329
QY 381 TrpAspSerArgLeuPheAsnTyxGlySerTrpGluValLeuArgPheLeuSerSer 400
DB 1330 TGGGATTCGCGTGTCTCACTACGCGGAATAGAGATTAAGATTCACTTCCAT 1389
QY 401 AlaArgTrpLeuGluGluTyxLysPheAspGlyPheArgPheAspGlyValThraSer 420
DB 1390 GCAAGATGATGCTTACGAAATTAAGTTCGATGATGATGATGATGATGATGATGAT 1449
QY 421 MetMetTyxThraHsHsGlyLeuGluMetThraPheThraGlyAsnTyxGlyTyxPhe 440
DB 1450 ATGATGTATACCAACCATGATTAACAAGTACCTTTACAGGAGACTACATGATATTTT 1509
QY 441 GlyPheAlaThraSpValaSpAlaValTyxLeuMetLeuValaAspLeuLlHs 460
DB 1510 GCGTTTCCACGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1569
QY 461 GlyLeuHsProAspAlaValSerLlGlyLysAspValSerGlyMetProThraPheCys 480
DB 1570 GCGCTTATCTGAGAGCGTTCATTTGTTGAGAGATTTTGTGAAAGCTTACATTTGCC 1629
QY 481 LleProValProAspGlyGlyValGlyPheAspTyxArgLeuHsMetAlaValAlaAsp 500
DB 1630 CTTCCTGTTCAAGTGTGGGGTGTGGTTGATGATGATGATGATGATGATGATGATGAT 1689
QY 501 LysTrpLlGluLeuLeuLysGlnSerAspLysSerTrpLysMetGlyAspLlValHs 520
DB 1690 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1749
QY 521 ThrLeuThraAspArgArgTrpLeuGluLysCysValThraLysGluSerHsAspGln 540
DB 1750 AACTTAACAATAGAGGTGTGAAAGGTGTGATCTTATGCTGAAGTCATGATCAA 1809
QY 541 AlaLeuValGlyAspLysTrpLlLeaPheTrpLeuMetAspLysAspMetTyxAspPhe 560
DB 1810 GCACCTGTTGAGACAAAGATATTCATTCCTGTTGAGACAAAGATATTCATTCATTCAT 1869
QY 561 MetAlaLeuAspArgProSerTrpProArgLlLeaSpArgGlyLlAlaLeuHsLysMet 580
DB 1870 ATGGCTCTGACGACCTTCGACACCTTAATATGATGCGGAAATAGACATGCAATTAATG 1929
QY 581 LleArgLeuValThraMetGlyLeuGlyGlyGlyTyxLeuAsnPheMetGlyAspGlu 600
DB 1930 ATTAGCTTATCAATAGCTTATGAGAGAGAGGCTTATCTTATCTTATGAGAAATGAG 1989
QY 601 PheGlyHsProGluTrpLlLeaAspPheProArgGlyProGlnThraLeuProThraGlyLys 620
DB 1990 TTGGGCACTCTGAATGATGATCTTCCAAAGAGCCCAACAAGTATTCACATCTGTAAG 2049
QY 621 ValLeuProGlyLysAsnAsnSerTyxAspLysCysArgArgArgPheAspLeuGlyAsp 640
DB 2050 TTCTATCCCAAGAAATACAAAGATTACGACAAATAGCCGTGCAAGATTGACCTGGGTAT 2109
QY 641 AlaAspPheLeuArgTyxHsGlyMetGlnLysPheAspGlnAlaMetGlnHsLeuGlu 660
DB 2110 GCGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2169

QY 661 GluLysTyxGlyPheMetThraSerGluHsGlnTyxValSerArgLysHsGluGluAsp 680
DB 2170 GAAAAATGTGCTTATATACATCAAGACCAAGTACGATCTCGGAAACACGAGAGAT 2229
QY 681 LysValLlLeuPheGluArgGlyAspLeuValPheValPheAsnPheHsTrpSerSer 700
DB 2230 AAGGTGATCGCTTGTGAAAGAGGACCTTGATTTGTCTTCACTTCCACTGAGATAT 2289
QY 701 SerPheAspTyxArgValGlyCysSerArgProGlyLysTyxTyxValAlaLeuAsp 720
DB 2290 AGCATTTTCGACTACCGGGTGGTGTCTTAAGCGCTGGAGATGACAGAGGTGTTAGAC 2349
QY 721 SerAspAspAlaLeuPheGlyGlyPheSerArgLeuAspHsAspValAspTyxPheThr 740
DB 2350 TCAGACGCTGACCTCTTGTGTGATTTGTGTAGATTCATCACTGAGAGCACTTCACT 2409
QY 741 ThrGluHsProHsAspAspArgProArgSerPheSerValTyxThraProSerArgThr 760
DB 2410 AATGCTGCCAACAATGACACACAGGCCCATTCGTTCTCAGTGTACCTCTAGCAGAAC 2469
QY 761 AlaValAlaTyxAla 765
DB 2470 TGTGTGTCTAGCT 2484

RESULT 4
US-10-336-753-55
; Sequence 55, Application US/10336753
; Publication No. US2003026176A1
; GENERAL INFORMATION:
; APPLICANT: Guan, Hanping
; APPLICANT: Keeling, Peter L.
; TITLE OF INVENTION: PLANT LIKE STARCHES AND THE METHOD OF MAKING THEM IN
; TITLE OF INVENTION: HOSTS
; FILE REFERENCE: 2461-52
; CURRENT APPLICATION NUMBER: US/10/336,753
; PRIOR FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US/09/402,254
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US98/06660
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/042,939
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-04-04
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 2640
; TYPE: DNA
; ORGANISM: Zea mays
US-10-336-753-55

Alignment Scores:
Pred. No.: 0 Length: 2640
Score: 3342.00 Matches: 608
Percent Similarity: 86.98% Conservative: 67
Best Local Similarity: 78.35% Mismatches: 79
Query Match: 80.16% Indels: 22
DB: 12 Gaps: 4

US-09-508-377-12 (1-768) x US-10-336-753-55 (1-2640)

QY 4 PheAlaValSerGlyAlaThraLeuGlyVal-----AlaArgProProAla 18
DB 108 TTCTTAACCTCGGGGTGCTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 167
QY 19 AlaAlaGlnProGluGluLeuGlnLlLeuProGluAspLlGluGluGlnThraLlAlaVal 38
DB 168 GCCGCGCCAGGAAGCGGTCACTGCTTCTGAGGGGAGAAATAT----- 212
QY 39 AsnMetThrGlyTyxHsGlyLysLeuGluSerSerLys----- 52
DB 213 -----GGCTCGCATCAAGGGCTGACTCGGCTCAATTCACAGTCGATGAATG 260

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Db 261 GAGTACACAGACATTTCTGAAAGACAGACGTCGTCTGCT-----GGTGTGCTGATGCT 314
Qy 73 ValValGlyGlyLeuProArgValValProLysProGlyAspGlyGlnLysIlePheGlu 92
Db 315 CAAGCCTTGAACAGAGTTCGAGTGTCTCCCAACAGCATGAGCAAAAATATTTCCAG 374
Qy 93 IleAspProThrLeuLysAspPheArgSerHisLeuAspTyrArgTyrSerGlyLysArg 112
Db 375 ATTGACCCCATGTTCCAAAGCTATTAAGTACATCTTGAGTATCGGTACAGCTCATATGA 434
Qy 113 ArgIleArgAlaAlaIleAspGlnHisGlyGlyGlyLeuGlnAlaPheSerArgGlyTyr 132
Db 435 AGATCCGCTCAGACATTTGATGAACATGAAGAGGCTTGGAAGCCTTCTCCGCTGATTAT 494
Qy 133 GlyLysLeuGlyPheThrArgSerAlaGlyGlyLysIleThrTyrArgGlyTyrAlaProGly 152
Db 495 GAGAAAGTTTGATTTAATGCCAGCGCGGAGAGTATCACATTCGAAATGGGCTCTCCGA 554
Qy 153 AlaHisSerAlaAlaLeuValGlyAspPheAsnAsnTyrPasnProAsnAlaAspThrMet 172
Db 555 GCATTTTCTGACGATTCGTGGTGGTGAAGCTCAACAATCTGGATCCAAATGACAGATGTATG 614
Qy 173 ThrArgAspAspTyrGlyValTyrGlnIlePheLeuProAsnAsnAlaAspGlySerPro 192
Db 615 AGCAAAATAGATGTTGGTGTGGGAAATTTTCTGCTTAACAATGCAGATGTGTACATCA 674
Qy 193 AlaIleProHisGlySerArgValLysIleArgMetAspThrProSerGlyValLysAsp 212
Db 675 CTAATTCCTCATGATCTCGTGAAGGTGAGATGATCTCCATCGAGGATTAAGAT 734
Qy 213 SerIleSerAlaTyrIleLysPheSerValGlnAlaProGlyGlnIleProPheAsnGly 232
Db 735 TCATTTCCAGCCTCGATCAAGTACTCACTGACGCGCCCAAGAAATACCATATGATGGG 794
Qy 233 IleTyrTyrAspProProGlyGlyGlyLysTyrValPheGlnHisProGlnIlePheArg 252
Db 795 ATTATATATGATCTCTCGAAGAGGCTAAAGTATGTGTTCAGCATCGCGAACCTTAACA 854
Qy 253 ProGlnSerLeuArgGlyIleTyrGlySerHisIleGlyMetSerSerProGlyProLysIle 272
Db 855 CCAAAATATGCGGATATATGAACACATGTCGAAATGAGTACCCCGAACCAGAAATGA 914
Qy 273 AsnSerTyrAlaAsnPheArgAspGlyValLeuProArgIleLysArgLeuGlyTyrAsn 292
Db 915 AACACATATGTAATCTTAAAGGATGAATGCCCTCCCAAGAAATAAAAAATTGATGATCAAT 974
Qy 293 AlaValGlnIleMetAlaIleGlnGlnHisSerTyrTyrAlaSerPheGlyTyrHisVal 312
Db 975 GCACTGCAAAATATATGAGCATCCAAAGACATCATATATATGAAAGCTTTGAAATACCATGA 1034
Qy 313 ThrAsnPhePheAlaProSerSerArgPheGlyTyrProGlyAspLeuLysSerLeuIle 332
Db 1035 ACTATATTTTTTGGCCCAAGTATGCTGTTGGTATCCCAAGAGATTTGAAGTCTTTGATT 1094
Qy 333 AspArgAlaHisGlyLeuGlyLeuLeuValLeuMetAspIleValHisSerHisSerSer 352
Db 1095 GATAGAGACATGACATTTGTTGCTAGTCTCATGATGTGTTGATCATGATCATGCGCTCA 1154
Qy 353 AsnAsnThrLeuAspGlyLysAsnGlyPheAspGlyThrAspThrHisTyrPheHisGly 372
Db 1155 AGTATATCTCTGGATGGGTGATGTGATGTGATGATGATGATGATGATGATGATGATGAT 1214
Qy 373 GlyProAspGlyValHisTyrMetTyrPasnSerArgLeuPheAsnTyrGlySerTyrGlu 392
Db 1215 GGTCCACGTGGCCATCATCTGAGTGTGGATTTCTCGCTATTTTACATATGGGAATGGGA 1274
Qy 393 ValLeuArgPheLeuLeuSerAsnAlaArgTyrTyrLeuGlyGlyLysPheAspGly 412
Db 1275 GTTTTAAAGTTCTCTCTCCATGCTAGATGTGCTCGAAGAAATATAAGTTGATGAT 1334
Qy 413 PheArgPheAspGlyValThrSerMetMetTyrThrHisIleGlyLeuGlnMetTyrPhe 432

Db 1335 TTCGCTTTGATGATGTGATCTCCATGATGATACATCACACGAGATTACAGTAACTTT 1394
Qy 433 ThrGlyAsnTyrGlyGlyTyrPheGlyPheAlaThrAspValAspAlaValTyrLeu 452
Db 1395 ACGGGGAATCTGAAGATATTTTGGCTTTGCCACGATGTATGATGATGATGATGATGAT 1454
Qy 453 MetLeuValAsnAspLeuIleHisGlyLeuHisProAspAlaValSerIleGlyGluAsp 472
Db 1455 AGCTCGTGAATGATCTTAATTCATGATGATGATGATGATGATGATGATGATGATGAT 1514
Qy 473 ValSerGlyMetProThrPheCysIleProValProAspGlyGlyValGlyPheAspTyr 492
Db 1515 GTTATGTAATGCTTCAATTTGCTTCTCTGTTACAGATGTGGGTAGTTTGAATCAT 1574
Qy 493 ArgLeuHisMetAlaValAlaAspLysTyrIleGlyLeuLeuLysGlnSerAspGlySer 512
Db 1575 CGATGTCATATGCTGTGCTGCTGACCAATGATGATGATGATGATGATGATGATGATGAT 1634
Qy 513 TyrPheMetGlyAspIleValHisTyrLeuThrAsnArgTyrTyrLeuGlyLysCysVal 532
Db 1635 TGGAAATGAGGTGATATTTGTGACACACTGACAAATATGAGGTGTGTAGAAAGTGTGA 1694
Qy 533 ThrTyrAlaGlySerHisAspGlnAlaLeuValGlyAspLysThrIleAlaPheTyrLeu 552
Db 1695 ACTTATGCTGAATGATCATGATCAAGCATATGCTGGCGACAAAGCATATTTGGTTG 1754
Qy 553 MetAspLysAspMetTyrAspPheMetAlaLeuAspArgProSerThrProArgIleAsp 572
Db 1755 ATGACAAAGATATGATGATGATTTCAATGCCCTGATGACCTTCAATCTCCATCATTGAT 1814
Qy 573 ArgGlyIleAlaLeuHisLysMetIleArgLeuValPheMetGlyLysGlyGlyGly 592
Db 1815 CGGGATATGATCATTAATGAATGATGATGATGATGATGATGATGATGATGATGATGAT 1874
Qy 593 TyrLeuAsnPheMetGlyAsnGlyPheGlyHisProGlyTyrIleAspPheProArgGly 612
Db 1875 TATCTTAATTTCTGGAATATGATGATGATGATGATGATGATGATGATGATGATGAT 1934
Qy 613 ProGlnThrLeuProThrGlyLysValLeuProGlyAsnAsnAsnSerTyrAspLys 632
Db 1935 CCGCAAAAGCTTCCAAAGTGTGATGATTTATCCAGGAGATTAACAACAGTTAGACAAATGT 1994
Qy 633 ArgArgArgPheAspLeuGlyAspAlaAspPheLeuArgTyrHisGlyMetGlnLysPhe 652
Db 1995 CGTCGAAGATTTAATCCGTGGGTGATGACAGCTATTTTGATGATGATGATGATGATGAT 2054
Qy 653 AspGlnAlaMetGlnHisLeuGlyGlyLysTyrGlyPheMetThrSerGlnHisGlnTyr 672
Db 2055 GATCAGCAATGCAACATCTTGAGCAAAATATATCAATCATGATCATGATCACAAGTAT 2114
Qy 673 ValSerArgLysHisGlyGlyAspLysValIleIlePheGlyLysGlyAspLeuValPhe 692
Db 2115 ATTTCCCGGAAACATGAGAGATGAAGTATGTGTGCGAAAGGAGATTGGTATTT 2174
Qy 693 ValPheAsnPheHisTyrPasnSerSerPhePheAspTyrArgValGlyCysSerArgPro 712
Db 2175 GTGTTCACATTCACATGCAACACACAGCTATTTTATACCTATGATGATGATGATGATGAT 2234
Qy 713 GlyLysTyrLysValAlaLeuAspSerAspAspAlaLeuPheGlyGlyPheSerArgLeu 732
Db 2235 GGGGTGATATAGAGGTGCTTGATGCTCGACCGCTGACATATTTGGTGGATTTAGCGAGAT 2294
Qy 733 AspHisAspValAspTyrPheThrThrGlnHisProHisAspAsnArgProArgSerPhe 752
Db 2295 CATCACCGACCGGACCTTACCGCGGACGCTGTCGATGATTAATAGGCATATTCATTC 2354
Qy 753 SerValTyrThrProSerArgThrAlaValValTyrAlaLeuThrGlu 768
Db 2355 TCGGTTATACCAACACAGACATGTGTCTCTATGCTCCAGTGGAG 2402

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/ Patent No. US20020002713A1
/ GENERAL INFORMATION:
/ APPLICANT: Allen, Steve
/ APPLICANT: Beckles, Diane M.
/ APPLICANT: Butler, Karla
/ APPLICANT: Pearlstein, Rich
/ TITLE OF INVENTION: Starch Branching Enzyme IIB
/ FILE REFERENCE: BB1439 US NA
/ CURRENT APPLICATION NUMBER: US/09/792,127
/ PRIOR FILING DATE: 2001-02-23
/ PRIOR APPLICATION NUMBER: 60/186098
/ NUMBER OF SEQ ID NOS: 5
/ SOFTWARE: Microsoft Office 97
/ SEQ ID NO 1
/ LENGTH: 2559
/ TYPE: DNA
/ ORGANISM: Triticum aestivum
US-09-792-127-1

Alignment Scores:
Pred. No.: 0 Length: 2559
Score: 3329.00 Matches: 589
Percent Similarity: 94.06% Conservative: 60
Best Local Similarity: 85.36% Mismatches: 41
Query Match: 79.85% Indels: 0
DB: 9 Gaps: 0

US-09-508-377-12 (1-768) x US-09-792-127-1 (1-2559)

QY 76 GULYSPROARGLYVALPOLYSPROGLYASPGLYGLNLYSILEYRGHILEASPRO 95
DB 9 GAGNAATTACGCAATTCCTGCCACACCCGGAAATGACAGCAAAATATACGAAATTGACCCCA 68
QY 96 THRLLEULYASPHARGSERHISLEUASPTLYRARGYRSEGLYTYRARGYLEARG 115
DB 69 AGCCTCGAGACTTAAAGTACCATCTGAGATGATGATAGCTTATACGAGAAATAGCT 128
QY 116 AALALEILEASPHINISGLUGLYGLYLEUGLUALPHESERARGLYTYRGLULEU 135
DB 129 TCAGACATTGATGACACGAGAGGAGCATGATGATTTCCCGGTAGAGAGATTT 188
QY 136 GLYPHETHARGSERALAGUGLYILETHRYARGLUTPALAPROGLYALHISER 155
DB 189 GGAATTATGGCAGCGCTGAAGGATACCTTACCGAATAGGCTCCTGGAGCAGATTCT 248
QY 156 AALALEULVALGLYASPHASANTTPASNPROASNPALASPTNMTHTHARGSP 175
DB 249 GCGAGCATAGTGTGGCACTTCACAAATGGGATCCAATGACAGCCATATAGCAAAAT 308
QY 176 ASPTYGLYVALTRPGIULIEPHELEUPROASNPALASPGLYSERPROALILEPRO 195
DB 309 GACCTTGAGTGTGGGAGATTTTCTCCCAACAATGAGTGTGGCCACCAATTCCT 368
QY 196 HISGLYSERARGYLYSILEARGMETASPTHTPROSEGLYVALLYASPSERTLESER 215
DB 369 CACGGCTCCGAGGAGAGTGAAGTGAATGATACCTCATCTGGATGAAGATTCATTCCT 428
QY 216 ALATPRLIEYSPHESERVALGINALPROGLYGLIULIEPHEASNPGLYLETYRXYR 235
DB 429 GCTTGATCAAGTACTCGGACGACTCCGAGAGATATACATCAATGAGATATATAT 488
QY 236 ASPPROGILUGLUGLULYLYTYRVALPHESINISPROGLINPOLYARSPROGLINSE 255
DB 489 GATCTCCCGAAGAGAGAGATGATGATTCACGATCCTCAACTAAACGCAAAATCA 548
QY 256 LEUARGILEYRGUSERHISILEGLYMECSERSEPROGLUPOLYSLIASERTYR 275
DB 549 TTGCGGATATATATAAACAATGTTGGCATGATGAGCCCGGAACCAAGATCAACATAT 608
QY 276 ALAASNPHARGSPGIVULIEUPROARGLILEYARGLEUGLYTYRASPALVALGIN 295
DB 609 GCAAACTTCAGGAGTGGTGTCTTCAAGAAATTAAAGACTTGATACATGACGTGCA 668

QY 296 ILEMETALILEGLINGLHISERTYRVALASERPHENGLYTRYHISVALTHASNPHE 315
DB 669 ATAAATGGCAATCAAGAGACATCATATGAAAGCTTTGGGATCCATGTTACCAATTTTC 728
QY 316 PHEALAPROSERSEARGHNEGLYTHRPROGLIASPLEULYSEULEULEASPARALA 335
DB 729 TTGACCAAGTAGGCCGTTTGGTCCCAAGAGATTTAAACCTTGATGATGAGAGCT 788
QY 336 HISGLULEUGLYLEULVALLEUMECASPILEVALHISERTHISSEASNPASTHR 355
DB 789 CACGAGCTTGCGCTGTTGTTCTCCTCAGATGTTGTTACAGTCAAGCGCTCAAAATATACC 848
QY 356 LEUASPGLYLEUASNGLYPHEASPGLYTHRASPTRYHISILEYRGILEYPROARG 375
DB 849 TTGACGCGGTTGAATGGTTTGTATGGCAGGATACACATTCCTCCATGCGGTTCAAGG 908
QY 376 GLYHISHTPMETTRHASPSEARGLEUPHEASNTYGLYSERTPGIULVALLEUARG 395
DB 909 GGCATCACTGGATGGGATTCCTCCGTGTGTTAACTATGGGAATAGAGATTAAGG 968
QY 396 PHELEUSERASNPALARGTRTPRPLEUGLULYTYRSPHESAPGLYPHEARGPHE 415
DB 969 TTTCTACTTTCCAAATGCAAGATGCTGCTAGAGAGATTAAGTTGATGTTCCGATTC 1028
QY 416 ASPGLYVALTHRSEMETMETTYRTHRHISGLYLEUGLIMETHRPHEHNGLYASN 435
DB 1029 GATGGCGGCACTTCATGATGATATACCATCATGATTAACAAGTAACTTACAGAGAAC 1088
QY 436 TYRGLYGLUTYRPHGLYPHEALATHRASPVALASPALVALVALYTRYLEUMETLEUVAL 455
DB 1089 TACCATGAAATATTTTGGCTTCCCATGATGATGAGCGGTCTTTTACCTGATGCTATG 1148
QY 456 AENASPLEULEILEGLYLEUHHISPROASPALASVALISERTILEGLYGLUASPSALSERGLY 475
DB 1149 AATGATCTHATTCATGCGGTTTATCTCTGAAGCCGTAACTHATCGGTGAAGATGTTAGTGA 1208
QY 476 METPROTHRPHESILEPROVALPROASPGLYGLYPHEASPTLYRARGLEUHHIS 495
DB 1209 ATGCTTACATTTGCCCTTCTGTTCAAGTTGGGCGGTGTTTGTGCTATCGCTTACAT 1268
QY 496 METALAVALEASPLYERTPRILEGLULEULYGLISERTASPGIUSERTPLYMET 515
DB 1269 ATGGCTGTGGCCGACAAAGATGATGAACTTCCAAAGAAACATGAGAGCTTGGAGATG 1328
QY 516 GLYASPILEVALHISETHRLEUTHRAENARGATGTRPLEUGLULYSCYVALTHRYTALA 535
DB 1329 GGTATATTTGTCCACACTTAACAAACAGAGGTGCTGGAAGATGTGTACTATAGCT 1388
QY 536 GLUSERHISASPGNALALEULVALGLYASPLYETHRILEALPHETRPLEUMETASPLY 555
DB 1389 GAAAGTCAAGATCAAGCACTTGTGGAGACAAAGACTATGCAATCTGTTGATGAGAACAG 1448
QY 556 ASPMETTYRASPHEMETLILEUMASPARGPROSETHRPROARGILEASPARGLYLE 575
DB 1449 GATATGATGATTTCAATGCGGTGAACGAGACTTCAACGCTTAATATGATCGGGATA 1508
QY 576 AALAEUHHISLYMETILEARGLEUVALTHRMETGLYLEUGLYGLUGLYTRYLEUASN 595
DB 1509 GCACGTGATTAATATGATGATTAACAAATGCGCTAGAGAGAGAGGTTATCTTAAC 1568
QY 586 PHEMETGLYASNGLUPHEGLYHISPROGLUTPRILEASPHPROARGLYPROGLINTHR 615
DB 1569 TTTATGGGAAATAGAGTTCGGGATCCTGATGATGATGATTCACAAAGGCCCAAGATA 1628
QY 616 LEUPROTHNGLYLYVALLEUPROGLYANASNPASERTYRASPPLYSCYARGARG 635
DB 1629 CTTCAAGGTGTAAGTTATCCAGGAAACAAACAGTTTACAGCAATGCGGTGCAAGA 1688
QY 636 PHEASPLEUGLYASPALASPHLEUARGTRYHISGLYMETGLINGLUPHEASPGIUALA 655
DB 1689 TTTGACCTCGGATGAGCAAGAAATTTCTTAGGTATCATGATGACAGGATTTGATCAGGCA 1748
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QY 656 MetGlnHisLeuGluGluLysTyrGlyPheMetHisSerGlnHisGlnTyrValSerArg 675
 DB 1749 ATGCAGCATCTTGAGGAAAAATATGTTTATGATCATGACCAACAGTATCTCGG 1808
 QY 676 LysHisGluGluAspLysValIleIlePheGluArgGlyAspLeuValPheValPheAsn 695
 DB 1809 AAACATGAGGAAGATAGGTGATCTGTTGAAAAAGGGAGCTTGATTTTGTTCAAC 1868
 QY 696 PheHisTpsSerAsnSerPhePheAspTyrArgValGlyCysSerArgProGlyLysTyr 715
 DB 1869 TTCACCTGAGTAGTACCTATTGCACTTACCGGTCGCTGTTTAAAGCTCGGAAGTAC 1928
 QY 716 LysValAlaLeuAspSerAspAspAlaLeuPheGlyGlyPheSerArgLeuAspHisAsp 735
 DB 1929 AAGGTGCTTAAAGTCTCGGAGCTGGAAGCTTGTGGTGGATTGGTAGATCATCACT 1988
 QY 736 ValAspTyrPheThrThrGluHisProHisAspAsnArgProArgSerPheSerValTyr 755
 DB 1889 GCAGAGCAGCTCACTTCTGACTGCCAACAATGCAAGGCCCATTCATTCTCAGTAC 2048
 QY 756 ThrProSerArgThrAlaValValTyrAla 765
 DB 2049 ACTCTACAGAACCTGTGTCTTATGCT 2078
 RESULT 6
 US-10-424-599-130849
 ; Sequence 130849, Application US/10424599
 ; Publication No. US20040031072A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa Thomas J
 ; APPLICANT: Kovalic David K
 ; APPLICANT: Zhou Yihua
 ; APPLICANT: Cao Yongwei
 ; TITLE OR INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(53223)B
 ; CURRENT APPLICATION NUMBER: US/10/424,599
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 285684
 ; SEQ ID NO 130849
 ; LENGTH: 5164
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_89164C.1
 US-10-424-599-130849
 Alignment Scores:
 Pred. No.: 0 Length: 5164
 Score: 3305.50 Matches: 601
 Percent Similarity: 87.56% Conservative: 75
 Best Local Similarity: 77.85% Mismatches: 75
 Query Match: 79.29% Indels: 22
 DB: 12 Gaps: 5
 US-09-508-377-12 (1-768) x US-10-424-599-130849 (1-5164)
 QY 18 AlaAlaAlaGlnProGluGluLeuGlnIleProGluAspIleGluGluGlnThrAlaGlu 37
 DB 599 TCTGCATCTTACAGATCACTTAAGTAACTCCGATGATTAACCTCAAGATCAACAGAAC 658
 QY 38 Val--AsnMetThrGlyGlyThrAlaGluLysLeuGlnSerSerGluProThr----- 54
 DB 659 TTAGAGGATTTAACATGAGAGATGAGATAAATCAACATTAGTGAAGCAGCTAGACAT 718
 QY 55 -----GlnGly-----IleValGluThrIleLeuAsp----- 63
 DB 719 TACAGCATATTGAGAGTGAAGAGCTCTGTTGATCATCATCTGTAGATGGAACATT 778
 QY 64 -----GlyValThrLysGlyValLysGluLeuValValGlyGlu----- 76
 DB 779 CCGGCCAAGAAACGCTCGGTATCTGTTGATGAGAAATCAAGATATGATGATGAAGTT 838

QY 77 LysProArgValValProLysProGlyAspGlyGlnLysIleTyrGluIleLeuAspProThr 96
 DB 839 AAACCTAA-GTCAATCCCCCAGCTGGCAGTGAAGAAAAATATATGATGATGATCACT 897
 QY 97 LeuLysAspPheArgSerHisLeuAspTyrArgTyrSerGluTyrArgArgIleArgAla 116
 DB 898 TTGCTAGCTCAGCGTACCACTTGTGATTTCCGTTATGACAAATCAAAAGTTGTGTTAT 957
 QY 117 AlaIleAspGlnHisGluGlyGlyLeuGluAlaPheSerArgGlyTyrGluLysLeuGly 136
 DB 958 GAAATTCAGACATGAAGCGGCTCGCATACATTTTCTGTGTATGAAAAATTGGC 1017
 QY 137 PheThrArgSerAlaGluGlyIleThrTyrArgGluThrAlaProGlyAlaHisSerAla 156
 DB 1018 TTCAATACGCACTGCTCAGGCATTTACTTACAGAGAGTGGGCACCTGGAGCTAAGTACGA 1077
 QY 157 AlaLeuValGlyAspPheAsnAsnThrAsnProAsnAlaAspThrMetThrArgAspAsp 176
 DB 1078 GCATTAATGAGACCTTCAACAAATTGAAATCCAAATGCAATGTAATACAGAGATGA 1137
 QY 177 TyrGlyValIleProGluIlePheLeuProAsnAsnAlaAspGlySerProAlaIleProHis 196
 DB 1138 TTGGTGTGGAGATCTTCTGCCAACAATGTGATGGTTCACCAACCAATCCCAT 1197
 QY 197 GlySerArgValLysIleArgMetAspThrProSerGlyValLysAspSerIleSerAla 216
 DB 1198 GGTTCCTCGGTCAAGATCCCATGAGATACCTCCCTGGAATCAAGAGACTCAATTCCTCT 1257
 QY 217 ThrIleLysPheSerValGlnAlaProGlyGluIleProPheAsnGlyIleTyrTyrAsp 236
 DB 1258 TGATTAATGATTTCTGTACAGGCTCTCGTGAAATTCATACAGCGAAATATATCATGAT 1317
 QY 237 ProProGluGluGluLysTyrValPheGlnHisProGlnProLysArgProGluSerLeu 256
 DB 1318 CCCCAGAAAGGAAAAATATGCTTCTCAACATCCACAGCCAAAGAGCCAAATCATCTT 1377
 QY 257 ArgIleTyrGluSerHisIleGlyMetSerSerProGluProLysIleAspSerTyrAla 276
 DB 1378 AGAATATATAGTACCACTGCAATGATAGCAGTCCGAGCCAAATCAATATATATGTC 1437
 QY 277 AsnPheArgAspGluValIleuProArgIleLysArgLeuGlyTyrAsnAlaValGlnIle 296
 DB 1438 AATTTTGAATGATGATGATGCTGCTCCGATTAAGGCTTGCTGATGCTGCAGATT 1497
 QY 297 MetAlaIleGlnGlnHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhePhe 316
 DB 1498 ATGGCTATCCAAAGACATTTCTTATTATGCCAGCTTGGGTACCATGTTCAAAATTTCTTT 1557
 QY 317 AlaProSerSerArgPheGlyThrProGluAspLeuLysSerLeuIleAspArgAlaHis 336
 DB 1558 GCACTTACGAGCCGATTTGGAATCCAGAGAACTTAAAGTCTGATGACAGAGCCCAT 1617
 QY 337 GluLeuGlyLeuLeuValIleuMetAspIleValHisSerHisSerSerAsnAsnThrLeu 356
 DB 1618 GAACTGGCTGCTGCTTCTGATGATGATATGATACAGGCATGATCAAAATATATCATTTG 1677
 QY 357 AspGlyLeuAsnGlyPheAspGlyThrAspThrHisTyrPheHisGlyGlyProArgGly 376
 DB 1678 GATGCGCTGAACATGTTTGAATGGAACGAAAGTCAATTCCTTCACCTCGGGTCAAGAGGT 1737
 QY 377 HisHisThrMetThrPaspSerArgLeuPheAsnTyrGlySerTrpGlyValLeuArgPhe 396
 DB 1738 TATCATGAGATGAGATTCCTGCGCTTTTAACTACGAAAGCTGGAACTTAAAGTAT 1797
 QY 397 LeuLeuSerAsnAlaArgTrpIleProGluGluLysTyrLysPheAspGlyPheArgPheAsp 416
 DB 1798 CTACTTTCGAATGCAAGATGCTGCTGATGATATCAAGTTGATGATTTGATTTGATTTGAT 1857
 QY 417 GlyValThrSerMetTyrThrHisHisGlyLeuGlnMetThrPheThrLysAsnTyr 436
 DB 1858 GGTGTATCATCAAGATGATCATCATCATGATGATGAGGATGATGATTTTCACTGGAATTTC 1917
 QY 437 GlyGluTyrPheGlyPheAlaThrAspValAspAlaValValTyrLeuMetLeuValAsn 456

D	1918	AATGAGTATTTGGTTTGGCAACGAGTGGATCTGTGATTTACCGTAGTCTACTAAT	1977
Q	457	AspLeuIleHISGlyLeuHisProAspAlaValSerIleGlyIAspValSerGlyMet	476
D	1978	GATGTACTTACATGGCGCTGTCCCTCGAGCGTGTTCATTTGGTGAAGATGTACGGCAATG	2037
Q	477	ProThrPheCysVilIProValProAspGlyGlyValGlyPheAspTyrArgLeuHisMet	496
D	2038	CCAAACATCTTCGCTTCCTCCACCGAAGATGGTGGGTTGGCTTTGATTTACGCTGACATG	2097
Q	497	AlaValAlaAspLysTrpIleGlyLeuLeuGlnSerAspGlnSerTrpLysMetGly	516
D	2098	GCCATTGACAGCAAGTGGATTGAAGTTTCTCAAGAAATGATGAAAGCTGAAATGGGT	2157
Q	517	AspIleValHisThrLeuThrAsnArgArgTrpLeuGlnLysCysValThrTyrAlaGlu	536
D	2158	GATATTGTCACACATTAAACAACAGAAAGGCGCTGGAAATATGTATGACTTAGCTGAA	2217
Q	537	SerHisAspGlnAlaLeuValGlyAspLysThrIleAlaPheTrpLysMetAspLysAsp	556
D	2218	AGTATATACCAAGCGCTTGTTGGTGGACAGCAATTCGATTGTGGTAGAGCAAGAT	2277
Q	557	MetTyrAspPheMetAlaLeuAspArgProSerThrProArgIleAspArgGlyIleAla	576
D	2278	ATGATATACCTTCATGGCTTTTAGACAGACATCCACACTATTATAGTCGGTATAGCG	2337
Q	577	LeuHisLysMetIleArgLeuValThrMetGlyLeuGlyGlyGlyTyrLeuAsnPhe	596
D	2338	TTGCACAAATATGATTAGCTTATATACATAGCGTCTTGGTGGTGAAGGGTATTTAAATTT	2397
Q	597	MetGlyAsnGluPheGlyHisProGluTrpIleAspPheProArgGlyProGlnThrLeu	616
D	2398	ATGGGGAATGAATTTGGCCATCCCGAGTGGATTATTTCCAGGGGTGATCAACATCTT	2457
Q	617	ProThrGlyLysValLeuProGlyAsnAsnAsnSerTyrAspLysCysArgArgPhe	636
D	2458	CCCTACTGGCGGAAATGATTCACAGGAAATACAACAGTTTGATTAATACAGCGGACGATTT	2517
Q	637	AspLeuGlyAspAlaAspPheLeuArgTyrHisGlyMetGlnGluPheAspGlnAlaMet	656
D	2518	GACTTGGGTGTGGGACTATCAAGATTCGAGGAATGCAAGATTTGATCAGGCCATG	2577
Q	657	GlnHisLeuGlnGlyLysTyrGlyPheMetThrSerGlnHisGlnTyrValSerArgLys	676
D	2578	CAGCATCTAAGAGAAAGTTGGTTTCATGACTGTCGACCAATATATTTTACCGAAA	2637
Q	677	HisGlnGluAspLysValIleIlePheGlnArgGlyAspLeuValPheValPheAsnPhe	696
D	2638	AATTAAGAGTACAAATATTAAGTTCGAAAGGGGCAACCTCACTTGTGCTTCAATTT	2697
Q	697	HisTrpSerAsnSerPhePheAspTyrArgValGlyCysSerArgProGlyLysTyrLys	716
D	2698	CATTGGAACAAGCTATTCAGATTACAGAGTTGGCTGTTCACCCCTGGGAATATAAG	2757
Q	717	ValAlaLeuAspSerAspAspAlaLeuPheGlyGlyPheSerArgLeuAspHisAspVal	736
D	2758	ATTGTCTTGGATTCAGATGATAGCTTGTGGTGGCTTCAGTCCGCTCAATCACAATGCT	2817
Q	737	AspTyrPheThrThrGlnHisProHisAspAsnArgProArgSerPheSerValTyrThr	756
D	2818	GAGACTTCACTCAAGAAAGATGATATGATGACCACTGATCTTTTATCTATGCA	2877
Q	757	ProSerArgThrAlaValValTyrAlaLeuThrGlu	768
D	2878	CCCTCTAGAACAGCAGTGTATTAGCCCTTGCAAT	2913

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: APPLICANT: Kreps, Joel
: APPLICANT: Wang, Xun
: APPLICANT: Zhu, Tong
: TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
: TITLE OF INVENTION: SAME, AND METHODS OF USE
: FILE REFERENCE: SCRIPT300-3
: CURRENT APPLICATION NUMBER: US/09/938,842A
: CURRENT FILING DATE: 2001-08-24
: PRIOR APPLICATION NUMBER: US 60/227,866
: PRIOR FILING DATE: 2000-08-24
: PRIOR APPLICATION NUMBER: US 60/264,647
: PRIOR FILING DATE: 2001-01-16
: PRIOR APPLICATION NUMBER: US 60/300,111
: PRIOR FILING DATE: 2001-06-22
: NUMBER OF SEQ ID NOS: 5379
: SEQ ID NO 872
: LENGTH: 2418
: TYPE: DNA
: ORGANISM: Arabidopsis thaliana
US-09-938-842A-872

Alignment Scores:
Pred. No.: 0 Length: 2418
Score: 3258.00 Matches: 584
Percent Similarity: 86.48% Conservative: 75
Best Local Similarity: 76.64% Mismatches: 71
Query Match: 78.15% Indels: 32
B: 9 Gaps: 4

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US-09-508-377-12 (1-768) X US-09-938-842A-872 (1-2418)

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18 AlaAlaGlnProGluGluLeuGlnIleProGlu----- 29

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Db 175 GCTATCTCTGCTTCTGAGAAAGTCTTAGTACTGATAATCTTGATGATGATCCAGAGGT 234

30 -----AspIleGluGluThrAlaGluValAsnMetThrGlyThr 44

Db 235 TTTTCACAGATATTGGATCTAGAAAGTCAACAATGGAATAT----- 27

45 AlaGluLysLeuGluSerSerGluProThrGlnGlyIleValGluThrIleThrAspGly 64

Db 277 ACTGAGCAGTACGACGAGACCAACATGACGTT----- 31

65 ValThrLysGlyValIlySGIuLeuValValGlyGlyLysProArgValValProlLysPro 84

Db 316 -----GTCAGGAGAGA-----GGGTGAACCAAGATAGTTCCTCCCAACCG 35

QY 85 GlyAspGlyGlnLysIleTyrGluIleAspProThrLeuLysAspPheArgSerHisLeu 10

Db 358 GGTGATGGCAGAAATTATGAGATAGACCCCATGTTACGACTTACACAATCATCTT 411

105 ASPTyrArgTyrSerGluTyrArgArgIleArgAlaAlaIleAspGlnHisGluGly 12

Db 418 GATTACCGTTATGGACAGTATAAAGATTGCCGTGAGGAATAGACAAGTATGAGCGTGT 477

125 LeuGluAlaPheSerArgGlyTyrGluLysLeuGlyPheThrArgSerAlaGluGlyIle 14

Db 478 CTTGAGGCATTCTCTCGTGGCTATGAAGAATTAGGATTTTCGCCAGTGATGCCGTATA 53

145 ThrTyrArgGluTrpAlaProGlyAlaHisSerAlaAlaLeuValGlyAspPheAsnAsn 16

Db 538 ACTTATAGAGAGTGGCGCCTGGAGCTAAGGCTGCATCACTTATCGGAGATTCAACAAC 599

165 TRPASNPROASNLAASPThrMetThrArgaspPTyrgIValITrgIuIlePheLeu 18

Db 598 TGAATTCTAATGCAGATATCATGACTCGGAATGAATTGGTGTTCGGAGATCTTTTG 65

185 PROASNA¹LA²SPGLY³SER⁴PRO⁵ALA⁶ILE⁷PRO⁸HSGLY⁹SER¹⁰ARG¹¹VAL¹²LYS¹³LEU¹⁴ARG¹⁵MET¹⁶ 20

Db 658 CCCAACACACTGATGTTCCGCTGCAATTCCTCATGGCTCACCCTGAAGATTCGTATG 71

205 AspThrProSerGlyValLysAspSerIleSerAlaTrpIleLysPheSerValGlnAla 22

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Db      718 GATACCTCAGTGGATTAAGACTCAATTCCTGCTGATCAAGTCTCGTGCAAGCT 777
Qy      225 ProGlyGluLeuPheAsnGlyIleTyrThrAspProGluGluGlyLeuVal 244
Db      778 CCGGGGAAATCCCATTCATGAGCATATGATATCTCCAGAGAGAGAGATGTA 837
Qy      245 PheGlnHisProGlnProLysArgProGluSerLeuArgIleTyrGluSerHisIleGly 264
Db      838 TTCAAATCTCTCAACCAAGAGAGCTAAGTCGCTAAGATTATGAAGCAATGTTGGC 897
Qy      265 MetSerSerProGluProLysIleAsnSerTyrAlaAsnPheArgAspGluValLeuPro 284
Db      898 ATGAGTAGCAGGAGCAATGATGCAATAGATGCTAATCTTAGAGATGATGTTCTTCC 957
Qy      285 ArgIleLeuArgLeuGlyTyrAsnAlaValGlnIleMetAlaIleGlnGlnHisSerTyr 304
Db      958 CGCATCAAAAGCTGGATATTAATGCTGTTCAAAATATGSCCATACAAAGACATTCATAT 1017
Qy      305 TyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaProSerSerArgPheGlyThr 324
Db      1018 TATGCCAGCTTTGGGTACCATGTCACAAACCTTTTGGCCCAAGAGAGTGGTGGAAC 1077
Qy      325 ProGluAspLeuLysSerLeuIleAspArgAlaHisGluLeuGlyLeuLeuValLeuMet 344
Db      1078 CCAAGAGAACTAAATCACTGATAGATGAGCTCAGAGCTTAGGCTGTGATGTTCTGATG 1137
Qy      345 AspIleValHisSerHisSerSerAsnAsnThrLeuAspGlyLeuAsnGlyPheAspGly 364
Db      1138 GATATCCTTCAATACCATGCTTCAAAAAACATTCGATGAGCTGAACATGTTATGGA 1197
Qy      365 ThrAspThrHisTyrPheHisGlyGlyProArgGlyHisIleTyrMetTyrAspSerArg 384
Db      1198 ACTGATGCTCTCTATTTTCACTCTGAGACTCGGGATACCATGATGGATTCAGCA 1257
Qy      385 LeuPheAsnTyrGlySerTyrGluValLeuArgPheLeuLeuSerAsnAlaArgTyrTyr 404
Db      1258 CTTTCAATTATGGAGAGCTGGAGAGATTAATGATATCTCTTCAATGACAGCGTGTTGG 1317
Qy      405 LeuGluGlyTyrLysPheAspGlyPheArgPheAspGlyValThrSerMetMetTyrThr 424
Db      1318 CTAAAGAGATCAAGTTGATGATGATTGATTGATGATGATGATGATGATGATGATGAT 1377
Qy      425 HisHisGlyLeuGlnMetThrPheThrGlyAsnTyrGlyGlyTyrPheGlyPheAlaThr 444
Db      1378 CATCATGAGACTCTCGCTTGATTACTGGGAACTACACCGAATACCTTGATGGAACCT 1437
Qy      445 AspValAlaAspAlaValValTyrLeuMetLeuValAsnAspLeuIleHisGlyLeuHisPro 464
Db      1438 GATGGAGATGCTGATGATATATCTCATGCTGCTTAATGATATGATATGATGATGATGAT 1497
Qy      465 AspAlaValSerIleGlyGluAspValSerGlyMetProThrPheCysIleProValPro 484
Db      1498 GAAGGATTAACCGTTGGTGAAGATGTTAGTGTATGCCAACATTCGATTTCTGTCCAA 1557
Qy      485 AspGlyGlyValGlyPheAspTyrArgLeuHisMetAlaValAlaAspTyrTyrIleGlu 504
Db      1558 GATGTGGCGTTGATTTGATACACGTTTACACATGGCCATAGCTATGAAGTAGAAGA 1617
Qy      505 LeuLeuLysGlnSerAspGluSerTyrLysMetGlyAspIleValHisIleThrLeuThrAsn 524
Db      1618 ATGCTCAAGAGAGATGATACATGCGCAAAAGGGGAGATCATCTTATACCACTTACCAAC 1677
Qy      525 ArgArgTyrLeuGlyLysCysValThrTyrAlaGluSerHisAspGlnAlaLeuValGly 544
Db      1678 AGAAGGTGCTCAGAGAGATGATCTTATGCTGGAAGTCACATCAAGCTTGTGTTGGT 1737
Qy      545 AspLysThrIleAlaPheTyrLeuMetAspLysAspMetTyrAspPheMetAlaLeuAsp 564
Db      1738 GATTAAGCAATTCCTTGTGTTATGACAAAGATATGATGATTTCAAGCAGTAGAGAC 1797
Qy      565 ArgProSerThrProArgIleAspArgGlyIleAlaLeuHisIleYsMetIleArgLeuVal 584
Db      1798 AGACCATCAACTCTTATGATGATGAGAAATGCTTGAACAAAGATGATGAGCTTATA 1857

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Qy      585 ThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGlyAsnGluPheGlyHisPro 604
Db      1858 ACTATGGGATTAGGGGGTGAAGGTTACTTAATTTTATGGAACGAATTCGAGACATCCA 1917
Qy      605 GluTyrPheAspPheProArgGlyProGlnThrLeuProThrGlyLysValLeuProGly 624
Db      1918 GATATGATGATTTTCCAGAGAGCGAGCGATCTTCTGATGATGATGATGATGATGATGAT 1977
Qy      625 AsnAsnAsnSerTyrAspLysCysArgArgArgPheAspLeuIleAspAlaAspPheLeu 644
Db      1978 AACAAATTCAGTTATGACAAATGCGCCGACGATTTGATCTTGGGATGACGATTAATCTC 2037
Qy      645 ArgTyrHisGlyMetGlnGluPheAspGlnAlaMetGlnHisLeuGluGlyTyrGly 664
Db      2038 AGATACCGCGGACTACAAAGATTTGATCAGGCAATGCAATCTTGAAGAGAAATTACGCT 2097
Qy      665 PheMetThrSerGluHisGlnTyrValSerArgLysHisGluGluLysPyrSvalIleIle 684
Db      2098 TTTATGACTTCGAGACCAATTCATATCAAGAAAGACAGACAGATGATGATGATGATGAT 2157
Qy      685 PheGluArgGlyAspLeuValPheValPheAsnPheHisIleTyrSerAsnSerPheAsp 704
Db      2158 TTGGAAGAGGTGATCTCGTCTTGTCTTTAATCTTCACTGACGACAGCAGACTACTTGAT 2217
Qy      705 TyrArgValGlyCysSerArgProGlyLysTyrLysValAlaLeuAspSerAspAla 724
Db      2218 TACCGGATGTTGTTGCCAAGCTCGGAAATATAGATCGATTTGAGCTCGAGATCCT 2277
Qy      725 LeuPheGlyGlyPheSerArgLeuAspPheHisAspValAspTyrPheThrGlnHisPro 744
Db      2278 CTCTTGGTGGATTCATATGAGCTGATGCGCAGAGCAGATCACTTATGATGAGCTTA 2337
Qy      745 HisAspAsnArgProArgSerPheSerValTyrThrProSerArgThrAlaValTyr 764
Db      2338 TACGAGCAACGACCTGCTCTCTTCAATGATGATGATGATGATGATGATGATGAT 2397
Qy      765 AlaLeu 766
Db      2398 GCTTTA 2403

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RESULT 8
 US-09-938-842A-872
 ; Sequence 872, Application US/09938842A
 ; Publication No. US20040009476A9
 ; GENERAL INFORMATION:
 ; APPLICANT: Harper, Jeff
 ; APPLICANT: Kreppe, Joel
 ; APPLICANT: Wang, Xun
 ; APPLICANT: Zhu, Tong
 ; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
 ; FILE REFERENCE: SCRIP1300-3
 ; CURRENT APPLICATION NUMBER: US/09/938, 842A
 ; CURRENT FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: US 60/227, 866
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: US 60/264, 647
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/300, 111
 ; PRIOR FILING DATE: 2001-06-22
 ; NUMBER OF SEQ ID NOS: 5379
 ; SEQ ID NO 872
 ; LENGTH: 2418
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 ; US-09-938-842A-872

Alignment Scores:
 Pred. No.: 0
 Score: 3258.00
 Percent Similarity: 86.48%
 Best Local Similarity: 76.64%

Length: 2418
 Matches: 584
 Conservative: 75
 Mismatches: 71

QY 442 PheAlThrAspValAspAlaValValTyrLeuMetLeuValAspLeuIleHisGly 461
DB 1530 CTGGCAACTGATGATGCTGTTGATGATGCTGCTCAACGATCTTATTCATGGG 1589
QY 462 LeuHisProAspAlaValSerIleGlyGluAspValSerGlyMetProThrPheCysIle 481
DB 1590 CTTTCCCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1649
QY 482 ProValProAspGlyValValGlyPheAspTyrArgLeuHisMetAlaValAlaAspLys 501
DB 1650 CCGCTTCAAGATGGGGGTGTTGGCTTGGATGATGATGATGATGATGATGATGATGAT 1709
QY 502 TrpIleGluLeuLeuLysGlnSerAspGlySerTrpLysMetGlyAspIleValHisThr 521
DB 1710 TGGATTGAGTTGCTCAAGAAACGGAGATGAGATGAGATGAGATGAGATGATGATGAT 1769
QY 522 LeuThrAspArgArgTrpLeuGluLysCysValThrTyrAlaGlySerHisAspGlnAla 541
DB 1770 CTGACAAATGAGATGCTGCGAAAGTGTTCATTCGCTGAAAGTCATGATCAAGCT 1829
QY 542 LeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyrAspPheMet 561
DB 1830 CTAGTGGTGATATAAATAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1889
QY 562 AlaLeuAspArgProSerThrProArgIleAspArgGlyIleAlaLeuHisLysMetIle 581
DB 1890 GCTGTGATGACCGTCACATCATTAATGATGATGATGATGATGATGATGATGATGAT 1949
QY 582 ArgLeuValThrMetGlyLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 601
DB 1950 AGCGTTGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2009
QY 602 GlyHisProGluTrpIleAspPheProArgGlyProGlnThrLeuProThrGlyLysVal 621
DB 2010 GGCACACCCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2069
QY 622 LeuProGlyLysMetAspSerTyrAspLysCysArgAlaGlyPheAspLeuGlyAspAla 641
DB 2070 ATTCACCGGAAACCAATTCAGTTATGATGATGATGATGATGATGATGATGATGAT 2129
QY 642 AspPheLeuArgTyrHisGlyMetGlnGluPheAspGlnAlaMetGlnHisLeuGluGlu 661
DB 2130 GATTATTATTAAGATTCGCTGGTGTGCAAGATTTGACCGGCTATGCAATGATTTGAAGAT 2189
QY 662 LysTyrGlyPheMetThrSerGlnHisGlnTyrValSerArgLysHisGlnGluAspLys 681
DB 2190 AATATATAGTTTATGATTCGAAACCAAGTTCATATCAGCAAGAGATGAGAGATAGG 2249
QY 682 ValIleIlePheGluArgGlyAspLeuValPheValPheAspPheHisTrpSerAspSer 701
DB 2250 ATGATTGATTTGAAAAAGAAACCTAGTTTGTCTTAATTTTCACTGCGCAAAAAAGC 2309
QY 702 PhePheAspTyrArgValGlyCysSerArgProGlyLysTyrLysValAlaLeuAspSer 721
DB 2310 TATTCACATTAATCCCATAGGCTGCTGCAAGCTCGAAAAATACAAAGTTGCCCTTGAACCTG 2369
QY 722 AspAspAlaLeuPheGlyGlyPheSerArgLeuAspHisAspValAspTyrPheThrThr 741
DB 2370 GATGATCACTTTTGGTGGCTTTGGGAGATGATGATGATGATGATGATGATGATGATGAT 2429
QY 742 GluHisProHisAspAspAspProArgSerPheSerValTyrThrProSerArgThrAla 761
DB 2430 GAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2489
QY 762 ValValTyrAlaLeuThrGlu 786
DB 2490 GTGGTTATGACCTAGTAGAC 2510

RESULT 10
US-10-056-454A-17
; Sequence 17, Application US/10056454A
; Publication No. US20030166919A1
; GENERAL INFORMATION:

APPLICANT: National Starch and Chemical Investment Holding Corporation
TITLE OF INVENTION: Improvements in or Relating to Plant Starch Composition
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: National Starch and Chemical Investment Holding Corporation
STREET: 1000 Unidema Blvd.
CITY: Newcasttle
STATE: Delaware
COUNTRY: United States of America
ZIP: 19720
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 25-Jun-2002
APPLICATION NUMBER: US/10/056,454A
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 2529 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-10-056-454A-17
SEQ ID NO: 17:
Alignment Scores:
Pred. No.: 0 Length: 2529
Score: 3196.00 Matches: 586
Percent Similarity: 82.53% Conservative: 80
Best Local Similarity: 72.61% Mismatches: 93
Query Match: 76.66% Indels: 48
DB: 14 Gaps: 6
US-09-508-377-12 (1-768) x US-10-056-454A-17 (1-2529)
QY 2 AlaThrPheAlaValSerGlyAlaThrLeu-----GlyValAlaArgProProAlaAla 19
DB 92 TCAACAGTTGACGATCGGGGAAAGTCTTGCTGCGTGAAYCCAGATGATAGCTCTCA 151
QY 20 AlaGlnProGluGluLeuGlnIleProGlu----- 29
DB 152 TCCTCAACAGACCAATTGATGATCTAGTCAAGACATCTCCAGAAATTCGCCAGATCAACT 211
QY 30 AspIleGluGluGlnThrAlaGlu----- 37
DB 212 GATGTGATAGATTCACATGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 271
QY 38 -----ValAsnMetThrGlyGlyThrAlaGlu----- 46
DB 272 GAGCCGCTCAAGGATCTTACAGAGAGTGTGAAGAGCTGATTTGCTTCATCACTACAA 331
QY 47 -----LysLeuGlnUserSerGluProThrGlnGlyIleValGluThrIle 61
DB 332 CTACAAAGAGTGTAACTGAGAGAGTCTAAACATTAATTAATCTTGAAGAGACATTT 391
QY 62 ThrAspGlyValThrIleGlyValLysGluLeuValValGlyGluLysProArgValVal 81
DB 392 ATTGATGATTCGATAGG-----ATCAGAGAG-----AGGGGCAATC 427
QY 82 ProLysProGlyAspGlyGlnLysIleTyrGluIleAspProThrLeuLysAspPheArg 101
DB 428 CCTCCACCTTGACCTTGCTGAGAGATTTATGAATATAGACCCCTTTGACAAACTATGCT 487
QY 102 SerHisLeuAspTyrArgTyrSerGluTyrArgArgIleArgAlaIleAspGlnHis 121
DB 488 CAACACCTTGATTAACGATTCATTCACAGTACAGAAATCGAGGAGGCAATTCAGACAGAT 547
QY 122 GluGlyGlyLeuGluAlaPheSerArgGlyTyrGlyLysLeuGlyPheThrArgSerAla 141
DB 548 GAGGAGGTTTGGAACTTTTCTCGGTGTTATGAAAAAATGGGTTTCATCTGATGCT 607

QY 142 GluGlyIleThrTYRArgGluTrrPalaProGlyAlaHisSerAlaAlaLeuValGlyAsp 161
 Db 608 ACAGGTATCATCTTACCGTGAAGGGCTCTGGTGCACGATGCGCTCATTTGGAGAT 667
 QY 162 PheAsnAntPasnProAsnAlaAspThrMetThrArgAspAspTyrGlyValTrrGlu 181
 Db 668 TTCAACAAATTGGGACGCAAAATGCTGACATTAGACTCGGAATGAATTTGGTCTGGGGAG 727
 QY 182 IlePheLeuProAsnAsnAlaAspGlySerProAlaIleProHisGlySerArgVallys 201
 Db 728 ATTTTTCGCAAAATATGTGGATGTCTCTGCAATTCCTCAATGGGTCCGAGTGAAG 787
 QY 202 IleArgMetAspThrProSerGlyValIlysAspSerIleSerAlaTrrPleLysPheSer 221
 Db 788 ATACGATGACACCTCCATCAGGTGTTAAGATTCATTCCTGCTGGATCAACTACTCT 847
 QY 222 ValGlnAlaProGlyGluIleProPheAsnGlyIleTyrTyrAspProProGluGlu 241
 Db 848 TTACAGCTTCTCGATGAATTCATATATGAATGAATATATATGATCCACCAGAGGAG 907
 QY 242 LysTyrValPheGlnHisProGlnProLysArgProGluSerLeuArgTleTyrGlySer 261
 Db 908 AGGTATTCCTTCACACCCAGCCGCAAGAAACCAAGTCCCTGAGATTAATGATCT 967
 QY 262 HisIleGlyMetSerSerProGluProLysIleAsnSerTyrAlaAsnPheArgAspGlu 281
 Db 968 CATATTGAAATGAGTATGTCGAGCTGAATTAATTAATTAATTAATTAATTAATTAAT 1027
 QY 282 ValLeuProArgGlyLeuArgLeuGlyTyrAsnAlaValGlnIleMetAlaIleGlnGlu 301
 Db 1028 GTTCTCTCTCCATAAAAAASCTTGGGTACATGCGGTGCAAAATATATGCTATTCAAGAG 1087
 QY 302 HisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaProSerSerArg 321
 Db 1088 CATCTTATTTATGCTAGTTTGGTATCATGTCACAAAATTTTTCACACAGCCCT 1147
 QY 322 PheGlyThrProGluAspLeuLysSerLeuIleAspArgAlaHisGluLeuGlyLeuLeu 341
 Db 1148 TTGGAAACGCCGACGACCTTAAGTCTTGAATTAAGTCAATGATGAGTAAGTAATGTT 1207
 QY 342 ValLeuMetAspIleValHisSerHisSerSerAsnAsnThrLeuAspGlyLeuAsnGly 361
 Db 1208 GTTCCATGACATGATGTCACAGCCATGATCAAAATTAATTAATTAATTAATTAATTAAT 1267
 QY 362 PheAspGlyThrAspThrHisTyrPheHisGlyGlyProArgGlyHisHisTrrMetTrr 381
 Db 1268 TTTCAGCGACAGATAGTGTACTTCTCTGAGAGCTCGTGATATCATTTGGATGTGG 1327
 QY 382 AspSerArgLeuPheAsnTyrGlySerTrrPgluValLeuArgPheLeuLeuSerAsnAla 401
 Db 1328 GATTCGCCGCTTTTAATCATATGAAACCTGGAGAGTCACTTGAATCTTCTCAAAATGCG 1387
 QY 402 ArgTrrTrrPleGluGlyTyrLysPheAspGlyPheArgPheAspGlyValThrSerMet 421
 Db 1388 AGATGTGTGTGGATGAGTCAAAATTTGATGATTTAGATTGATGATGATGATGATGATGAT 1447
 QY 422 MetTyrThrHisHisGlyLeuGlnMetThrPheThrGlyAsnTyrGlyGluTyrPheGly 441
 Db 1448 ATGTATATCTCACACGAGATTAATCGGTGGATTCACCTGGAACTACAGAGAAATCTTTGGA 1507
 QY 442 PheAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeuIleHisGly 461
 Db 1508 CTCGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1567
 QY 462 LeuHisProAspAlaValSerIleGlyGluAspValSerGlyMetProThrPheCysIle 481
 Db 1568 CTTTTCGAGATGCAATTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1627
 QY 482 ProValProAspGlyGlyValGlyPheAspTyrArgLeuHisMetAlaValAlaAspLys 501
 Db 1628 CCCGTTCAAGATGGGGCTGTGGCTTTGACTATCGGCTGCAATGGAATTTGCTGATTA 1687
 QY 502 TrrPleGluLeuLeuLysSerAspGlySerTrrPlyMetGlyAspIleValHisThr 521

Db 1688 TGGATTGAGTGTCTCAAGAAACGGGATGAGGATTTGGAGGTGGTGTATTGTTCATCA 1747
 QY 522 LeuThrAsnArgArgTrrPleGluLysCysValThrTyrAlaGlySerHisAspGlnAla 541
 Db 1748 CTCACAAATRGAAGATGCTGGAAATGCTGTTTCAATCCCTGAAATGATCAAGTCAAGCT 1807
 QY 542 LeuValGlyAspLysThrIleAlaPheTrrPleuMetAspLysAspMetTyrAspPheMet 561
 Db 1808 CTAGTCGTGATTAACATATAGCATTCGCTGATGAGCAAGGATATGATGATTTATG 1867
 QY 562 AlaLeuAspArgProSerTrrProArgIleAspArgIleIleAlaLeuHisLysMetIle 581
 Db 1868 GCTGTGATGACCGCAACAYCATTAATATGATGATGATGATGATGATGATGATGATGAT 1927
 QY 582 ArgLeuValThrMetGlyLeuGlyGlyGlyTyrLeuAsnPheMetGlyAsnGluPhe 601
 Db 1928 AGCTTGTATCTATGGATTAAGAGAGAGAGGATTAATTAATTAATTAATTAATTAATTAAT 1987
 QY 602 GlyHisProGluTrrPleAspPheProArgGlyProGlnThrLeuProThrGlyLysVal 621
 Db 1988 GGCACCCCTGAGTGAATGATTTCCCTAGGGCTGARGACACCTCTGATGATGCTCACTA 2047
 QY 622 LeuProGlyAsnAsnAsnSerTyrAspLysCysArgArgArgPheAspLeuGlyAspAla 641
 Db 2048 ATTCGCGGAAACCAATTCAGTATGATTAATGACAGCGAGATTTGACCTGGAGATGCA 2107
 QY 642 AspPheLeuArgTyrHisGlyMetGlnGluPheAspGlnAlaMetGlnHisLeuGluGlu 661
 Db 2108 GAATATTTAAGATACATGCTGTTGCAAGATTTTACCGGGCTATGACATTAATTTGAAGAT 2167
 QY 662 LysTyrGlyPheMetThrSerGluHisGlnTyrValSerArgLysHisGlyGluAspLys 681
 Db 2168 AAATATGAGTTTATGACTTCAAGAACACAGTTCATCAACAAAGATGAGGAAATGAG 2227
 QY 682 ValIleIlePheGluArgGlyAspLeuValPheValPheAsnPheHisTrrSerAsnSer 701
 Db 2228 ATGATGTATTTGAAGAAGAACCTTGTGTGTCTTAAATTTTCACTGACGCAAAATGAC 2287
 QY 702 PhePheAspTyrArgValGlyCysSerArgProGlyLysTyrLysValAlaLeuAspSer 721
 Db 2288 TATTCAGACATATCCCATAGCTGCTGAGCTTGAAATCAAGTGTGGCTTGACATCA 2347
 QY 722 AspAspAlaLeuPheGlyGlyPheSerArgLeuAspHisAspValAspTyrPheThrThr 741
 Db 2348 GATGATCCATTTTGTGGCTTGGGAGAAATGATCATTAATGCCGAATATTTCACCTCT 2407
 QY 742 GluHisProHisAspAsnArgProArgSerPheSerValTyrThrProSerArgThrAla 761
 Db 2408 GAAGGATCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2467
 QY 762 ValValTyrAlaLeuThrGlu 768
 Db 2468 GTGCTCATGACATAGTAAGAC 2488

RESULT 11
 US-10-056-454A-19
 Sequence 19, Application US/1005645A
 Publication No. US20030166919A1
 GENERAL INFORMATION:
 APPLICANT: National Starch and Chemical Investment Holding Corporation
 TITLE OF INVENTION: Improvements in or Relating to Plant Starch Composition
 NUMBER OF SEQUENCES: 20
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: National Starch and Chemical Investment Holding Corporation
 STREET: 1000 Unigema Blvd.
 CITY: Newcastle
 STATE: Delaware
 COUNTRY: United States of America
 ZIP: 19720
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible

[illegible]

QY 82 ProlyserProGlyAspGlyGlnIleYrGlnIleAspProThrLeuIleAspPheArg 101
Db 702 CTCCACACCTGGAGCTTGGTCAGAGATTATGAAATGACCCCTTTGGACAAATCATACGT 761
QY 102 SerHisLeuAspTyrArgTyrSerGluTyrArgArgIleArgAlaIleAspGlnHis 121
Db 762 CAACACCTTGAATTACAGGATTCACAGTACAGAACTGAGGAGGACAAATTGACAAATAT 821
QY 122 GluGlyGlyLeuGlnIleAspSerArgIlyTyrGlnIleGlyLeuIlePheThrArgSerAla 141
Db 822 GAGGGTGGTTGGAGCTTTTCTCGTGGTTGAAAAAATGGGTTTCACTCGTAGTGCT 881
QY 142 GluGlyIleThrTyrArgIleUtrPalaProGlyValHisSerAlaAlaLeuValGlyAsp 161
Db 882 ACAGGATACCTTACCGTAGTGAGGCTCGTGCCAGTCCAGTCCCTCATTTGGAGAT 941
QY 162 PheAsnAsnTyrAsnProAsnAlaAspThrMetThrArgAspAspTyrGlyValTyrGlu 181
Db 942 TTCAACAATGGGACCCCAATGCTGACATTATGACTCGGAATGAATTTGGTGTGGAG 1001
QY 182 IlePheLeuProAsnAlaAspGlySerProAlaIleProHisGlySerArgValIys 201
Db 1002 ATTTTTCGCCAAATATATGATGATGTTCTCTGCAATTCCTCATGGGTCCAGAGTAG 1061
QY 202 IleArgMetAspThrProSerGlyValIleAspSerIleSerAlaTyrPheIleYrPheSer 221
Db 1062 ATACGTATGGACATCCATCAGGTGTTAAGATTCCATTCCTGCTGGATCAACTCTCT 1121
QY 222 ValGlnAlaProGlyGluIleProPheAsnGlyIleTyrTyrAspProProGluGlnIle 241
Db 1122 TTACAGCTTCTCGATGAAATTCATATATGAAATATATATATATATATATATATATAT 1181
QY 242 LysTyrValPheGlnHisProGlnProLysArgProGlnSerLeuArgIleTyrGlnIle 261
Db 1182 AGGTATATCTCCACACACCCAGCCGCAAGAAACCAAGTCGTGAGAAATATATGATCT 1241
QY 262 HisIleGlyMetSerSerProGluProLysIleAsnSerTyrAlaAsnPheArgAspGlu 281
Db 1242 CATATTTGATAGATGATGCTCCGAGCTTAAATTAATCTCATACGTGAATTTTAAAGATGA 1301
QY 282 ValLeuProArgIleLysArgLeuGlyTyrAsnAlaValGlnIleMetAlaIleGlnIle 301
Db 1302 GTTCTTCTCCGATAAAAAGCTTGGGTACATGCGGTGCMAATTTATGGTTATTCANAG 1361
QY 302 HisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaProSerSerArg 321
Db 1362 CATCTTTATATAGCATGTTTGGTTATCATGTCACAAATTTTNGACCAACAGCCGT 1421
QY 322 PheGlyTyrProGluAspLeuLysSerLeuIleAspArgAlaHisGluLeuGlyLeuLeu 341
Db 1422 TTTGGAACCCCGACGACCTTAAGTCTTGAATGATTAAGCTCATAGCTAGAGAAATGTT 1481
QY 342 ValLeuMetAspIleValHisSerHisSerSerSerAsnThrLeuAspGlyLeuAsnGly 361
Db 1482 GTTTCATAGCATTTGTTTACAGCCATGCATCAATTAATCTTTAGATGACGAAACATG 1541
QY 362 PheAspGlyTyrAspThrHisTyrPheHisGlyIleProArgGlyHisHisTyrMetTyr 381
Db 1542 TTTGACGCGACAGATGATGTTACTTCACTCGAGCTCGTGTATATCATTTGAGATGTG 1601
QY 382 AspSerArgLeuPheAsnTyrGlySerTyrPgluValLeuArgPheLeuLeuSerAspAla 401
Db 1602 GATTCGCCGCTCTTAACTATGAGAACTGGAGGTCTTAAGTATCTTCTCTAAAGCG 1661
QY 402 ArgTyrProLeuGluGluTyrLysPheAspGlyPheArgPheAspGlyValTyrSerMet 421
Db 1662 AGATGGTGGTTGATGATGATTCAAATTTGATGATTTAGATTTGATGATGATGATGATGAT 1721
QY 422 MetTyrThrHisHisGlyLeuGlnMetThrPheThrGlyAsnTyrGlyTyrPheGly 441
Db 1722 ATGTATACTCACACGAGATTATCGGTGATTCATCTGGGAACTACAGAGAAATCTTTGA 1781

Db 1782 CTGCAACTGATGAGAGCTGTGTGTATCGAATGCTGGTGAACGATCTTATTCATGGG 1841
QY 462 LeuHisProAspAlaValSerIleGlyGluAspValSerGlyMetProThrPheCysIle 481
Db 1842 CTTTCCAGATGCAATTAACATTTGTTGTAAGTGTAGCGGAATGGCAGATTTTMTAT 1901
QY 482 ProValProAspGlyValGlyPheAspTyrArgLeuHisMetAlaValAlaAspLys 501
Db 1902 CCCGTTCAAGATGGGGGTGTGGCTTTGATGATCTCGGCTCATATGCAATTCGTGATAAA 1961
QY 502 ThrIleGluLeuLeuGlnSerAspGlySerTyrPheMetGlyAspIleValHisThr 521
Db 1962 TGGATGATGTTGCTCAAGAAACGGGATGAGATGAGAGTGGAGTGGATGATTTCTTACA 2021
QY 522 LeuThrAsnArgArgTyrProLeuGluLysCysValIleTyrAlaGlySerHisAspGlnAla 541
Db 2022 CTGCAAAATAGAGATGCTCGGAAAGTGTGTTTATACGCTGAAAGTCATGATCAAGCT 2081
QY 542 LeuValGlyAspLysThrIleAlaPheTyrPheMetAspLysAspMetTyrAspPheMet 561
Db 2082 CTAGTCGGGTATTAACATATAGCATTCGTGCTGATGAGAGAAAGATATGATATTTATG 2141
QY 562 AlaLeuAspArgProSerThrProArgIleAspArgGlyIleAlaLeuHisLysMetIle 581
Db 2142 GCTGTGATAGACCTTCAACATCATTAATAGATCGTGGATAGCATTCGACAAAGATGAT 2201
QY 582 ArgLeuValThrMetGlyLeuGlyGlyGlyTyrLeuAsnPheMetGlyAsnGluPhe 601
Db 2202 AGGCTTGAATTAATAGGATTTGAGAGAGAAAGGATCTTAATTTGATGGAAATGAAATTC 2261
QY 602 GlyHisProGluTyrPheAspPheProArgGlyProGlnThrLeuProThrGlyVal 621
Db 2262 GGCCACCTGATGATGATTTCCCTAGGGCTGAACAACCTCTCATGATGCTCAGAT 2321
QY 622 LeuProGluAsnAsnAsnSerTyrAspLysCysArgArgArgPheAspLeuGlyAspAla 641
Db 2322 ATTCGCCGAAACCAATTCAGATATGATTAATGACAGAGGAAATTTGACCTGGAGATGCA 2381
QY 642 AspPheLeuArgTyrHisGlyMetGlnIlePheAspGlnAlaMetGlnHisLeuGluGlu 661
Db 2382 GAATATTTAATATACCGTGGTTCGACAAATTTGACCGGCTATGAGATCTTGAAGAT 2441
QY 662 LysTyrGlyPheMetThrSerGlnHisGlnTyrValSerArgLeuHisGluGluAspLys 681
Db 2442 AAATATGATTTATGACTTCGAAACACACAGTTCATATACGAAAGATGAAAGATGATG 2501
QY 682 ValIleIlePheGluArgGlyAspLeuValPheValPheAsnPheHisTyrSerAsnSer 701
Db 2502 ATGATGATTTGAAAGAAAGAACTAGATTTTGTCTTAAATTTTCACTGGACAAAGAGC 2561
QY 702 PhePheAspTyrArgValGlyCysSerArgProGlyLysTyrLysValAlaLeuAspSer 721
Db 2562 TATTCAGCTATTCGATAGGCTGCTGAAGCTGGAATAATACAAAGTCTCTTGAAGCTCA 2621
QY 722 AspAspAlaLeuPheGlyGlyPheSerArgLeuAspHisAspValAspTyrPheThrThr 741
Db 2622 GATGATCACTTTTGGTGGCTTCGGGAAATGATGATCAATTAAGCCGAAATTTTCACTTT 2681
QY 742 GluHisProHisAspAsnArgProArgSerPheSerValTyrThrProSerArgThrAla 761
Db 2682 GAAAGATGGTATGATGATGATGCTTCCTTCATTAATGATGATGATGATGATGATGATG 2741
QY 762 ValValTyrAlaLeuThrGlu 768
Db 2742 GTGGTATATGACATAGTAGAC 2762

RESULT 13
US-10-056-454A-16
Sequence 16, Application US/10056454A
Publication No. US20030166919A1
GENERAL INFORMATION.

TITLE OF INVENTION: Improvements in or Relating to Plant Starch Composition
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSER: National Starch and Chemical Investment Holding Corporation
STREET: 1000 Unidema Blvd.
CITY: Newcasle
STATE: Delaware
COUNTRY: United States of America
ZIP: 19720
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 25/10/056,454A
FILING DATE: 25-Jun-2002
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 2576 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-056-454A-16

Alignment Scores:
Pred. No.: 0 Length: 2576
Score: 3164.50 Matches: 584
Percent Similarity: 82.40% Conservative: 81
Best Local Similarity: 72.37% Mismatches: 94
Query Match: 75.91% Indels: 49
Gaps: 6

US-09-508-377-12 (1-768) x US-10-056-454A-16 (1-2576)
QY 2 AlathrhealvalaIseryAlathrleu-----GlyValAlaArgProProAlaala 19
DB 99 TCTACAGTGCAGATCGGGGAAAGTCTTGCTCGAACCAGAGTATGATCTCTCA 158
QY 20 AlagInProglugluLeuGlnleProglu----- 29
DB 159 TCCCAACAAACCAATTGATGCTCAGACATCTCCAGAAATTTCCAGACATCACT 218
QY 30 AsplleglugluInthrAlaglu----- 37
DB 219 GATGTAGTATGTTCAACAATGGAACACGCTAGCCAGATTAAACTGAGAACATGACGTT 278
QY 38 -----ValAsnMetThrGlyGlyThralaglu----- 46
DB 279 GAGCGGTCAAGATCTTACAGAAAGTGTGAAGAGCTGAAATTGCTTCATCATCAACA 338
QY 47 -----LysleugluSerSerGluProthrglnGlyLevalGluThrile 61
DB 339 CTACAGAAGGTGTAACTGAGAGAGTAAACATTAAATACCTTCTGAGAGAACATT 398
QY 62 ThrAspGlyValThrleGlyVallySerGluLeuValGlyGluSerProArgVal 81
DB 399 ATTGATGAATCTGATAGG---ATCAGAGG-----AGGGGATC 434
QY 82 ProlySerProGlyAspGlyGluLysileYrgLulLeaSPProThrleuLysAspPheArg 101
DB 435 CCTCACCGGAGCTGGTGCAGAAAGTTTAAATAGACCCCTTTTGACAACTATCGT 494
QY 102 SerHisleuAspTyrArgTyrSerGluYrArgArgIleArgAlaAlaIleAspGlnHis 121
DB 495 CAACACCTTGATTTACGGTATTCACAGTACAGAACTGAGGAGGCAATTGACACAGTAT 554
QY 122 GluGlyGlyLeuGluAlaPheSerArgGlyTyrGluLysleuGlyPheThrArgSerAla 141
DB 555 GAGGGGTGTTGGAGCTTTTCTCGTGGTTATGAAAAATGGGTTTCACTCGATGCGT 614

DB 615 ACAGGTATCACTTACCGGATGAGGGCTCTGTGCTGCACATCACTGCTCATGTAGAT 674
QY 162 PheAsnAsnTyrPAsnProAsnAlaAspThrMetThrArgAspAspTyrGlyValTyrGlu 181
DB 675 TTCAACAATTGGAGACGAATGCTGACATTATGACTCGGAATGAATTTGGTGTCTGGAG 734
QY 182 IlePheLeuProAsnAsnAlaAspGlySerProAlaIleProHisGlySerArgValIys 201
DB 735 ATTTTCTGCCAAATATGATGATGTTCTCTGCAATTCCTCATGAGTCAAGAG 794
QY 202 IleArgMetAspThrProSerGlyVallyAspSerIleSerAlaTyrIleLysPheSer 221
DB 795 ATACGTATGACATCTCATCAGATGTTAAGATTCATTCCTGCTGGATCACTACTCT 854
QY 222 ValGlnAlaProGlyGluIleProPheAsnGlyIleTyrTyrAspProProGluGlu 241
DB 855 A--CAGCTTCTGATGAATTCATTAATGAAATATATATGATCCACCCGAGAGAG 912
QY 242 LysTyrValPheGlnHisProGlnProlyArgProGlnSerLeuArgIleTyrGluSer 261
DB 913 AGGTATATCTTCCACACCCAGCCCAAGAAACCAAGTGTGAGAAATATGATCT 972
QY 262 HisIleGlyMetSerSerProGluProlyIleAsnSerTyrAlaAsnPheArgAspGlu 281
DB 973 CATATTTGATAGATGATGCTCGAGCTTAATTAATTAATCACTACGTGATTTAGATGAA 1032
QY 282 ValLeuProArgIleLysArgleuGlyTyrAsnAlaValGlnIleMetAlaIleGlnGlu 301
DB 1033 GTTCTTCTCGCATATAAAAAAGCTTGGTCAATGAGCTGCATAATTAATGCTATCAAGAG 1092
QY 302 HisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPheAlaProSerSerArg 321
DB 1093 CATCTTATTATGCTAGTGGTTTGTATCATGTCACAAATTTTGTGACCAAGACCGT 1152
QY 322 PheGlyThrProGluAspLeuLysSerLeuIleAspArgAlaHisGluLeuGlyLeuLeu 341
DB 1153 TTGGAAACCGCCAGACACCTTAAGTCTTATGATTAAGTCACTAGCTGAGATGTT 1212
QY 342 ValLeuMetAspIleValHisSerHisSerSerAsnAsnThrLeuAspGlyLeuAsnGly 361
DB 1213 GTTCTCATGACATGTTGTCAACCCATGACATCAAAATATCTTTAGATGACTGAACATG 1272
QY 362 PheAspGlyThrAspThrHisTyrPheHisGlyGlyProArgGlyHisIleTyrMetTyr 381
DB 1273 TTGGAGGACCCATGATGTTGTTACTTCACTCTGAGCTGTGGTTATCATTTGATGAG 1332
QY 382 AspSerArgLeuPheAsnTyrGlySerTyrGluValLeuArgPheLeuSerAsnAla 401
DB 1333 GATTTCCGCTTTTAACTATGAGAACTGGAGGATCTAGATTCCTCTCAAAATCG 1392
QY 402 ArgTyrTyrleuGluGluTyrLysPheAspGlyPheArgPheAspGlyValThrSerMet 421
DB 1393 AGATGGGTGGTGTGATGATCAATTTGATGATTTGATGATGATGATGATGATGATG 1452
QY 422 MetTyrThrHisHisGlyLeuGlnMetThrPheThrGlyAsnTyrGlyTyrPheGly 441
DB 1453 ATGTATACACACAGGATTTATCGGGGATTCCTGGAACTACGAGAAATACCTTTGA 1512
QY 442 PheAlaThrAspValaAspAlaValaTyrleuMetLeuValaAsnAspLeuIleHisGly 461
DB 1513 CTGCAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1572
QY 462 LeuHisProAspAlaValSerIleGlyGluAspValSerGlyMetProThrPheCysIle 481
DB 1573 CTTTTCCAGATGATGATTAATCATTTGATGATGATGATGATGATGATGATGATG 1632
QY 482 ProValProAspGlyGlyValGlyPheAspTyrArgleuHisMetAlaValaAspLys 501
DB 1633 CCGGTCAAGTGGGGGTGGCTTTTACATTCGCTGATATGCAATTCGATGATAA 1692
QY 502 TyrIleGluLeuLeuLysSerAspGluSerTyrLysMetGlyAspIleValHisThr 521

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Db      1693  IGGATTGAGTTGCTCCAGAAACCGGATGACGATTGCAAGAGGGGATGATTGTTATCA 1752
QY      522   LeuThrAsnaGArGTpDLeuGluLysCysValThrTYraAlaGluSerHisAspGlnAla 541
Db      1753  CTGCAAAATGAGAAATGGTCCGGAAAAAGTGTGTTTCAATCCGCTGAAGATCATGATCAACT 1812
QY      542   LeuValAlaGlyAspLysThrIleAlaPheThrLeuMetAspLysAspMetTyrAspPheMet 561
Db      1813  CTAACTCGGTGTAATAAATCAATAGCAATTCGGCTGATGGAACAAGATATGATGATTTATG 1872
QY      562   AlaLeuAspArgProSerThrProArgIleAspArgGlyIleAlaLeuHisLysValIle 581
Db      1873  GCTTGTGATGACCGCCCAACATCATTAATAGATCCTGGGATGACATTCGACAAAGATGATT 1932
QY      582   ArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGlyAsnGluPhe 601
Db      1933  AGCGTTGTAATTAATGAGATTAGAGAGAAAGGGTACCTAAATTTTCATGGGAAATGAAATTC 1992
QY      602   GlyHisProGluTyrPLeuAspPheProArgGlyProGlnThrLeuProThrGlyLysVal 621
Db      1993  GGGCAACCCCTGGTGGATGATTGTTCCCTGAAGGCTGAACAACCTCTCGATGACTCAAGA 2052
QY      622   LeuProGluAsnAsnAsnSerTyrAspLysCysArgArgArgPheAspLeuGlyAspAla 641
Db      2053  ATTCGCCGAAACCAATTGATGATTATGATTAATATGACACCGAATTTGACTCGGAGATGCA 2112
QY      642   AspPheLeuArgTyrHisGlyMetGlnGluPheAspGlnAlaMetGlnHisLeuGluGlu 661
Db      2113  GAATATTTAAGATACCGTGGGTGCAAGAAATTTGACCGGGCTATGACAGATCTTGAAAGAT 2172
QY      662   LysTyrGlyPheMetThrSerGlnHisGlnTyrValSerArgLysHisGluLysLys 681
Db      2173  AAAATATGAGTTTATGACTTCGAACACACAGTTCATATACGAAAGATGAAAGATATAGG 2232
QY      682   ValIleIlePheGluArgGlyAspLeuValPheValPheAsnPheHisTyrSerAsnSer 701
Db      2233  ATGATGTTGATTTGAAAAAGAAACCTAGTTTGTCTTAAATTTTCACTGACAAAAAAGC 2292
QY      702   PhePheAspTyrArgValGlyCysSerArgProGlyLysTyrLysValAlaLeuAspSer 721
Db      2293  TATTCAGACTATCGATGATGGCTGCCTGAAGCCTGAAATAACAAAGTTGCCCTTGACCTCA 2352
QY      722   AspAspAlaLeuPheGlyGlyPheSerArgLeuAspHisAspValAspTyrThrThrThr 741
Db      2353  GATGATCCACTTTTGTGGTGGCTTCGGGAGAAATTGATCATTAATGACCGAATATTTCACCTT 2412
QY      742   GluHisProHisAspAsnArgProArgSerPheSerValIleTyrThrProSerArgHisAla 761
Db      2413  GAAAGAGATGATGATGATGCTCTCTGTCATTAATGATGATGACCTTTGTAAGAACAGCA 2472
QY      762   ValValIleTyrAlaLeuThrGlu 768
Db      2473  GTGGTCTATGCACTAGTAGAC 2493

RESULT 14
US-10-056-454A-18
; Sequence 18, Application US/10056454A
; Publication No. US20030166919A1
;
GENERAL INFORMATION:
APPLICANT: National Starch and Chemical Investment Holding Corporation
TITLE OF INVENTION: Improvements in or Relating to Plant Starch Composition
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESS: National Starch and Chemical Investment Holding Corporation
STREET: 1000 Unigema Blvd.
CITY: Newcasttle
STATE: Delaware
COUNTRY: United States of America
ZIP: 19720
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

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[illegible]

Query Match:	75.668	Indels:	16
DB:	9	Gaps:	3
US-09-508-377-12 (1-768) x US-09-938-842A-337 (1-2577)			

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Db      2377 AACCTTTATTGGAGGCTTCAACGGCTAGATGACTCCGGGGAGTTTTCACCTTGAT 2436
Oy      743  HlSPROHlSAsPaSnARgProARgSerPheSerValTYrThrProSerARgThrAlaVal 762
Db      2437 GGAAGGCACGACGATAGGCTTGCTCTCATGTGTATGACCGTGACGAGAACCGCTGTA 2496
Oy      763  ValTYrAlaLeuThrGlu 768
Db      2497 GTTACGCTGCACTAGAT 2514
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Search completed: April 18, 2004, 00:00:18
Job time : 665 secs

1	4031.5	96.7	2853	4	US-09-609-450-3	Sequence 9, Appl
2	3588.5	86.1	2446	4	US-09-731-166-9	Sequence 9, Appl
3	3351	80.4	2720	4	US-09-731-166-1	Sequence 11, Appl
4	3342	80.2	2725	3	US-08-941-445A-14	Sequence 14, Appl
5	3341	80.1	2665	4	US-09-257-894-1	Sequence 1, Appl
6	3189	76.5	3074	3	US-09-087-277-1	Sequence 1, Appl
7	3189	76.5	3074	3	US-09-658-499-1	Sequence 1, Appl
8	2924	70.1	2087	4	US-03-257-884-9	Sequence 9, Appl
9	2917	70.0	2165	4	US-09-257-894-8	Sequence 8, Appl
10	2227	53.4	1393	3	US-09-087-277-3	Sequence 3, Appl
11	2227	53.4	1393	4	US-09-658-499-3	Sequence 3, Appl
12	51.6	3198	2	US-08-716-448-1	Sequence 1, Appl	

1 MetAlaThr-pheAlaValSerGlyAlaThrLeuGlyValAlaArgPro----- 16

QY 689 PleuValPheValPheAspPheHisTrpSerAsnSerPhePheAspTyrArgValGlyCys 709
DB 2262 TTGGTATTTGTTTTCACCTCCAGCAGCAATAGCTTTTTCATACCGTGTGGGTG 2321
QY 709 SSerArgProGlyValTyrValValAlaLeuAspSerAspAlaLeuPheGlyGlyPhe 729
DB 2322 TTCACAGCTGGAGAGTACAGAGTGGCTTGGACTCCGACAGATGCACCTTTGGTGATT 2381
QY 729 eSerArgLeuAspHisAspValAspTyrPheThrThrGluHisProHisAspAsnArgPhe 749
DB 2382 CAGCAGGCTGTGATCAAGATGCTCAGTACCTTCAACACGCAATCCGATGCAACACAGCC 2441
QY 749 oArgSerPheSerValTyrThrProSerArgThrAlaValTyrAlaLeuThrGlu 768
DB 2442 GCGCTCTTCTCGGTGTACCTCCGACGAGCAACTGCGGTGTGTATGCCCTTACAGAG 2499

RESULT 2
US-09-731-166-9
; Sequence 9, Application US/09731166
; Patent No. 6639126
; GENERAL INFORMATION:
; APPLICANT: Sewalt, Vincent J. H.
; APPLICANT: Singletary, George W.
; TITLE OF INVENTION: Production of Modified Polysaccharides
; FILE REFERENCE: 35718/206348
; CURRENT APPLICATION NUMBER: US/09/731,166
; CURRENT FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: 60/1169,993
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2446
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURES:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: SBE11a
; OTHER INFORMATION: Genbank Accession No. 6639126 U65948
; NAME/KEY: CDS
; LOCATION: (2)...(2446)
US-09-731-166-9

Alignment Scores:
Pred. No.: 0 Length: 2446
Score: 3588.50 Matches: 662
Percent Similarity: 88.75% Conservative: 32
Best Local Similarity: 84.65% Mismatches: 49
Query Match: 86.08% Indels: 39
Gaps: 4

US-09-508-377-12 (1-768) x US-09-731-166-9 (1-2446)

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DB 377 CCAGAGATGGCGCAACGAATATATGAGATTGACCCCAATTTGGAAAGGTTTGGGGGTGAC 436
QY 104 LeuAspTyrArgTyrSerGlyTyrArgArgIleArgAlaAlaIleAspGluHisGlyGly 123
DB 437 CTGGACTACCAATACAGTAATATATAGATTATACGCGCGCTATTCATCACTGAAAGGT 496
QY 124 GlyLeuGluAlaPheSerArgGlyTyrGluLysLeuGlyPheThrArgSerAlaGluGly 143
DB 497 GGTGTGATGCTTTTTCACGCGGTTCAGAAAGGCTTGAATTTTCTGCGACGCGTGAAGGT 556
QY 144 IleThrTyrArgGluTyrAlaPheProGlyAlaHisSerAlaAlaLeuValGlyAspPheAsn 163
DB 557 ATCACTTACAGAGATGGGCTCTGAGCATATCTGACGACATTATAGGTGACTTCAAC 616
QY 164 AsnTrpAsnProAsnAlaAspThrMetThrArgAspAspTyrGlyValTrpGluIlePhe 183
DB 617 AACTGAAACCAAAATGCTGATGCTATGGCCAGAAATGATGATCGCGCTTGGAGATTTC 676
QY 184 LeuProAsnAsnAlaAspGlySerProAlaIleProHisGlySerArgValLysIleArg 203
DB 677 CTGCTTAACAATGCTGATGATTCCTCTGATTCCTCATGCTCAGCTGTAAGATACG 736
QY 204 MetAspThrProSerGlyValLysAspSerIleSerAlaTrpIleLysPheSerValGln 223
DB 737 ATGACACACATCTGCTGCTTATAGATTCATCTCGCTCGATGATCAAGTTTCTGTGACG 796
QY 224 AlaProGlyGluIleProPheAsnGlyIleTyrTyrAspProProGluGluGlyTyr 243
DB 797 GCTCCAGGTGAATATCCATACCAACGATATATATATGACCCACTTAAGAGGAAATAT 856
QY 244 ValPheGluHisProGlnProLysArgProGluSerLeuArgIleTyrGluSerHisIle 263
DB 857 GTATTCAACACCTTCAACCTTAAGCGCCCAAGTCACTCGGATATATGATATCATGTT 916
QY 264 GlyMetSerSerProGluProLysIleAsnSerTyrAlaAsnPheArgAspGluValLeu 283
DB 917 GGAATGATTAAGCCCGGACCAAAATATATACATATGTAATCTGACAGATGAGGTCTT 976
QY 284 ProArgIleLysArgLeuGlyTyrAsnAlaValGlnIleMetAlaIleGlnGluHisSer 303
DB 977 CCAGAAATTAATAAAGCTTGGATGATACATGCAATGCAATATGCAATCCGAAACACTCT 1036
QY 304 TyrTyrAlaSerPheGlyTyrHisValThrAsnPheAlaProSerSerArgPheGly 323
DB 1037 TATTATGCAAGCTTGGGTACATGTTACGAATTTTTCGCCCAAGTACCGCTTTGGG 1096
QY 324 ThrProGluAspLeuLysSerLeuIleAspArgAlaHisGlyLeuGlyLeuValLeu 343
DB 1097 ACTCCAGAGGACCTAAATCTCTTATGATAAAGCCATGAGCTTGCTGTAGTCTT 1156
QY 344 MetAspIleValHisSerHisSerSerAsnAsnThrLeuAspGlyLeuAsnGlyPheAsp 363
DB 1157 ATGATATATGTTCAATAGCTATTCATCAATTAATATACCTTGATGGTGTGAATGGTTGAT 1216
QY 364 GlyThrAspThrHisTyrPheHisGlyValProArgGlyHisIleTrpMetTrpAspSer 383
DB 1217 GGCACCGATACATTACTTCAATGATGATCCAGAGCCATATATGATGATGATCTT 1276
QY 384 ArgLeuPheAsnTyrGlySerTrpGluValLeuArgPheLeuLeuSerAsnAlaArgTyr 403
DB 1277 CGCTATTCATTAATGAGGAGTGGGAAATTTGAGATTCTATTTGCAATATGCGAGATGG 1336
QY 404 TrpLeuGluGluTyrLysPheAspGlyPheArgPheAspGlyValHisSerMetMetTyr 423
DB 1337 TGGCTTGAAAGATTAATAATTTATGATGGTTGATTTGATGGGTGACCTTCATGATATAT 1396
QY 424 ThrHisHisGlyLeuGlnMetThrPheThrGlyAsnTyrGlyValLysTyrPheGlyPheAla 443
DB 1397 ACTCAACATGATTTCAAGTACATTTCACTGGGAATATATGCGAATATTTTGGATTGGCC 1456

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Db      2357  CCGCATGACACAGCCCGTGTCTTCTGCTATGACCCAGGACGAAACACCCGCTGCA 24
Oy      764   TTTAATA 765
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Db      2417  TATGCA 2422

RESULT 3
US-09-731-166-11
; Sequence 11, Application US/09731166
; Patent No. 6639126

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Db 590 GAGAAATTGCTTAATTCGACCGCGAAGATTCACACATTCGAGATGGGCTCTCGGA 64
QY 153 AIAHLSSEAIALALEVALGIVAAPPHLEASASTTTPASNPQVQANALAASTThmet 17
Db 650 GCAATTTCTCGACGACATGCTGGGTGACTTCAACAATCGGATTCCAATGCGATCGATG 70
QY 173 ThTAgBAspAspTgLYVAlTppGLIePhLeuPrbAmenALAApGLISeFPro 19
Db 710 ACCAATAAAGAGATTGGTGTGGGAATTTTCTGCTCAACATGCGATGTCACATCA 76

Tue Apr 20 10:02:29 2004

us-09-508-377-12.rn1

Page 5

QY 193 AlaIleProHieGlySerArgValIlysiIleArgMetAspThrProSerGlyValIyAsp 212
Db CCTATTCTCCAGAGACTCGTGTAAAGGTGAAGATGATCTCATAGGGATAAAGAT 829
QY 213 SerIleSerAlaIleIlePheSerValGlnAlaProGlyGluIleProPheAsnGly 232
Db TCATATCCAGCCTGGATCAAGTACTCAGTCGACGCCCGAGAGAAATACCATGTGATGGG 889
QY 233 IleTyrTyrAspProGluGluGluIlyTyrValPheGlnIleProGluIleProIyAsp 252
Db ATTTATTATGATCTCTCGTGAAGAGTAAAGTATGTTCAGCATGGCAACCTTAAACGA 949
QY 253 ProGluSerIleuArgIleTyrGluSerHisIleGlyMetSerSerProGluProIySile 272
Db CCAAAATCATTCGGATATATGAAACACATGTGGAATGATGCCCGGAAACGAGATA 1009
QY 273 AsnSerTyrAlaAspPheArgAspGluValIleuProArgIleuYsArgIleuGlyTyrAsn 292
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QY 353 AsnAsnThrIleuAspGlyLeuAsnGlyPheAspGlyThrAspThrHisTyrPheHisGly 372
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QY 373 GlyProArgGlyHisIleStrMetIleProSerArgPheAsnTyrGlySerIleGlu 392
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QY 393 ValIleuArgPheIleuSerAsnAlaArgIleTyrIleuGluGluIlyTyrYsPheAspGly 412
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QY 413 PheArgPheAspGlyValIleuSerMetMetTyrThrHisGlyLeuGluMetThrPhe 432
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QY 433 ThrGlyAsnTyrGlyGlyIlyTyrPheGlyPheAlaIleuAspValAlaValIleu 452
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QY 513 TyrIleuMetGlyAspIleValHisThrIleuThrAsnArgArgIleuGluIlyCysVal 532
Db TGAAGATGGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1789
QY 533 ThrTyrAlaGluSerHisAspGlnAlaLeuValGlyAspIlyThrIleAlaIleThrIleu 552
Db ACTATGCTGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1849

QY 553 MetAspIlyAspMetTyrAspPheMetAlaLeuAspArgProSerThrProArgIleAsp 572
Db ATGACAAAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1909
QY 573 ArgGlyIleAlaLeuHisIleuMetIleArgIleuValIleuMetGlyLeuGlyGluGly 592
Db CGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1969
QY 593 TyrIleuSerPheMetGlyAsnGluPheGlyHisProGluIleAspPheProArgIly 612
Db TATCTTAATTTCAATGGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2029
QY 613 ProGluThrIleuProThrGlyIlyValIleuProGlyAsnAsnAsnSerTyrAspIly 632
Db CCGCAAGACTTCCAAAGTGTATGATTTCCAGGGAATTAACAAAGTATGACAAATGT 2089
QY 633 ArgArgArgPheAspLeuGlyAspAlaAspPheLeuArgTyrHisGlyMetGlnIlePhe 652
Db CGTGAAGATTTGACCTGGTGTATGATGATGATGATGATGATGATGATGATGATGATGAT 2149
QY 653 AspGlnAlaMetGlnHisIleuGluGluIlyTyrGlyPheMetThrSerGluHisGlnTyr 672
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QY 693 ValPheAsnPheHisIleProSerAsnSerPheAspTyrArgValGlyCysSerArgPro 712
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QY 713 GlyIlyTyrIlyValAlaLeuAspSerAspAlaLeuPheGlyGlyPheSerArgIleu 732
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QY 733 AspHisAspValAspTyrPheThrThrGluHisProHisAspAsnArgProAspSerPhe 752
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QY 753 SerValIlyThrProSerArgThrAlaValIlyTyrAlaLeuThrGlu 768
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RESULT 4
US-08-941-445A-14
Sequence 14, Application US/08941445A
Patent No. 6107060
GENERAL INFORMATION:
APPLICANT: Keeling, Peter
APPLICANT: Guan, Hanning
TITLE OF INVENTION: Starch Encapsulation
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS: Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle
CITY: Boulder
STATE: CO
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/941,445A
FILING DATE: 30-SEP-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,855
FILING DATE: 30-SEP-1996
INVENTOR:

```

? NAME: Wimmer, Ellen P
? REGISTRATION NUMBER: 28, 547
? REFERENCE/DOCKET NUMBER: 89-97
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (303) 499-8080
? TELEFAX: (303) 499-8089
? INFORMATION FOR SEQ ID NO: 14:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 2725 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: not relevant
? MOLECULE TYPE: mRNA
? HYPOTHEetical: NO
? ORIGINAL SOURCE:
? ORGANISM: Zea mays
? FEATURE:
? NAME/KEY: sig_peptide
? LOCATION: 91..264
? FEATURE:
? NAME/KEY: mat_peptide
? LOCATION: 265..2487
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 91..2490
?
? OS-08-941-445A-14

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Db 1780 ATTATGCTGAAGATGATGATCAAGCATTTGCGGCAAGACTATGCGTTTGTTG 1839
Qy 553 MetAspLysAspMetTyrAspPheMetAlaLeuAspArgProSerThrProArgIleAsp 572
Db 1840 ATGGACAAGATATGATGATTTTCATGCGCCCTCGATGAGACTTCACCTCCACGATTGAT 1839
Qy 573 ArgGlyTleAlaLeuHisLysMetCileArgLeuValThreGlyLeuGlyGlyGly 592
Db 1900 CCGGATGATGCAATTACATGAAGATGATGATGATGATGATGATGATGATGATGATGAT 1959
Qy 593 TyrLeuAsnPheMetGlyAsnGluPheGlyHisProGluTrpIleAspPheProArgGly 612
Db 1960 TATCTTAATTTTCATGCGAATGATGATGATGATGATGATGATGATGATGATGATGAT 2019
Qy 613 ProGlnThrLeuProThrGlyLysValLeuProGlyAsnAsnAsnSerTyrAspLysCys 632
Db 2020 CCGCAAGACTTCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2079
Qy 633 ArgArgArgPheAspLeuGlyAspAlaAspPheLeuArgTyrHisGlyMetGlnLysPhe 652
Db 2080 CGTCGAAGATTTGACCTGGGTGATGACAGACTATCTTGGTATCATGCTATGCAAGAGTTT 2139
Qy 653 AspGlnAlaMetGlnHisLeuGluGluLysTyrGlyPheMetThrSerGluHisGlnTyr 672
Db 2140 GATCAGGCAATGCAACATCTTGAGCAAAATATGAAATTCATGACATCTGATCACCAGTAT 2139
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Qy 693 ValPheAsnPheHisTyrSerAsnSerPhePheAspTyrArgValGlyCysSerArgPro 712
Db 2260 GTGTTCAACTTCCACGCAACAGCTATTTTGACTACCGTATGCTTGGTTCGCAAAACCT 2319
Qy 713 GlyLysTyrLysValAlaLeuAspSerAspAspAlaLeuPheGlyGlyPheSerArgLeu 732
Db 2320 GGGGATTAATAGGTGCTTGAGACTCCGACGCTGAGACTATTTGGTGAATTTAGAGGATC 2319
Qy 733 AspHisAspValAspTyrPheThrThrGluHisProHisAspAsnArgProArgSerPhe 752
Db 2380 CATCAGCAGCGAGAGACTTCAACGCCGACTGTTCCGATGATATATAGCCATATTCATTC 2439
Qy 753 SerValTyrThrProSerArgThrAlaValValTyrAlaLeuThrGlu 768
Db 2440 TCGGTTTATACACCAAGACAGATGTCGTCTATGCTCCAGTGGAG 2487

RESULT 5
US-09-257-894-1
Sequence 1, Application US/09257894
Patent No. 6376749
GENERAL INFORMATION:
APPLICANT: Broglie, Karen E.
APPLICANT: Klein, Theodore M.
APPLICANT: Hubbard, Natalie L.
APPLICANT: Lightner, Jonathan B.
TITLE OF INVENTION: No. 6376749el Starches via Modification of
TITLE OF INVENTION: Expression of Starch Biosynthesis
TITLE OF INVENTION: Enzyme Genes
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. du Pont de Nemours and Company
STREET: 1007 Market Street
CITY: Wilmington
STATE: Delaware
COUNTRY: USA
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows 95
SOFTWARE: Version 7.0a

APPLICATION NUMBER: US/09/257,894
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/091,052
FILING DATE: JUNE 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Majarian, William R.
REGISTRATION NUMBER: 41,173
REFERENCE/DOCKET NUMBER: BB-1066-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4926
TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2665 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 79..2476
US-09-257-894-1
Alignment Scores:
Pred. No.: 0 Length: 2665
Score: 3341.00 Matches: 608
Percent Similarity: 86.98% Conservative: 67
Best Local Similarity: 78.35% Mismatches: 79
Query Match: 80.14% Indels: 22
Gaps: 4
US-09-508-377-12 (1-768) x US-09-257-894-1 (1-2665)
Qy 4 PheAlaValSerGlyAlaThrLeuGlyVal-----AlaArgProProAla 18
Db 181 TTCTTAATCGGGGCTGCTCGAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 240
Qy 19 AlaAlaGlnProGluGlnLeuGlnIleProGluAspIleGluGlnThrAlaGluVal 38
Db 241 GCCGGCGCAGAGAGCGCGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 265
Qy 39 AsnMetThrGlyGlyThrAlaGluLysLeuGluSerSerGlu-----52
Db 286 -----GGCTCCGACCAAGGCTGACTCGGCTCAATTCCAGTCGATGACTG 333
Qy 53 ProThrGlnGlyIleValGluThrIleThrAspGlyValThrLysGlyValLysGluLeu 72
Db 334 GAGGTACAGACATTTCTGAGAGAGACACACGCTGCTGCT-----GCTGCTGCTGCT 387
Qy 73 ValValGlyGluLysProArgValValProLysProGlyAspGlyGluLysIleTyrGlu 92
Db 388 CAAAGCTTGAACAGAGTTCGAGTGTCCGCCCAACAGAGATGAGCAAAAATATTCAG 447
Qy 93 IleAspProThrLeuLysAspPheArgSerHisLeuAspTyrArgTyrArgGlyTyrArg 112
Db 448 ATTTGACCCCATGTTGCAAGGCTATAGTACCACTTGTGATGATGATGATGATGATGATGAT 507
Qy 113 ArgIleArgAlaAlaIleAspGlnHisGluGlyGlyLeuGluAlaPheSerArgGlyTyr 132
Db 508 AGAATCCCTTCAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 567
Qy 133 GluLysLeuGlyPheThrArgSerAlaGluGlyIleThrTyrArgGluTrpAlaProGly 152
Db 568 GAGAAGTTTGATTTAATGCCAGCGCGAAGGATACACATATGAGAAATGGGCTCCTCGA 627
Qy 153 AlaHisSerAlaAlaLeuValGlyAspPheAsnAsnTrpAsnProAsnAlaAspIleMet 172
Db 628 GCATTTTCTGAGCATTTGTGGTGTGATCTTCAACATGGGATCCAAATGCAATGCTGATG 687
Qy 173 ThrArgAspAspTyrGlyValTrpGluIlePheLeuProAsnAsnAlaAspIleSerPro 192

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Db      688 AGCAAAATAGATTGTTGGTTTGGGAAATTTTCTGCTTAAACAATGCAGATGCATCA 747
QY      193 AAlleProh1esglSerArGVallys1learyKerAspThrProserGlyValIysAsp 212
Db      748 CCAATTCCTCATGCATGATCTCGTTAAAGTGAAGATGATGATCTCATCGAGATAAAGAT 807
QY      213 Ser11SerAlaTrp11elysPheSerValGlnAlaProGlyGlu11leProPheAsnGly 232
Db      808 TCATTCACACCTCGATCAAGTACTCATGTCAGGCCCGCAGAGAAATCCATATGATGGG 867
QY      233 11eTyTrAspProProGluGluGlu11sTyValPheGln11sProGluPro11sArg 252
Db      868 ATTATATATATATCTCTGAAAGAGCTTAAAGTATGTTCTTCAAGCATGGCAACCTTAAAGA 927
QY      253 ProGluSerLeuArg11eTyGluSerHis11eGlyMetSerSerProGluPro11sArg 272
Db      928 CCAAAATCATTCGGCATATATGAAACATGTCGGAATGAGTAGCCCGAACCAGAAAGATA 987
QY      273 AsnSerTyAlaAsnPheArgAspGluValLeuProArg11elysArgLeuGlyTyTrsn 292
Db      988 AACACATATGTAATCTTAGGGATGAAGTCTCCCAAGATTAATAAACTTGATATCAAT 1047
QY      293 AlaValGln11leMetAla11eGlnGluHisSerTyTyTrAlaSerPheGlyTyTrHisVal 312
Db      1048 GCAGTGCATAATATGCGATCCAAAGACATCATATTTATGAAAGCTTTGGATACATGTA 1107
QY      313 ThrAsnPhePheAlaProSerSerArgPheGlyThrProGluAspLeu11sSerLeu11e 332
Db      1108 ACTATATTTTGGGCCAAGTAGTGTGTTGGTACCCAGAAAGATTGAAGCTTGTGAT 1167
QY      333 AspArgAlaHisGluLeuGlyLeuLeuValLeuMetAsp11eValHisSerHisSerSer 352
Db      1168 GATAGACACATGAGCTTGTGCTTGTCTCATGATGATGTTGTTGTTGTTGTTGTTGTTGTTA 1227
QY      353 AsnAsnThrLeuAspGlyLeuAsnGlyPheAspGlyTrpAspThrHis11sTyPheHisGly 372
Db      1228 AGTAATCTCTGAGGGGTGATGATGTTTGTATGATGATGATGATGATGATGATGATGATGAT 1287
QY      373 GlyProArgGlyHis11sTyPheTrpAspSerArgLeuPheAsnTyTrGlySerTrpGlu 392
Db      1288 GGTCCACCTGGCCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1347
QY      393 ValLeuArgPheLeuLeuSerAsnAlaArgTrpTrpLeuGluGluTyTrsPheAspGly 412
Db      1348 GTTTTAAATTTCTCTCTCCAAATGCTAGATGTTGCTCGAGAAATATAGTTTGAATGGT 1407
QY      413 PheArgPheAspGlyValThrSerMetTyTrHis11sGlyLeuGlnMetThrPhe 432
Db      1408 TTCCGTTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1467
QY      433 ThrGlyAsnTyGlyGluTyTrPheGlyPheAlaThrAspValAspAlaValAlaTyTrLeu 452
Db      1468 ACGGGGAACCTTCAATGATATTTTGGCTTGGCACCGAGTATGATGATGATGATGATGATGATGAT 1527
QY      453 MetLeuValAsnAspLeu11eHisGlyLeuHis11sProAspAlaValSer11eGlyGluAsp 472
Db      1528 ATGCTGTAAATGATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1587
QY      473 ValSerGlyMetProThrPheCys11eProValProAspGlyGlyValGlyPheAspTyTr 492
Db      1588 GTTAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1647
QY      493 ArgLeuHisMetAlaValAlaAspTyTrTrp11eGluLeuLeu11sGlnSerAspGluSer 512
Db      1648 CGGATGCAATAGCTGTGGCTGTCGAATGATGATGATGATGATGATGATGATGATGATGATGAT 1707
QY      513 TrpTyMetGlyAsp11eValHis11sThrLeuThrAsnArgTrpTrpLeuGluTyTrVal 532
Db      1708 TCGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1767
QY      533 ThrTyAlaGluSerHisAspGlnAlaLeuValGlyAspTyTrThr11eAlaPheTrpLeu 552

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QY      553 MetAspTyTrAspPheMetAlaLeuAspArgProserThrProArg11eAsp 572
Db      1828 ATGACCAAGGATATATGATTTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1887
QY      573 ArgGly11eAlaLeuHis11sMet11eArgLeuValThrMetGlyLeuGlyGlyGly 592
Db      1888 CCGGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1947
QY      593 TyTrLeuAsnPheMetGlyAsnGluPheGlyHis11sProGluTrp11eAspPheProArgGly 612
Db      1948 TATCTTAAATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2007
QY      613 ProGlnThrLeuProThrGlyTyValLeuProGlyAsnAsnAsnSerTyTrAspTyCys 632
Db      2008 CCGCAAAAGCTTCCAAATGTTTATTTTCCAGGAAATACAAAGTTATGCAAAATGT 2067
QY      633 ArgArgArgPheAspLeuGlyAspAlaAspPheLeuArgTyTrHisGlyMetGlnGluPhe 652
Db      2068 CCGTCAAGATTTGACCTGGGTGATGACACTATCTTAGATCATCGTATGCAAGAGTTT 2127
QY      653 AspGlnAlaMetGlnHisLeuGluGluTyTyGlyPheMetThrSerGluHisGlnTyTr 672
Db      2128 GATCAGGCAATGCAACATCTTGAGCAAAATATGAAATCATGATGATGATGATGATGATGATGAT 2187
QY      673 ValSerArgTyHisGluGluAspTyVal11e11ePheGluArgGlyAspLeuValPhe 692
Db      2188 ATTTCCCGAAGATATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2247
QY      693 ValPheAsnPheHis11sTrpSerAsnSerPhePheAspTyTrArgValGlyCysSerArgPro 712
Db      2248 GTTTCACCTTCCATCGCAACAACAGCTATTTGATGATGATGATGATGATGATGATGATGATGAT 2307
QY      713 GlyTySerTyTrTyValAlaLeuAspSerAspAspAlaLeuPheGlyGlyPheSerArgLeu 732
Db      2308 GGGGTATATGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2367
QY      733 AspHisAspValAspTyTrPheThrThrGluHis11sProHisAspAsnArgProArgSerPhe 752
Db      2368 CATCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2427
QY      753 SerValTyTrProSerArgThrAlaValAlaTyTrAlaLeuThrGlu 768
Db      2428 TCGGTTATATACCAAGCAAGACATGTGTGTATGCTCTCATGCTCATGAG 2475

RESULT 6
US-09-087-277-1
/ Sequence 1, Application US/09087277B
/ Patent No. 6169226
/ GENERAL INFORMATION:
/ APPLICANT: EK, BO
/ APPLICANT: KHOSNODI, Jamshid
/ APPLICANT: LARSSON, Claes-Tomas
/ APPLICANT: LARSSON, Hakan
/ APPLICANT: RASK, Lars
/ TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
/ FILE REFERENCE: 003300-486
/ CURRENT APPLICATION NUMBER: US/09/087, 277B
/ CURRENT FILING DATE: 1998-05-29
/ EARLIER APPLICATION NUMBER: PCT/SE96/01558
/ EARLIER FILING DATE: 1996-11-28
/ EARLIER APPLICATION NUMBER: SE 9504272-7
/ EARLIER FILING DATE: 1995-11-29
/ EARLIER APPLICATION NUMBER: SE 9601506-0
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 1
/ LENGTH: 3074
/ TYPE: DNA
/ ORGANISM: Unknown
/ FEATURE:
/ OTHER INFORMATION: Description of Unknown Organism: bett gene

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OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
 OTHER INFORMATION: (potato)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (189) ..(2825)
 FEATURE:
 NAME/KEY: sig_peptide
 LOCATION: (189) ..(332)
 FEATURE:
 NAME/KEY: mat_peptide
 LOCATION: (333) ..(2825)
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (92) ..(2156)
 OTHER INFORMATION: Nucleotides 92, 285, 1406, 1430, 1897 and 2156 are
 OTHER INFORMATION: n wherein n = A, C, G or T.
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (285) ..(287)
 OTHER INFORMATION: Amino acid -16 is Xaa wherein Xaa = Ile, Leu, Val
 OTHER INFORMATION: or Phe.
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1405) ..(1406)
 OTHER INFORMATION: Amino acid 358 is Xaa wherein Xaa = Leu or Phe.
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1428) ..(1430)
 OTHER INFORMATION: Amino acid 366 is Xaa wherein Xaa = Thr.
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1896) ..(1898)
 OTHER INFORMATION: Amino acid 522 is Xaa wherein Xaa = Tyr, Ser, Cys
 OTHER INFORMATION: or Phe.
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (2154) ..(2156)
 OTHER INFORMATION: Amino acid 608 is Xaa wherein Xaa = Pro.
 US-09-087-277-1
 Alignment Scores:
 Pred. No.: 0 Length: 3074
 Score: 3189.00 Matches: 585
 Percent Similarity: 82.78% Conservative: 83
 Best Local Similarity: 72.49% Mismatches: 91
 Query Match: 76.49% Indels: 48
 DB: 3 Gaps: 6
 US-09-508-377-12 (1-768) x US-09-087-277-1 (1-3074)
 QY 2 AlaThrPheAlaValSerGlyAlaThrLeu-----GlyValAlaArgProProAlaAla 19
 DB 366 TCTACAGTTGCGACGATCGGGGAAAGTCCTTGCTGCGGAAACCCAGAGTAGATGCTCTCA 425
 QY 20 AlaGlnProGluGluLeuGlnIleProGlu----- 29
 DB 426 TCCTCAACAGCCAAATTGATGATCACTGAGACATCTCCAGAAAATTCGCCAGCATCACT 485
 QY 30 AsPIleGluGluGlnThrAlaGlu----- 37
 DB 486 GATGTRGATGATTCACAAATGACACGCTAGGCAGATTAAACTGGAACGATGAGCTT 545
 QY 38 -----ValAsnMetThrGlyGlyThrAlaGlu----- 46
 DB 546 GAGCCGTCAAGATCTTACAGAGAAAGTGTGAAGAGCTGATTGCTTCATCACTACAA 605
 QY 47 -----LysLeuGluSerSerGluProThrGlnGlyIleValGluThrIle 61
 DB 606 CTACAGAAAGGTGCTAACTGAGAGAGTCTAAACATTAATATCTTGTGAAGAGCAATT 665
 QY 62 ThrAspGlyValThrLysGlyValLysGluLeuValValGlyGluLysProArgValVal 81
 DB 666 ATTGATGATCTGATGATGAG-----ATCAGAGAG-----AGGGGATC 701

QY 82 ProLysProGlyAspGlyGlnLysIleTyrGluIleAspProThrLeuLysAspPheArg 101
 DB CCTCCACCTGGACCTTGTCAGAAAGATTATGAAATGAGACCCCTTTGCAACATCTGCT 761
 QY 102 SerHisLeuAspTyrArgTyrSerGluTyrArgArgIleArgAlaIleAspGlnHis 121
 DB CAACACCTTGATTAAGGATTACAGATCAAGAACTGAGAGGAGGACCATTAAGCAAGTAT 821
 QY 122 GluGlyGlyLeuGluAlaPheSerArgGlyTyrGluLysLeuGlyPheThrArgSerAla 141
 DB GAGGTGGTTGGAGGCTTTTCTCGTGGTTATGAAAAATGGCTTCACTCGTAGTGCT 881
 QY 142 GluGlyIleThrTyrArgGluTyrAlaProGlyAlaHisSerAlaAlaLeuValGlyAsp 161
 DB ACAGGTATCACTTACCGTAGAGGGCTCCTGGTGGCCAGTCAGCTCCCTCATTTGAGAT 941
 QY 162 PheAsnAsnTyrAsnProAsnAlaAspThrMetThrArgAspAspTyrGlyValITPGLu 181
 DB TTCAACAAATTGGAGCGCAATGCTACATTATGACTCGGAAATGAAATTTGTTCTGGAG 1001
 QY 942 TTTTCGCGCAAAATATGATGATGTTCTCTGGCAATTCCTCATGCTCAGAGTGAAG 1061
 DB 1002 ATTTTTCGCGCAAAATATGATGATGTTCTCTGGCAATTCCTCATGCTCAGAGTGAAG 1061
 QY 202 IleArgMetAspThrProSerGlyValLysAspSerIleSerAlaThrIleLysPheSer 221
 DB 1062 ATACGTATGACACTCCATCAGGTGTAAAGATTCATTCCTGCTTGATCACTACTCT 1121
 QY 222 ValGlnAlaProGlyGluIleProPheAsnGlyIleTyrTyrAspProProGluGlu 241
 DB TTAACGCTTCGATGAATTCATATATGAAATATATATGATGACACCCGAAAGAGAG 1181
 QY 1122 TTAACGCTTCGATGAATTCATATATGAAATATATATGATGACACCCGAAAGAGAG 1181
 DB 242 LysTyrValPheGlnHisProGlnProLysArgProGluSerLeuArgIleTyrGluSer 261
 DB 1182 AGGTATATCTTCACAAACCCAGCGCAAGAAACCAAACTCCCTGAGATATATGATCT 1241
 QY 262 HisIleGlyMetSerSerProGluProLysIleAsnSerTyrAlaAsnPheArgAspGlu 281
 DB 1242 CATATTTGAATGATGATGATCGGAGCGCTAAATTAATCTCATGATGATTTTGAAGTGA 1301
 QY 282 ValLeuProArgIleLysArgLeuGlyTyrAsnAlaValGlnIleMetAlaIleGlnGlu 301
 DB 1302 GTTCTTCCTCGATTAATAAGCTTGAGTACATGCGGTGCATATTTGGCTATTCAAGAG 1361
 QY 302 HisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaProSerSerArg 321
 DB 1362 CATCTTATTTANGCATGTTTGGTTATCATGTCACAAATTTTNNGCACCAACACCGCT 1421
 QY 322 PheGlyThrProGluAspLeuLysSerLeuIleAspArgAlaHisGluLeuGlyLeu 341
 DB 1422 TTTGGAAACNCCCGAGACCTTAAGCTTTGATGATTAAGCTCATGATGATGAAATGTT 1481
 QY 342 ValLeuMetAspIleValHisSerHisSerSerAsnAsnThrLeuAspGlyLeuAsnGly 361
 DB 1482 GTTCTCATGACATTTGTTCAAGCCATGATCAATTAATACCTTATAGATGACGAAACATG 1541
 QY 362 PheAspGlyThrAspThrHisTyrPheHisGlyGlyProArgGlyHisIleStrMetTyr 381
 DB 1542 TTTGACGCGACAGATGATGTTGTTACTTCACTCGAGAGCTCGTGGTATCATGATGATG 1601
 QY 382 AspSerArgLeuPheAsnTyrGlySerTyrGluValIleAspPheLeuSerAsnAla 401
 DB 1602 GATTCGCGCTCTTAACTATGAAACCTGGAGGATCTTAAGATTTCTCTCAAAATGCG 1661
 QY 402 ArgTyrTrpLeuGluGluTyrLysPheAspGlyPheArgPheAspGlyValThrSerMet 421
 DB 1662 AGATGGTGTTGATGATGATTCAAATTTGATGATTTAGATTTGATGATGATGATCATG 1721
 QY 422 MetTyrThrHisHisGlyLeuGlnMetThrPheThrGlyAsnTyrGlyGluTyrPheGly 441
 DB 1722 ATGATATCTCAACACGATTTATCGGTGGATTCACGTGGAGATCAAGAGAAATATCTTTGA 1781

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Cy 442 PheAlaThrAspValAspAlaValAlaTyrLeuMetLeuValAsnAspLeuIleHisGly 461
Db 1782 CTCGAACTGATGATGCTGTTGTTGATCTGATGCTGCTGCAACGATCTTATTCATGCG 1841
Cy 462 LeuHisProAspAlaValSerIleGlyGluAspValSerGlyMetProThrPheCysIle 481
Db 1842 CTTTCCAGATGCAATTAACCTTGGTGAAGATGTTAGCGGAATGCCGACATTTTATTT 1901
Cy 482 ProValProAspGlyGlyValAlaGlyPheAspTyrArgLeuHisMetAlaValAlaAspIys 501
Db 1902 CCGCTTCAAGATGGGGGCTGTTGGCTTGTGCTATCGGCTCCAAATGCAATTCGTGATTA 1961
Cy 502 TrpIleGluLeuLeuLeuSerAspGluSerTrpIysMetGlyAspIleValHisThr 521
Db 1962 TGGATTGCTGCTCAAGAAACGGGATGAGATTGAGAGTGGGCTGATATTGTTCAATCA 2021
Cy 522 LeuThrAsnArgArgTyrPheGluIysCysValAlaThrTyrAlaGluSerHisAspGlnAla 541
Db 2022 CTGACAAATAGAAAGATGTCGGAAGAGTGTGTTTCTATCGCTGAAGTCAATGATCAAGCT 2081
Cy 542 LeuValAlaGlyAspIysThrIleAlaPheTrpLeuMetAspIysAspMetTyrAspPheMet 561
Db 2082 CTAGTCGGGATTAACCTATAGATTCCTGCTGATGAGAGATATGATATGATTTATG 2141
Cy 562 AlaLeuAspArgProSerThrProArgIleAspArgIleAlaLeuHisIleMetIle 581
Db 2142 GCTCTGATGATGCTCAACATCAATCAATTAATGATCGGGATGACATTCGCAAGATGATT 2201
Cy 582 ArgLeuValAlaThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGlyAsnGluPhe 601
Db 2202 AGGCTGTATCACTATGAGATTAAGAGAGAGGATCACTAAATTCATCGGAATATGATTC 2261
Cy 602 GlyHisProGluTrpIleAspPheProArgGlyProGlnThrLeuProThrArgIysVal 621
Db 2262 GCGCCACCCGATGATGATTCCTTACCTAGGCTGAAACACACCTCTCTGATGCTCAGTA 2321
Cy 622 LeuProGlyAsnAsnAsnSerTyrAspIysCysArgArgPheAspLeuGlyAspAla 641
Db 2322 ATTCGCGAAACCAATTCATGATTAATGATGATGATGATGATGATGATGATGATGATGAT 2381
Cy 642 AspPheLeuArgTyrHisGlyMetGlnGluPheAspGlnAlaMetGlnHisLeuGluGlu 661
Db 2382 GAATATTTAAGATACCGTGGGTGCAAGATTTGACCGGCTATGCGATCTTGAAGAT 2441
Cy 662 LysTyrGlyPheMetThrSerGluHisGlnTyrValSerArgIysHisGluGluAspIys 681
Db 2442 AATATAGATTTATGATCTTCAGAACCCAGTTCATATCAAGAAAGATGAGATGAGATGAG 2501
Cy 682 ValIleIlePheGluArgGlyAspLeuValPheValPheAsnPheHisTyrSerAsnSer 701
Db 2502 ATGATTTGATTTGAAAGAGAAACCTAGTTTGTCTTTAATTTTCTGACGACAAAAGC 2561
Cy 702 PhePheAspTyrArgValGlyCysSerArgProGlyLysTyrIysValAlaLeuAspSer 721
Db 2562 TATTCGACTATCGCAGTAGGCTCTGAAAGCTCGAAAATACAAAGTTGCTTGACTCA 2621
Cy 722 AspAspAlaLeuPheGlyGlyPheSerArgLeuAspHisAspValAspIyrPheThrThr 741
Db 2622 GATGATTCACATTTTGTGGCTTCGAGAGATTCATATATATCCGAATTTTCACCTTT 2681
Cy 742 GluHisProHisAspAsnArgProArgSerPheSerValTyrThrProSerArgThrAla 761
Db 2682 GAAAGATGATATATATCTCTCTCTCTCAATATATGATGATGATGATGATGATGATGAT 2741

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APPLICANT: EK, Bo
APPLICANT: KHOSNOODI, Jamehid
APPLICANT: LARSSON, Clas-Tomas
APPLICANT: LARSSON, Hakon
APPLICANT: RASK, Lars
TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
FILE REFERENCE: 003300-486
CURRENT APPLICATION NUMBER: US/09/658,499
CURRENT FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 09/087,277
PRIOR FILING DATE: 1998-05-29
PRIOR APPLICATION NUMBER: PCT/SE96/01558
PRIOR FILING DATE: 1996-11-28
PRIOR APPLICATION NUMBER: SE 9504272-7
PRIOR FILING DATE: 1995-11-29
PRIOR APPLICATION NUMBER: SE 9601506-0
PRIOR FILING DATE: 1996-04-19
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 3074
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: bell gene
OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
OTHER INFORMATION: (potato)
NAME/KEY: CDS
LOCATION: (189)..(2825)
NAME/KEY: sig_peptide
LOCATION: (189)..(332)
NAME/KEY: mat_peptide
LOCATION: (333)..(2825)
NAME/KEY: misc_feature
LOCATION: (92)..(2156)
OTHER INFORMATION: Nucleotides 92, 285, 1406, 1430, 1897 and 2156 are
OTHER INFORMATION: n wherein n = A, C, G or T.
NAME/KEY: misc_feature
LOCATION: (285)..(287)
OTHER INFORMATION: Amino acid -16 is Xaa wherein Xaa = Ile, Leu, Val
OTHER INFORMATION: or Phe.
NAME/KEY: misc_feature
LOCATION: (1404)..(1406)
OTHER INFORMATION: Amino acid 358 is Xaa wherein Xaa = Leu or Phe.
NAME/KEY: misc_feature
LOCATION: (1428)..(1430)
OTHER INFORMATION: Amino acid 366 is Xaa wherein Xaa = Thr.
NAME/KEY: misc_feature
LOCATION: (1896)..(1898)
OTHER INFORMATION: Amino acid 522 is Xaa wherein Xaa = Tyr, Ser, Cys
OTHER INFORMATION: or Phe.
NAME/KEY: misc_feature
LOCATION: (2154)..(2156)
OTHER INFORMATION: Amino acid 608 is Xaa wherein Xaa = Pro.
US-09-508-377-12
US-09-508-377-12 (1-768) x US-09-508-499-1 (1-3074)
Alignment Scores:
Pred. No.: 0
Score: 3189.00
Percent Similarity: 82.78%
Best Local Similarity: 72.49%
Query Match: 76.49%
DB: 4
Gaps: 6
US-09-508-377-12 (1-768) x US-09-508-499-1 (1-3074)
Cy 2 AlaThrPheAlaValSerGlyAlaThrLeu-----GlyValAlaArgProProAlaAla 19
Db 366 TCTACAGTTCGAGATCGGGGAAAGTCTTGTGCTGGAAACCAAGATGATAGCTCTCA 425
Cy 20 AlaGlnProGluGluLeuGlnIleProGlu----- 29
Db 426 TCTCAACAGACCAATTTGAGTTCACTGAGACATCTCCAGAAATTTCCCGACATCACT 485

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QY 30 AsplleGlugluThrAlaglu----- 37
 Db 486 GATGTAGATAGTTCACACATGGAACAGCTAAGCAATTAACTGAGAACGATGAGCT 545
 QY 38 -----ValasnMetHrglyGlyThraAlaglu----- 46
 Db 546 GAGCCGCTCAAGTGATCTTACAGGAAGGTGGAAGAGCTGGATTTGCTTCACTACATA 605
 QY 47 -----LysleuGluSerSerGluProHrgInglylleValGluThrIle 61
 Db 606 CTACAAAGAGGTGTAAACTGAGAGAGCTPAAACATTAAATACTTCTGAGAGACAACT 665
 QY 62 ThrAspGlyValThrLysGlyValLysGluLeuValGlyGluLysProArgValVal 81
 Db 666 ATTTGATGATCTGATAG--ATCAGAGAG-----AGGGGCATC 701
 QY 82 ProLysProGlyAspGlyGluLysIleTyrgLuuIleAspProThrLeuLysAspPheArg 101
 Db 702 CCTCCACCTGAGACTTGGTGAGAAAGATTATGAATAGACCCCTTTGACAACTATGCT 761
 QY 102 SerHisLeuAspTyraGlyTyrgSerGluTyraArgIleArgAlaAlaIleAspGlnHis 121
 Db 762 CAACACCTTGATTACAGGATTTCAACATACAGAACTGAGGGAGGCAATTGACAGATAT 821
 QY 122 GluGlyGlyLeuGluLuuIlePheSerArgGlyTyrgLuuLysleuGlyPheThrArgSerAla 141
 Db 822 GAGGGGTGTTGGAAGCTTTTCTCGTGGTTATGCAAAAAATGGTTTCACTCGTAGTCT 881
 QY 142 GluGlyIleThrTyraGluThrAlaProGlyAlaHisSerAlaAlaLeuValGlyAsp 161
 Db 882 ACAGGATACACTTACCTGAGTGGGCTGCTGGTCCAGTCAGCTGCCCTCATTTGAGAT 941
 QY 162 PheAsnAsnTyrAsnProAsnAlaAspThrMetThrArgAspAspTyrglyValITPGLu 181
 Db 942 TTCAAATAATGGAGCCAAATGCTGACATTATGACTGGAAATGATTGGTGTGAGAG 1001
 QY 182 IlePheLeuProAsnAsnAlaAspGlySerProAlaIleProHisGlySerArgValLys 201
 Db 1002 ATTTTCTGCCAAATATATGATGATGCTTCTCCGCAATTCCTCATGGGTCCAGAGTAG 1061
 QY 202 IleArgMetAspThrProSerGlyValLysAspSerIleSerAlaITPGLIleLysPheSer 221
 Db 1062 ATAAGTATGAGACACTCATCAGATGATTAGGATTCATTCCTGCTTGATCACTACTCT 1121
 QY 222 ValGlnAlaProGlyGluIleProPheAsnGlyIleTyrgTyraAspProProGluGlu 241
 Db 1122 TTAACACTTCTCGATATAATATCATATATATGATATATATATATATATATATATAT 1181
 QY 242 LysTyrgValPheGlnHisProGlnProLysArgProGluSerLeuArgIleTyrgLysSer 261
 Db 1182 AGGTATATCTTCCAAACACCCAGCCCAAAGAACCAAGATGCGTGAATATATATATCT 1241
 QY 262 HisIleGlyMetSerSerProGluProLysIleAsnSerTyraAlaAsnPheArgAspGlu 281
 Db 1242 CATATTGAGATGATGATGCTCGAGAGCTPAAATTAATCATATCGTAATTTAGAGATGA 1301
 QY 282 ValLeuProArgIleLysArgLeuGlyTyraAsnAlaValGlnIleMetAlaIleGlnGlu 301
 Db 1302 GTTCCTTCCGCAATAAAAGCTGGGTGACATGCGGTGCATAATTAATGCTATTCAGAG 1361
 QY 302 HisSerTyrgTyraIleSerPheGlyTyrgHisValThrAsnPhePheAlaProSerSerArg 321
 Db 1362 CATCTTATATATCTGATTTGTTGATCATGTCGAATTTTNGACACCAAGCCGT 1421
 QY 322 PheGlyThrProGluAspLeuLysSerLeuIleAspArgAlaHisGluLeuGlyLeuLeu 341
 Db 1422 TTGTGAAACCCCAAGCACTTAAGTCTTTGATGATTAAGCTCATGAGCTGGAATGTT 1481
 QY 342 ValLeuMetAspIleValHisSerHisSerSerAsnAsnThrLeuAspGlyLeuAsnGly 361
 Db 1482 GTTCTATGAGCAATGTTCAAGCCATGATCAATATATATCTTATGATGAGCACTGAACATG 1541

QY 362 PheAspGlyThrAspThrHisTyrgPheHisGlyGlyProArgGlyHisIleSTPMeTTrp 381
 Db 1542 TTGTGACGACAGATAGTTGTTACTTTCATCTCGAGAGCTCGTGGTATATCATTTGATGTGG 1601
 QY 382 AspSerArgLeuPheAsnTyrgLyserTyrgLuuValLeuArgPheLeuLeuSerAsnAla 401
 Db 1602 GATTCGCCCTCTTTAACTATGATGAACCTGGAGGTCTTAAGTATCTTCTCAAAATGCG 1661
 QY 402 ArgTPTrPLeuGluGluTyrgTyrgPheAspGlyPheArgPheAspGlyValIThrSerMet 421
 Db 1662 AGATGCTGTGGATGAGTCAAAATTTGATGATTTAGATTGATGTGAGATCGACATCAATG 1721
 QY 422 MetTyrgThrHisHisGlyLeuGlnMetThrPheThrGlyAsnTyrgLuuTyrgPheGly 441
 Db 1722 ATGTTACTCACACAGATATACGGGAGATTCACCTGGAACTACAGAGAAATCTTTGGA 1781
 QY 442 PheAlaThrAspValAspAlaValValTyrgLeuMetLeuValAsnAspLeuIleHisGly 461
 Db 1782 CTGCGAAGTATGATGATGCTGTGTATCTGATCTGCTCAACGATCTTATTCATGGG 1841
 QY 462 LeuHisProAspAlaValSerIleGlyGlyAspValSerGlyMetProThrPheCysIle 481
 Db 1842 CTTTCCAGATGCAATTAACATGTGTGAAGATGTTAGCGGAATGCCGACATTTTATTT 1901
 QY 482 ProValProAspGlyGlyValGlyPheAspTyraArgLeuHisMetAlaValAlaAspLys 501
 Db 1902 CCCGTTCAGATGGGGGTGTTGGCTTTGACTATCGGCTGCATATGGCAATGCTGATATA 1961
 QY 502 TrpIleGluLeuLeuLysGlnSerAspGluSerTyrgLysMetGlyAspIleValHisThr 521
 Db 1962 TGGATTGAGTTGCTCAAGAAACGGATGAGATTGGAGAGTGGGATATATTTGCTATACA 2021
 QY 522 LeuThrAsnArgArgTyrgLeuGluLysCysValThrTyraGluSerHisAspGlnAla 541
 Db 2022 CTGACAAATAGAAAGATGTCGGAAAGTGTGTTCTAGCGTGAAGTCAATGATCAAGCT 2081
 QY 542 LeuValGlyAspTyrgThrIleAlaPheTrpLeuMetAspLysAspMetTyraAspPheMet 561
 Db 2082 CTAGTCGGATATAAACHATATGATCTTCCGTGATGAGAGAAGATATATATATTTATG 2141
 QY 562 AlaLeuAspArgProSerThrProArgIleAspArgGlyIleAlaLeuHisLysMetIle 581
 Db 2142 GCTCGATAGACCTCAACATCATATATATATGATGATGATGATGATGATGATGATGAT 2201
 QY 582 ArgLeuValIThrMetGlyLeuGlyGlyGlyTyrgLeuAsnPheMetGlyAsnGluPhe 601
 Db 2202 AGGCTTGATCATATGATGATGATGAGAGAGGATATCTAAATTTCAATGGAAATGAATTC 2261
 QY 602 GlyHisProGluITrPLeuAspPheProArgGlyProGlnIThrLeuProThrGlyLysVal 621
 Db 2262 GCGCACCTGAGTGAATGATTTCCCTAGGGCTGAACCAACACTCTCTGATGGCTCAGTA 2321
 QY 622 LeuProGlyAsnAsnAsnSerTyraAspLysCysArgArgArgPheAspLeuGlyAspAla 641
 Db 2322 ATTCGGGAAACCAATTCAGTTATGATATAATCAGACGAGATTTTACCTGGAGATGCA 2381
 QY 642 AspPheLeuArgTyrgHisGlyMetGlnGluPheAspGlnAlaMetGlnHisLeuGluGlu 661
 Db 2382 GAATATTTAAGTACCGTGGTGTGCAAGATTTGACGGGCTATGCGATATCTTGAAGAT 2441
 QY 662 LysTyrgLysPheMetThrSerGluHisGlnTyrgValSerArgGlyHisGluGluAspLys 681
 Db 2442 AAATATGAGTTTATATCACTTCAAGAACCAAGTTCATATCAGAAAGATGAGAGATAGG 2501
 QY 682 ValIleIlePheGluLuuArgIleAspLeuValIleValPheAsnPheHisSTPSerAsnSer 701
 Db 2502 ATGATTGATTTGAAAAAGAAACCTAATGTTTGTCTTAAATTTTCACTGGAACAAAAAGC 2561
 QY 702 PhePheAspTyraArgValGlyCysSerArgProGlyLysTyrgTyrgValAlaLeuAspSer 721
 Db 2562 TATTCAGCTATGCAATGAGCTGCGTGAAGCTGGAAGAAATACAGAGTGTGCTTGACTCA 2621
 QY 722 AspAspAlaLeuPheGlyGlyPheSerArgLeuAspHisAspValAspTyrgPheThrThr 741


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Db      1210 GATCCACGTCGCGCATCTGATGATGGGATTCCTGCTATTACTATGGAAGTGGGAA 1269
Qy      393 ValLeuArgPheLeuLeuSerAsnAlaArgTrpLeuGluGluTrpLeuPheAspGly 412
Db      1270 GTTTTAAGATTCTCTCTCCCAATGCTAGTGGTGGCTGAGGAATATAAGTTGATGCT 1329
Qy      413 PheArgPheAspGlyValThrSerMetCysTrpHisHisGlyLeuGlnMetTrpPhe 432
Db      1330 TTCCGTTTGGATGGTGTGACCTCCAGATGATGATACACACACGGAATTAACAGTAACATTT 1389
Qy      433 ThrGlyAsnTrpGlyGluTrpPheGlyPheAlaThrAspValAlaValAlaValTrpLeu 452
Db      1390 ACGGGGAACCTCAATGATGATTTTGGCTTTGGCCACGATGTAATGATGATGATTTACTTG 1449
Qy      453 MetLeuValAsnAspLeuLeuHisGlyLeuHisProAspAlaValSerIleGlyGluAsp 472
Db      1450 ATGCTGGTAAATGATTAATTAATGATGATGATTTATCCTGAGGCTGTAACCATTTGGTGAAGAT 1509
Qy      473 ValSerGlyMetProThrPheCysIleProValProAspGlyGlyValGlyPheAspTrp 492
Db      1510 GTTACTGGATGCTCATTTGCTTCCCTGTTCCAGATGATGGGGTGGTGGTGGTGGTGGTAT 1569
Qy      493 ArgLeuHisMetAlaValAlaAspTrpIleGluLeuLeuGlnSerAspGluSer 512
Db      1570 CGGATGCAATATGCTGGTGGCTGCAATATGATGATGATTTCTCAAGCAAGATGATGAAGT 1629
Qy      513 TrpLeuMetGlyAspIleValHisThrLeuThrAsnArgTrpLeuGluGlyCysVal 532
Db      1630 TCGAAGATGGTGTGATTTGTCGCACTGCACTGCAAAATGAGAGGTGTAGAGAGTGTGTA 1689
Qy      533 ThrTrpAlaGluSerHisAspGlnAlaLeuValGlyAspTrpTrpIleAlaPheTrpLeu 552
Db      1690 ACTTATGCTGAAGAATGATGATCAAGCATTAAGTCGGGCGACAACTAATGGCTTTGGTGTG 1749
Qy      553 MetAspIleAspMetTrpAspPheMetAlaLeuAspArgProSerTrpProArgIleAsp 572
Db      1750 ATGGACAAAGATATGATGATTTTCATGAGCCCTGATGAGCTTCACCTCCATCCATGAT 1809
Qy      573 ArgGlyIleAlaLeuHisIleAspMetIleArgLeuValThrMetGlyLeuGlyGluGly 592
Db      1810 CCGTGGATAGCATTAATGAATGATGATTAAGCTTAATCAATGGTTTAAAGAGAGAGGCG 1869
Qy      593 TrpLeuAsnPheMetGlyAsnGluPheGlyHisProGluTrpIleAspPheProArgGly 612
Db      1870 TATCTTAATTTCAATGGAATAGATTTGATGATCCTGAATGATGATGATTTTCCAAAGAGT 1929
Qy      613 ProGlnThrLeuProThrGlyValValLeuProGlyAsnAsnAsnSerTrpAspGlyCys 632
Db      1930 CCGCAAAAGACTTCCAAAGGTGATTAATTAATCAAGGGAATTAACAACATTTAACAATGT 1989
Qy      633 ArgGlyArgPheAspLeuGlyAspAlaAspPheLeuArgTrpHisGlyMetGlnGluPhe 652
Db      1990 CGTCAAGATTTGACCTGGGTGATGCAAGTATCTTAATGATGATGATGATGATGATGATGAT 2049
Qy      653 AspGlnAlaMetGlnHisLeuGluGluValTrp 663
Db      2050 GATCAGGCAATGCAACATCTTGAGCAAAATAT 2082

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RESULT 9
US-09-257-894-8/c
; Sequence 8, Application US/09257894
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; GENERAL INFORMATION:
; APPLICANT: Biogile, Karen E.
; APPLICANT: Klein, Theodore M.
; APPLICANT: Hubbard, Natalie L.
; APPLICANT: Lightner, Jonathan E.
; TITLE OF INVENTION: No. 6376749el Starches via Modification of
; TITLE OF INVENTION: Expression of Starch Biosynthesis
; TITLE OF INVENTION: Enzyme Genes
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS

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ADDRESSER: E. I. du Pont de Nemours and Company
STREET: 1007 Market Street
CITY: Wilmington
STATE: Delaware
COUNTRY: USA
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows 95
SOFTWARE: Version 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/257,894
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/091,052
FILING DATE: JUNE 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Majarian, William R.
REGISTRATION NUMBER: 41,173
REFERENCE/DOCKET NUMBER: BB-1066-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4926
FAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 2165 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-257-894-8
Alignment Scores:
Pred. No.: 6,55e-316 Length: 2165
Score: 2917.00 Matches: 532
Percent Similarity: 87.48% Conservative: 55
Best Local Similarity: 79.28% Mismatches: 62
Query Match: 69.97% Indels: 22
Gaps: 4
US-09-508-377-12 (1-768) x US-09-257-894-8 (1-2165)
Qy      4 PheAlaValSerGlyAlaThrLeuGlyVal-----AlaArgProProAla 18
Db      1985 TTCTTAATCGCGGGGCTCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1926
Qy      19 AlaAlaGlnProGluGluGluGlnIleProGluAspIleGluGluGlnThrAlaGluVal 38
Db      1925 GCCCGCGCCAGAGAACGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1881
Qy      39 AsnMetTrpGlyGlyThrAlaGluLeuGluGluGluGluGluGluGluGluGluGluGlu 52
Db      1880 -----GGCTCGGATCAAGAGGCGGTGATCGGCTCAATTCAGTCGATGAACCTG 1833
Qy      53 ProThrGlnGlyIleValGluThrIleThrAspGlyValThrLeuGlyValValGluLeu 72
Db      1832 GAGGTACAGACATTTCTGAGAGAGCAACGTCGGTGT-----GATGGCTGATGCT 1779
Qy      73 ValValGlyGluValProArgValAlaProGlyProGlyAspGlyGlnValValValVal 92
Db      1778 CAAGCTTGAACAGAGTTCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1719
Qy      93 IleAspProThrLeuLeuAspPheArgSerHisIleAspTrpArgTrpSerGluTrpArg 112
Db      1718 ATTGACCCCATGTTTCAGAGGCTATAGATCAATCTTGAATATGATGATGATGATGATGATGAT 1659
Qy      113 ArgIleArgAlaAlaIleAspGlnHisGlyGlyValGluGluAlaPheSerArgGlyTrp 132
Db      1658 AGAATCCGTTCAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1599
Qy      133 GluValLeuGlyPheThrArgSerAlaGluGlyIleThrTrpArgGluTrpAlaProGly 152

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Db 1598 GAGAGATTGATTTAATGCCAGCGGAGAGGTATCACATATCGAAGATGGGCTCTCGA 1539
Qy 153 AAlaHisserAlaAlaLeuValGlyAspPheAsnAntTPAsnProAsnAlaAspTrMet 172
Db 1538 GCATTTCTGAGACATGGTGGGTGACGTCAACAACATGGGATCCAAATGCAATCGTAG 1479
Qy 173 ThrArgAspAspArgValValTrpGluIlePheLeuProAsnAsnAlaAspGlySerPro 192
Db 1478 AGCAAAATAGAGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1419
Qy 193 AlaIleProHisGlySerArgValIleArgMetAspThrProSerGlyValIleAsp 212
Db 1418 CCTATTCTCATGATCTCGTGTAAAGGAGAAATGATATCTCATCTCAGGGATAAAGGAT 1359
Qy 213 SerIleSerAlaTPuIleLeuPheSerValGlnAlaProGlyGluIleProPheAsnGly 232
Db 1358 TCATTTCCAGCTCGATCAAGTACCTCAGTGCAGGCCCCAGAGAAATACCAATGATGAG 1299
Qy 233 IleTyrTyrAspProPProGluGluIleValIleValIlePheGlnHisProGlnProLysArg 252
Db 1298 ATTTATTTATGATCTCTCTCGAAGAGGTAAAGTATGTTGTTCCAGGCAATCGCACTTAACA 1239
Qy 253 ProGluSerLeuArgIleTyrGluSerHisIleGlyMetSerSerProGluProLysIle 272
Db 1238 CCAAAATCATTTGCGGATATATCAACACATCGGAAATGATGATGATGATGATGATGATGAT 1179
Qy 273 AsnSerTyrAlaAsnPheArgAspGluValLeuProGlyIleLysArgLeuGlyTyrAsn 292
Db 1178 AACCAATATGTAACCTTGAAGATGAAGTCCCTCCAGAAATAAAAAATCTGGATACAT 1119
Qy 293 AlaValGlnIleMetAlaIleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisVal 312
Db 1118 GCAGTGCAAATATATGCAATCCAAAGCACTCATTTATGAAAGCTTTGATACCATGTA 1059
Qy 313 ThrAsnPhePheAlaProSerSerArgPheGlyThrProGluAspLeuLysSerLeuIle 332
Db 1058 ACTATATTTTGGCCCAAGTAGTGGTTTGGTACCCCAAGAGATTTGAAGCTTTGATT 999
Qy 333 AspArgAlaHisGluLeuGlyLeuLeuValLeuMetAspIleValHisSerHisSerSer 352
Db 998 GATGAGACATGACATGACCTTGGTGTAGTCTCATGAGATGATGATGATGATGATGATGAT 939
Qy 353 AsnAsnThrLeuAspGlyLeuAsnGlyPheAspGlyThrAspThrHisIleGlyLeuGly 372
Db 938 AGTAATATCTCGATGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 879
Qy 373 GlyProArgGlyHisIleTyrMetIlePheAspSerArgLeuPheAsnTyrGlySerTrpGlu 392
Db 878 GGTCCAGCTGCACATCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 819
Qy 393 ValLeuArgPheLeuLeuSerAsnAlaArgTTPuLeuGluIleTyrTyrPheAspGly 412
Db 818 GTTTTAAATTTCTCTCTCCATGCTAGATGATGATGATGATGATGATGATGATGATGATGAT 759
Qy 413 PheArgPheAspGlyValThrSerMetMetTyrThrHisIleGlyLeuGlnMetThrPhe 432
Db 758 TTCGTTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 699
Qy 433 ThrGlyAsnTyrGlyGluTyrPheGlyPheAlaThrAspValAlaAspAlaValIleLeu 452
Db 698 ACCGGGAACTCAAGATATTTGGCTTTGCCACGATGATGATGATGATGATGATGATGATGAT 639
Qy 453 MetLeuValAsnAspLeuIleHisGlyLeuHisProAspAlaValSerIleGlyGluAsp 472
Db 638 ATGCTGGTAATGATCAATTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 579
Qy 473 ValSerGlyMetProThrPheCysIleProValProAspGlyGlyValGlyPheAspTyr 492
Db 578 GTTAGTGAAGATCCATATTTGCCCTCTCTTCAAGATGATGATGATGATGATGATGATGATGAT 519
Qy 493 ArgLeuHisMetAlaValAlaAspLysTrpIleGluLeuLeuLysGlnSerAspGlySer 512

Db 518 CGGATGCATATGCTGTGCTGACAAATGATGATGATGATGATGATGATGATGATGATGAT 459
Qy 513 TrpLysMetGlyAspIleValHisThrLeuThrAsnArgArgTrpLeuGluLysCysVal 532
Db 458 TGGAAAGTGGTATATTTGACACACATGCAATATGAGAGTGGTGGTGGTGGTGGTGGTGGT 399
Qy 533 ThrTyrAlaGluSerHisAspGlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeu 552
Db 398 ACTTATGCTAAAGTATGATGATCAAGCATTTAGTGGCCCAAGACATATGCGTTTGGTTG 339
Qy 553 MetAspLysAspMetTyrAspPheMetAlaLeuAspArgProSerThrProArgIleAsp 572
Db 338 ATGACAAAGATATGATGATTTTCATGCGCCCTCATGATGATGATGATGATGATGATGATGAT 279
Qy 573 ArgGlyIleAlaLeuHisLysMetIleArgLeuValThrMetGlyLeuGlyGlyGluGly 592
Db 278 CGTGGATACATTTACATTAAGATGATTAAGACTTATCATGATGATGATGATGATGATGATGAT 219
Qy 593 TyrLeuAsnPheMetGlyAsnGluPheGlyHisProGluTrpIleAspPheProArgGly 612
Db 218 TATCTTATTTATGATGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 159
Qy 613 ProGlnThrLeuProThrGlyLysValLeuProGlyAsnAsnAsnSerTyrAspLysCys 632
Db 158 CCGCAAAAGCTTCCAGTGTGATGATTTATTCAGGGAATACCAACAGTTATGACAAATGT 99
Qy 633 ArgArgArgPheAspLeuGlyAspAlaAspPheLeuArgTyrHisGlyMetGlnGluPhe 652
Db 98 CGTGAAGATTTACCTGGGTGATGACACTATTTTGGTATCTGATGATGATGATGATGATGAT 39
Qy 653 AspGlnAlaMetGlnHisLeuGluGluLysTyr 663
Db 38 GATCAGCAATGCAACATCTTGAGCAAAATAT 6
RESULT 10
US-09-087-277-3
Sequence 3, Application US/09087277B
Patent No. 6169226
GENERAL INFORMATION:
APPLICANT: EK. BO
APPLICANT: KHOSNOODI, Jamedid
APPLICANT: LARSSON, Claes-Tomas
APPLICANT: LARSSON, Hakan
APPLICANT: RASK, Lars
TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
FILE REFERENCE: 003300-486
CURRENT APPLICATION NUMBER: US/09/087, 277B
CURRENT FILING DATE: 1998-05-29
EARLIER APPLICATION NUMBER: PCT/SE96/01558
EARLIER FILING DATE: 1996-11-28
EARLIER APPLICATION NUMBER: SE 9504272-7
EARLIER FILING DATE: 1995-11-29
EARLIER APPLICATION NUMBER: SE 9601506-0
EARLIER FILING DATE: 1996-04-19
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 1393
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Description of unknown Organism: beii gene fragment
OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
OTHER INFORMATION: (potato)
FEATURE:
NAME/KEY: CDS
LOCATION: (2)..(1393)
FEATURE:
NAME/KEY: misc feature
LOCATION: (424)..(1150)
OTHER INFORMATION: Nucleotides 424, 891 and 1150 are n wherein n = A,
OTHER INFORMATION: C, G or T.

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? NAME/KEY: misc_feature
? LOCATION: (422)..(424)
? OTHER INFORMATION: Amino acid 141 is Xaa wherein Xaa = Thr.
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (890)..(892)
? OTHER INFORMATION: Amino acid 297 is Xaa wherein Xaa = Tyr, Ser, Cys
? OTHER INFORMATION: or Phe.
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (1148)..(1150)
? OTHER INFORMATION: Amino acid 393 is Xaa wherein Xaa = Pro.
US-09-087-277-3

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TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: beil gene fragment
OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
OTHER INFORMATION: (potato)
NAME/KEY: CDS
LOCATION: (2)..(1393)
NAME/KEY: misc_feature
LOCATION: (424)..(1150)
OTHER INFORMATION: Nucleotides 424, 891 and 1150 are n wherein n = A,
OTHER INFORMATION: C, G or T.
NAME/KEY: misc_feature
LOCATION: (422)..(424)
OTHER INFORMATION: Amino acid 141 is Xaa wherein Xaa = Thr.
NAME/KEY: misc_feature
LOCATION: (890)..(892)
OTHER INFORMATION: Amino acid 297 is Xaa wherein Xaa = Tyr, Ser, Cys
OTHER INFORMATION: or Phe.
NAME/KEY: misc_feature
LOCATION: (1148)..(1150)
OTHER INFORMATION: Amino acid 383 is Xaa wherein Xaa = Pro.
US-09-508-499-3

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Alignment Scores:
Pred. No.: 5 066-239 Length: 1393
Score: 2227.00 Matches: 400
Percent Similarity: 93.09% Conservative: 31
Best Local Similarity: 86.39% Mismatches: 32
Query Match: 53.42% Indels: 0
Gaps: 0
US-09-508-377-12 (1-768) x US-09-658-499-3 (1-1393)

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QY 184 LeuProAsnAsnAlaAspGlySerProAlaIleProHisGlySerArgValIleArg 203
DB 2 CTGCAATATATATGATGGATGGTCTCTCTCAATCTCTCAATGGGTCAGAGTGAAGTACGT 61
QY 204 MetAspThrProSerGlyValIleAspSerIleSerAlaIleIleIleSerHisValGln 223
DB 62 ATGACACTCTCATCGAGGTGAAGATTCATCTCTGCTGATCACTACTCTTACAG 121
QY 224 AlaProGlyGluIleProPheAsnGlyIleTyrTyrAspProGluGluGluIleTyr 243
DB 122 CTTCCTGATGAATTCATATATATGATATATATATATATATATATATATATATATATAT 181
QY 244 ValPheGlnHisProGlnProIleAspProGluSerIleAspArgIleTyrGlnSerHisIle 263
DB 182 ATCTTCCACACCCGCGCCAAAGAACCAAGTCCGCTGAGATATATATATATATATATAT 241
QY 264 GlyMetSerSerProGluProIleIleAsnSerTyrAlaAsnPheArgSpGluValIleu 283
DB 242 GGAATGATAGTCCGAGCGCTTAAATTAATCACTCATACGTAATTTTGAAGATGAAGTCTT 301
QY 284 ProArgIleIleAspArgLeuGlyTyrAsnAlaValGlnIleMetAlaIleGlnGlnHisSer 303
DB 302 CCTGCGATTAATAAAGCTTGGTACATGCGGTGCGCAATTTTGGCTTTCATAGAGCATTTCT 361
QY 304 TyrTyrAlaSerPheGlyTyrHisValThrAsnPheAlaProSerSerArgPheGly 323
DB 362 TATATGCTAGATTGGTATCATGTCACAAATTTTTCGACCAAGCCGCTTTGAA 421
QY 324 ThrProGluAspLeuIleAspSerIleAspArgAlaHisGlnIleuGlyLeuValIleu 343
DB 422 ACNCCCGAGACTTAAGCTTTGATTTGAAGCTCATGAGCTGAGTAAGTATGTTGTTCTC 481
QY 344 MetAspIleValHisSerHisSerSerAspAsnThrLeuAspGlyLeuAsnGlyPheAsp 363
DB 482 ATGACATTTGTCACGCCATGATCAATTAATCTTTAGATGAGCTGAACAATGTTGAC 541
QY 364 GlyThrAspThrHisIleTyrPheHisGlyGlyProArgGlyHisIleIleIleIleIle 383
DB 542 GGCACAGATAGTGTACTTCTGAGAGCTCGTGGTATCATGATGATGAGTGGATTTCC 601

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QY 384 ArgLeuPheAsnTyrGlySerTyrProGluValIleuArgPheLeuLeuSerAsnAlaArgTyr 403
DB 602 CCCCCTTTTAATCTATGGAAGACTGGAGGACTTAAAGTATCTTCTCAATATGCAAGATGG 661
QY 404 TyrPheGluGluTyrIlePheAspGlyPheArgPheAspGlyValIleIleSerMetMetTyr 423
DB 662 TCGTTGATGAGTCTCAATTTGATGATGATTTAGATTTGATGATGATGATGATGATGATGAT 721
QY 424 ThrHisIleGlyLeuGlnMetThrPheThrGlyAsnTyrGlyGluTyrPheGlyPheAla 443
DB 722 ACTCACCGAGATTTATCGGTGGATTCACCTGGGAACTTACAGAAATTAATCTTTGAGCTGCA 781
QY 444 ThrAspValAspAlaValIleTyrLeuMetLeuValAsnAspLeuIleHisGlyLeuHis 463
DB 782 ACTGATGATGATGCTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 841
QY 464 ProAspAlaValSerIleGlyGluAspValSerGlyMetProThrPheCysIleProVal 483
DB 842 CCAGATGCAATTAACCATGCTGAGTGAAGATTTAGCGGAATGCCGACATTTTATTTCCGCTT 901
QY 484 ProAspGlyValGlyPheAspTyrArgLeuHisMetAlaValAlaAspIleTyrIle 503
DB 902 CAAGATGGGGGTGGTCTTGTGACTATCGGCTCATATGCGCAATGCTGATTAATGATTT 961
QY 504 GluLeuLeuIleGlnSerAspGluSerTyrIleMetGlyAspIleValHisThrLeuThr 523
DB 962 GAGTTCTCTAAGAAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1021
QY 524 AsnArgArgTyrPheGluIleCysValIleTyrAlaGluSerHisAspGlnAlaLeuVal 543
DB 1022 AATAGAAGATGGCGGAAAGTGTCTTCACTATGCGCTGAAGATCATGATCAAGCTCTAGTC 1081
QY 544 GlyAspIleThrIleAlaPheTyrPheMetAspIleAspMetTyrAspPheMetAlaLeu 563
DB 1082 GGTGATTAACATATACATTTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1141
QY 564 AspArgProSerThrProArgIleAspArgGlyIleAlaLeuHisIleMetIleArgLeu 583
DB 1142 GATAGACNTCAACATCATATATATATATATATATATATATATATATATATATATATATAT 1201
QY 584 ValThrMetGlyLeuGlyIleGlyIleTyrLeuAsnPheMetGlyAsnGluPheGlyHis 603
DB 1202 GTAACATGAGTATGAGAGGAAAGGTACTTAATTTCAATGGAAATGAAATTCGGCCAC 1261
QY 604 ProGluThrIleAspPheProArgGlyProGlnThrIleProThrGlyIleValLeuPro 623
DB 1262 CCGAGTGGATTAATTTCTTACGGCTGAACACACCTCTCTGATGCTGATGATGCTGATGCT 1321
QY 624 GlyAsnAsnAsnSerTyrAspIleCysArgArgIlePheAspLeuGlyAspAlaAspPhe 643
DB 1322 GGAACCAATCACTATATATATATATATATATATATATATATATATATATATATATATAT 1381
QY 644 LeuArgTyr 646
DB 1382 TTAAGATAC 1390

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RESULT 12

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US-08-716-449-1
Sequence 1, Application US/08716449
Patent No. 6103893
GENERAL INFORMATION:
APPLICANT: National Starch and Chemical Investment
APPLICANT: Holding Corporation
TITLE OF INVENTION: Method for Producing Altered Starch
TITLE OF INVENTION: from Potato Plants
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scott & Aylen
STREET: Box 194, 24th Floor, Toronto-Dominion Bank Tower
CITY: Toronto
STATE: Canada M5K 1H6
COUNTRY: Canada

```


426 HisGlyLeuGlnMetThrPheThiGlyAspThrGlyLysIleuTrpPheGlyPheAlaThrAsp 445
 1358 CATGAAATCAATATGGGATTTTACAGGAAACTATATGATGATTTTACAGCGAGCTCAAGAT 1417
 446 ValAspAlaValAlaTyrLeuMetLeuValAsnAspLeuIleHisGlyLeuHisProAsp 465
 1418 GTTATGCTGTGGTCTATTATTAATGTGGCCCAATATTCATGATTCACAAGATTTTCCAGAC 1477
 466 AlaValSerIleGlyGluAspValSerGlyMetProThrPheCysIleProValProAsp 485
 1478 GCAACTGTTATGGCCGAGATGTTCTCGTAATGGCCGGGCTTACCGGCGCTGTTCTGAG 1537
 486 GlyGlyValGlyPheAspTyrArgLeuHisMetAlaValAlaAspLysTrpIleGluLeu 505
 1538 GGAGGAATGGTGTTTGATTAATCCGCTGGCATATGCCAATCCAGATAGTGGATGATTAAT 1597
 506 LeuLys--GlnSerAspGlnSerTrpLysMetGlyAspIleValHisThrLeuThrAsn 524
 1598 TTAAAGATATAGAATAGATGAAGATTGGTCCCTGAGGAAGTAAATCATCGATTGGACAAAT 1657
 525 ArgArgTrpLeuGluLysCysValThrTrpLysGlnSerHisAspGlnAlaLeuValGly 544
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 545 AspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyrAspPheMetAlaLeuAsp 564
 1718 GACAAGACCATTTGCATTTCTCTCTAATGACAAGAGATGATTTCTGGCATGCTTGTCTTG 1777
 565 ArgProSerThrProArgIleAspArgGlyIleAlaLeuHisLysMetIleArgLeuVal 584
 1778 ACAGATGCTTCCCTGGTGGTATGATCCAGAAATGGGCTTCCAAAGATCATCATTTTTC 1837
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 1838 ACAATGGCGCTTGGGAGAGAGAGGAGGATCTCAATTTCATGGGTAAACGATTTGGCCATCT 1897
 605 GluTrpIleAspPheProArgGlyProGlnThrLeuProThrGlyLysValLeuProGly 624
 1898 GAGTGGATTTGATCTTCCCTAGA-----GAGGGC 1924
 625 AsnAsnAsnSerTyrAspLysCysArgArgArgPheAspLeuGlyAspAlaAspPheLeu 644
 1925 AATAAATTGGAGTTATGACAAATGTAGACGCCAGTGAACCTTCCGCGATAGCGAACACTTG 1984
 645 ArgTyrHisGlyMetGlnGluPheAspGlnAlaMetGlnHisLysGluGlyLysTyrGly 664
 1985 AGATACAAAGTTATGAATGATTTGATTAAGACTATGAATGGCTCGATGAAAGATTTCA 2044
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 2045 TTCCCTCGCATCGGAAAAACAGTAAATAGCACACATGATGATGATGAATAAAGATTTGTG 2104
 685 PheGluArgGlyAspPheValPheValPheAsnPheHisTrpSerAsnSerPhePheAsp 704
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 705 TyrArgValGlyCysSerArgProGlyLysTyrLysValAlaLeuAspSerAspAla 724
 2165 TATTAAGTTGATGTGACATTCGCCAGGGAAGTACAGAGTTGCACTGGGACGTGATCTTGG 2224
 725 LeuPheGlyGlyPheSerArgLeuAspHisAspValAspTyrPheThrThr----- 741
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 742 -----GluHisProHisAspAsnArgProArgSerPheSerValTyrThr 756
 2285 AATACCTGAGATCCAGAAACAATTTCAATGATGTCCTCAAAATTTCTTCAAAGTGGCTCT 2344
 757 ProSerArgThrAlaValValTyr 764
 2345 CTTGGCCGAACATGTGTGGCTTAT 2368

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US-09-731-166-13
/ Sequence 13. Application US/09731166
/ Patent No. 6639126
/ GENERAL INFORMATION:
/ APPLICANT: Sewalt, Vincent J. H.
/ TITLE OF INVENTION: Singleary, George W.
/ FILE REFERENCE: 35718/206348
/ CURRENT APPLICATION NUMBER: US/09/731,166
/ PRIOR FILING DATE: 2000-12-06
/ PRIOR APPLICATION NUMBER: 60/169,993
/ NUMBER OF SEQ ID NOS: 16
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 13
/ LENGTH: 2470
/ TYPE: DNA
/ ORGANISM: Zea mays
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (0)...(0)
/ OTHER INFORMATION: SBEI -- Genbank Accession No. 6639126 217959
/ NAME/KEY: CDS
/ LOCATION: (2)...(2470)
US-09-731-166-13

Alignment Scores:
Pred. No.: 1,52e-229 Length: 2470
Score: 2146.00 Matches: 395
Percent Similarity: 71.57% Conservative: 101
Best Local Similarity: 57.00% Mismatches: 171
Query Match: 51.48% Indels: 26
DB: Gaps: 6

US-09-508-377-12 (1-766) x US-09-731-166-13 (1-2470)

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QY 126 GluAlaPheSerArgLYTyrgLuleuGlyPheThrArgSerAlaGluGlyIleThr 145
DB 359 GAATCTTTTCTTAAAGGCTATTTGAAATTTGGGATTTAATCAAAATGAGAGTGAACCTGA 418
QY 146 TTTATGgGluTrrAlaProGlyLahHsSerAlaAlaLeuValGlyAspPheAsnEntTP 165
DB 419 TATCGGAATGGGCACTCTGCTGGCAGGAGGAGCAAGACTTATTTGTACTTCAATGACTGG 478
QY 166 AsnProAsnAlaAspThrMetThrArgAspAspTyrgLYValTPGluIlePheLeuPro 185
DB 479 AATGCGTCAAAACCATNAGATGGAAGAGATTAATTTGGTGTGGTCGATCAAAATTT--- 535
QY 186 AsnAsnAlaAspGlySerProAlaIleProHsIsgLYSerArgValLYsIleArgMetAsp 205
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QY 206 ThrProSerGlyValLYsAspSerIleSerAlaTPDileYsPheSerValGlnAlaPro 225
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QY 226 GlyGluIle-----ProPheAsnGlyIleTyrrAspProProGluGluGluLYsTyrr 243
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QY 244 ValPheGlnHsIleProGlnProLYsArgProGluSerLeuArgIleTyrgIuSerHsIle 263
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Db 836 CACGGCAATACGCAAAATTAATACACACAGTTGATGAGGATTAAGAGCATTCG 895
Qy 304 TTTTAlaSerPheGlyTyrHisValThrAsnPheAlaProSerSerArgPheGly 323
Db 896 TACTAGCTTCTTGGGTACCATGTGACAAATTTCTTGGGTAGCAGACAGATCAGC 955
Qy 324 ThrProGlnAspLeuLysSerLeuIleAspArgAlaHisGluLeuGlyLeuValIleu 343
Db 956 ACACCCAGAGGACCTCAAAATCTGTGTGATAGGCACACAGTTGGGTTTGGAGTTCTG 1015
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Qy 364 -----GlyThrAspThrHisTyrPheHisGlyGlyProArgGlyHisSerPheMet 380
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Qy 381 TTPAspSerArgLeuPheAsnTyrGlySerTTPGlyValIleuArgPheLeuLeuSerAsn 400
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Qy 401 AlaArgTTPLeuGluGlyTyrLysPheAspGlyPheArgPheAspGlyValThrSer 420
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Qy 461 GlyLeuHisProAspAlaValSerIleGlyGluAspValSerGlyMetProThrPheCys 480
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Qy 540 GlnAlaLeuValGlyAspLysThrIleAlaPheThrPheMetAspLysAspMetTyrAsp 559
Db 1616 CAGTCATTTGTCGCAAAAATATGATGCTTCTCTGATGCAAGCAAGAAATATCACT 1675
Qy 560 PheMetAlaLeuAspArgProSerThrProArgIleAspArgGlyIleAlaLeuHisLys 579
Db 1676 GGCATGTCAGACTTGCAGCTCTTCCTCAATATGATGAGGAGATTCACCTCAAAAG 1735
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Db 1736 ATGATTCACCTTCAACAAATGGCCCTTGAGGATGATGCTACCTTGAATTTATGGGAAAT 1795
Qy 600 GluPheGlyHisProGluTTPIleAspPheProArgGlyProGlnThrLeuProThrGly 619
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Qy 620 LysValLeuProGlyAsnAsnAsnSerTyrAspLysCysArgArgPheAspLeuGly 639

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Qy 640 AspAlaAspPheLeuArgTyrHisGlyMetGlnGluPheAspGlnAlaMetGlnHisLeu 659
Db 1883 GACACTGATCACTTGGCGGTACAAAGTACATGAATGCCCTTGACCAAGCGATGAATGCCCTC 1942
Qy 660 GluGluLysTyrGlyPheMetThrSerGluHisGlnTyrValSerArgLysHisGluGlu 679
Db 1943 GATGAGAGATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2002
Qy 680 AspLysValIleIlePheGluArgGlyAspLeuValPheValPheAsnPheHisTTPSer 699
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Qy 700 AsnSerPhePheAspTyrArgValGlyCysSerArgProGlyLysTyrLysValAlaLeu 719
Db 2063 AAACTTACAGAGGCTACAAAGTGGATCGATTTCTGCGAAATACAGATGACCTTG 2122
Qy 720 AspSerAspAspAlaLeuPheGlyGlyPheSerArgLeuAspHisAspValAspTyrPhe 739
Db 2123 GACTGTGATGCTGTGCTGTGCTGTGATGGAAGAGTTGGCCACGCGATCACTTC 2182
Qy 740 ThrThr-----GluHisProHisAspAsnArgProArgSer 751
Db 2183 ACGTGCCTGAAGGGGTGCGCAGGGGTGCCGAAACGAACTTCAACAAACCGCGAACTCG 2242
Qy 752 PheSerValTyrThrProSerArgThrAlaValTyr 764
Db 2243 TTCAAGTCTTCTTCGCCGCCGACCTGTGTGCTTAT 2281

RESULT 14
US-09-257-894-19/c
Sequence 19, Application US/09257894
Patent No. 6376749
GENERAL INFORMATION:
APPLICANT: Brogile, Karen E.
APPLICANT: Klein, Theodore M.
APPLICANT: Hubbard, Natalie L.
APPLICANT: Lightner, Jonathan E.
TITLE OF INVENTION: No. 6376749el Starches via Modification of
TITLE OF INVENTION: Expression of Starch Biosynthesis
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. du Pont de Nemours and Company
STREET: 1007 Market Street
CITY: Wilmington
STATE: Delaware
COUNTRY: USA
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows 95
SOFTWARE: Version 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/257,894
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/091,052
FILING DATE: JUNE 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Majarian, William R.
REGISTRATION NUMBER: 41,173
REFERENCE/DOCKET NUMBER: BB-1066-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4926
TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 2467 base pairs

QY 740 ThrThr-----GlnHisProHisAspAsnArgProArgSer 751
 Db 192 ACCTCCCTCGAAGGGGTGCAGGGGTGCCGAAACGAACCTTCACACACCGGCGCAACTCG 133
 QY 752 PheSerValThrThrProSerArgThrAlaValValTyr 764
 Db 132 TTCAAAGTCTTCTTCGCGCGCGCACTGTGTGCTTAT 94

RESULT 15
 US-09-257-894-24
 Sequence 24, Application US/09257894
 Patent No. 6376749

GENERAL INFORMATION:
 APPLICANT: Biogile, Karen E.
 APPLICANT: Klein, Theodore M.
 APPLICANT: Hubbard, Natalie L.
 APPLICANT: Lightner, Jonathan E.
 TITLE OF INVENTION: No. 6376749el Starches via Modification of
 TITLE OF INVENTION: Expression of Starch Biosynthesis
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: E. I. du Pont de Nemours and Company
 STREET: 1007 Market Street
 CITY: Wilmington
 STATE: Delaware
 COUNTRY: USA
 ZIP: 19898

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: Microsoft Windows 95
 SOFTWARE: Version 7.0A
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/257,894
 FILING DATE:

CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/091,052
 FILING DATE: JUNE 10, 1998
 ATTORNEY/AGENT INFORMATION:
 NAME: Majarian, William R.
 REGISTRATION NUMBER: 41,173
 REFERENCE/DOCKET NUMBER: BB-1066-A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 302-992-4926
 TELEFAX: 302-773-0164
 INFORMATION FOR SEQ ID NO: 24:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2565 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-09-257-894-24

Alignment Scores:
 Pred. No.: 1,62e-229 Length: 2565
 Score: 2146.00 Matches: 395
 Percent Similarity: 71.57% Conservative: 101
 Best Local Similarity: 57.00% Mismatches: 171
 Query Match: 51.48% Gaps: 26
 DB: 4 Gaps: 6

US-09-508-377-12 (1-768) x US-09-257-894-24 (1-2565)

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 Db 421 TATCGTAATGAGCACTCTGCTGCGAGAGCGAGACCTGATTTGGTGACTTCATTAATGCTGG 480
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 Db 481 AATGGTGCAACCATTAAGATGAGAAAGATTAATTTGGTCTTGGTGACCAAAATT--- 537
 QY 186 AsnAsnAlaAspGlySerProAlaIleProHisGlySerArgValLysIleArgMetAsp 205
 Db 538 GACCATGTCAAGGAGAAACCTCCATCCCTCACAATTCAGATTAATTCGCTTCTTA 597
 QY 206 ThrProSerGlyValLysAspSerIleSerAlaTyrIleLysPheSerValGlnAlaPro 225
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 QY 244 ValPheGlnHisProGlnProLysArgProGlnSerLeuArgIleTyrGlnSerHisIle 263
 Db 718 ACATTTAAGCATCTTCGCTTCAAGCCTGCTCCACGTATCATATGAGCCCATGTA 777
 QY 264 GlyMetSerSerProGlnProLysIleAsnSerTyrAlaAsnPheArgAspGlnValLeu 283
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 Db 838 CCAGCATACGAGCAAAATTAATACACACAGCTCACTGATGAGATGAGATGAGCATTCG 897
 QY 304 TyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaProSerSerArgPheGly 323
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 Db 958 ACACCAAGAGACCTCAAAATATCTTGTATTAAGGCACACAGTTGGTTGCCAGTTCTG 1017
 QY 344 MetAspIleValHisSerHisSerSerAsnAsnThrLeuAspGlyLeuAsnGlyPheAsp 363
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 QY 364 -----GlyThrAspThrHisTyrPheHisGlyGlyProArgGlyHisHisIleTyrMet 380
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 QY 381 ThrAspSerArgLeuPheAsnTyrGlySerTyrGlnValLeuArgPheLeuSerAsn 400
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 Db 1198 CTGAAATATTTGGTTGATTAATCATGTTTGAAGGCTTCGATTTGATGAGATTAATCA 1257
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 Db 1258 ATGCTGTATCATCACCATGTATCAATGTGGGCTTACTGGAACACTACAGGAATATTC 1317
 QY 441 GlyPheAlaThrAspValAspAlaValAlaTyrLeuMetLeuValAsnAspLeuIleHis 460
 Db 1318 AGTTTGACACACAGCTGTGATGCAAGTTTATCATGATGCTTGCACAAACATTAATGAC 1377
 QY 461 GlyLeuHisProAspAlaValSerIleGlyLysAspValSerGlyMetProThrPheCys 480
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QY 501 LysTrpIleGluLeuLeuLeuGlnSerAspGluSer---TrpLysMetGlyAspIleVal 519
Db 1498 AGATGGATTGACTTACCTTAAGATTAAGATGACTCTGAGTGTGATGGGTGAATATAGCG 1557
QY 520 HistTrpLeuThrAsnArgArgTrpLeuGlnLysCysValThrTyrAlaGluSerHisAsp 539
Db 1558 CATACTTGCATCAACAGAGATATCTGAAAATGATCGCATATGCTAGAGGCCATGAT 1617
QY 540 GlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyrAsp 559
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Db 1678 GGCATGTCAGACTTCAGCTCTGCTTCACCTACATTTGATCGAGGATTCGACTCCAAAG 1737
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Db 1798 GAGTTTGGTCACTCCAGAAATGATGACTTCCACAGA----- 1833
QY 620 LysValLeuProGlyAsnAsnAsnSerTyrAspLysCysArgArgAspPheAspLeuGly 639
Db 1834 -----GAAAGGAACAATGGAGCTATGATTAATTAATGACAGACAGACAGACCTTGTG 1884
QY 640 AspAlaAspPheLeuArgTyrHisGlyMetGlnGluPheAspGlnAlaMetGlnHisLeu 659
Db 1885 GACACTGATCACTTCGGGTACAGATACATGATGCGTTGACCAAGCATGATGCGCTC 1944
QY 660 GluGluLysTyrGlyPheMetThrSerGluHisGlnTyrValSerArgLysHisGluGlu 679
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QY 680 AspLysValIleIlePheGluArgGlyAspLeuValPheValPheAsnPheHisTrpSer 699
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QY 700 AsnSerPhePheAspTyrArgValGlyCysSerArgProGlyLysTyrIleValAlaLeu 719
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Db 2125 GACTCTGATGCTCTGCTTCTTCGTTGACATGGAAGATTCGCGCACGATGATCACTTC 2184
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Db 2185 ACGTGCCTGAAGGGGTGCGAGGGGTGCCCGAAACGAACTTCAACACCGGCCGAACCTCG 2244
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Search completed: April 17, 2004, 22:37:41
Job time : 180 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 17, 2004, 18:29:50 ; Search time 540 Seconds
(without alignments)

6041.882 Million cell updates/sec

Title: US-09-508-377-12

Sequence: 1 MATFAVSGATLGVARRPPAAA.....PRSFVYTPERTAVVATL 768

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Egapop 6.0 , Egapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS-human40.ccd
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pct -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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8: genesegn2003bs:*
9: genesegn2003cs:*
10: genesegn2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4169	100.0	2726	5	AAH78337
2	3685	88.4	3015	2	AAV05639
3	3363	80.7	3039	6	ABK15494
4	3362	80.6	2919	2	AAQ73750
5	3352	80.4	2968	5	AAH78342
6	3351	80.4	2640	2	AAV70961
7	3342	80.2	2725	2	AAV29757
8	3341	80.1	2655	2	AAH69729

9	3337.5	80.1	2655	7	ADA71289	Ada71289	Rice	gene
10	3292	79.0	3090	2	AAV38720	AAV38720	Full	leng
11	3258	78.1	2418	6	AB213067	AB213067	Arabidops	
12	3258	78.1	2418	7	ADA68438	ADA68438	Arabidops	
13	3241.5	77.8	2913	2	AAV38719	AAV38719	Full	leng
14	3197	76.7	2531	2	AAH17267	AAH17267	Class A	s
15	3197	76.7	2563	5	ABK50301	ABK50301	Potato	cd
16	3193	76.6	3074	2	AAH69587	AAH69587	Potato	st
17	3189	76.5	2529	2	AAH42637	AAH42637	Class A	s
18	3189	76.5	2578	2	AAH42631	AAH42631	Class A	s
19	3164.5	75.9	2307	9	ADC07807	ADC07807	Rice	DNA
20	3164	75.9	3231	6	AAH42632	AAH42632	Class A	s
21	3155	75.7	2577	6	AB212532	AB212532	Arabidops	
22	3155	75.7	2715	3	AAH45939	AAH45939	Arabidops	
23	3152.5	75.6	2576	2	AAH42634	AAH42634	Class A	s
24	3152	75.6	3003	2	AAH42634	AAH42634	Class A	s
25	3135	75.2	3033	2	AAH42630	AAH42630	Class A	s
26	3133	75.1	2975	2	AAH42635	AAH42635	Class A	s
27	3083.5	73.9	2304	9	ADC08218	ADC08218	Rice	DNA
28	2824	70.1	2087	2	AAH69737	AAH69737	Corn	star
29	2917	70.0	2165	2	AAH69736	AAH69736	Corn	star
30	2900	69.6	2307	3	AAH29938	AAH29938	DNA	encod
31	2336.5	56.0	11475	5	AAH78338	AAH78338	Nucleotid	
32	2301	55.2	11473	2	AAH34650	AAH34650	starch	br
33	2233	53.6	1919	2	AAH38722	AAH38722	Corn	star
34	2196	52.7	4563	4	AAH30910	AAH30910	Wheat	sta
35	2166.5	52.0	2733	3	AAH62135	AAH62135	Rice	star
36	2163.5	51.9	3128	2	AAH00774	AAH00774	Potato	st
37	2157.5	51.8	2733	2	AAH54674	AAH54674	Rice	star
38	2155	51.7	2289	7	ADA71346	ADA71346	Rice	gene
39	2155	51.7	2289	9	ADC08304	ADC08304	Rice	DNA
40	2146	51.5	2487	2	AAH69747	AAH69747	Corn	star
41	2146	51.5	2565	2	AAH69752	AAH69752	Corn	star
42	2146	51.5	2763	2	AAV29758	AAV29758	Zea	may's
43	2146	51.5	2771	2	AAH02457	AAH02457	Branching	
44	2146	51.5	2772	2	AAH69740	AAH69740	Plasmid	p
45	2140	51.3	2899	4	AAH02926	AAH02926	Human	she

ALIGNMENTS

RESULT 1

AAH78337 standard; cDNA; 2726 BP.

AAH78337	AAH78337	standard; cDNA; 2726 BP.
AC	AAH78337	
XX	AAH78337	
DT	26-NOV-2001	(first entry)
DE	Nucleotide sequence of wheat starch branching enzyme 9 (BE1a).	
XX	Wheat; starch branching enzyme; BE1a; BE1d; SBE; transgenic plant;	
KW	starch biosynthetic pathway; amylopectin; amylose; ss.	
XX		
OS	Triticum sp.	
XX		
FN	W0200162934-A1.	
FD	30-AUG-2001.	
XX		
PF	21-FEB-2001; 2001WO-AU000175.	
XX		
FR	21-FEB-2000; 2000AU-00005742.	
XX		
PA	(CSIR) COMMONWEALTH SCI & IND RES ORG.	
PA	(GOOD-) GOODMAN FIELDS LTD.	
PA	(LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.	
XX		
PI	Morell M, Rahman S;	
XX		
DR	WPI; 2001-570635/64.	
XX		
PT	Nucleic acids encoding wheat starch branching enzyme (tb useful for	

altering the amylose and amylopectin content of cereal plants, e.g. wheat and barley.

Example 1, Fig 1, 103bp; English.

The present sequence encodes wheat starch branching enzyme 9, designated CC BR1a. The specification describes BR1b. BR1b is a type II starch branching enzyme (SBE). The BR1b nucleic acids may be used to CC genetically transform cereal plants such as wheat or barley and for CC altering their nutritional content by modulating the starch biosynthetic CC pathway to vary levels of amylopectin and/or amylose produced in the CC plant

Sequence 2726 BP, 726 A, 564 C, 701 G, 735 T, 0 U, 0 Other;

Alignment Scores:
Pred. No.: 0 Length: 2726
Score: 4169.00 Matches: 768
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-508-377-12 (1-768) x AAH76337 (1-2726)

QY 1 MetLathrPheAlaValSerGlyAlaThrLeuGlyValAlaArgProProAlaAla 20
DB 124 ATGGCGAGGTTCGGGTGTCGGCGCGACCCCTCGGTGGCGGGCGCGCGCGCGG 183
QY 21 GlnProGluGluLeuGlnIleProGluAspIleGluGluGlnThrAlaGluValAsnMet 40
DB 184 CAACCTGAAGAATTACAGATACCTGAAGACATCGAGCAACCGCTGAAGTAAACATG 243
QY 41 ThrGlyGlyThrAlaGluLeuLeuGluSerSerGluProThrGlnGlyIleValGluThr 60
DB 244 ACAAGGGGAGCTGCGAAGAACTTGAATCTTCAGAACCGACTCAAGGCATTGGGAAACA 303
QY 61 IleThrAspGlyValThrLeuGlyValIleGlySerLeuValValGluLeuProAspVal 80
DB 304 ATCACTGATGGTGAAACCAAGAGAGTTAAGGAACTAGTGTGGGGAGAAACCGCAAGTT 363
QY 81 ValProLysProGlyAspGlyGlnLysIleTyrGluIleAspProThrLeuLysAspPhe 100
DB 364 GTCCCAAAACCAAGAGATGGGCGAAGAAATTAAGGATTGACCCAAACGCTGAAGATTTT 423
QY 101 ArgSerHisLeuAspTyrArgTyrSerGlyTyrArgGlyIleArgAlaAlaIleAspGln 120
DB 424 CGAGGACCATCTTGACTACCGATACAGCGAATACAGAGAAATTCGTCTCTATTGACCA 483
QY 121 HisGluGlyGlyLeuGluAlaPheSerArgGlyTyrGluLysLeuGlyPheThrArgSer 140
DB 484 CATGAAGGTGATGTGAAGCATTTTCTCGGTATGAAAGCTTGGAATTTACCCGCAAGT 543
QY 141 AlaGluGlyIleThrTyrArgGluTyrAlaProGlyAlaHisSerAlaIleValAlaGly 160
DB 544 GCTGAAGGTATACCTTACCGAAGATGGGCTCTCGAGCGCATTTCTGACAGATTAGAGGT 603
QY 161 AspPheAsnAspTyrAsnProAsnAlaAspThrMetThrArgAspAspTyrGlyValTyr 180
DB 604 GACTTCAACAATTGGAATCGAATGAGATGACTATACACAGATATATATGCTGTTGG 663
QY 181 GluIlePheLeuProAsnAspAlaAspGlySerProAlaIleProHisGlySerArgVal 200
DB 664 GAGATTTCCTCCCTACACATGCTGATGAGATCCCGCATTTCTTCTGATGCTCAAGTGA 723
QY 201 LysIleArgMetAspThrProSerGlyValLysAspSerIleSerAlaTyrIleLysPhe 220
DB 724 AAGATACCGATGGATCTCATCTGTGTGAAGATTCAATTTCTGCTTGATCAAGTTTC 783
QY 221 SerValGlnAlaProGlyGluIleProPheAsnGlyIleTyrTyrAspProProGluGlu 240
DB 784 TCTGTGCGAGGCTCCAGGTGAATATCAATTCAGTGGCATATATTATATGATCCACTGAAGAG 843

QY 241 GluLysTyrValPheGlnHisProGlnProLysArgProGluSerLeuArgIleTyrGlu 260
DB 844 GAGAGTATGTTCTCCACATCTCTCAACCTAAACGACAGATGACATGAGGATTTATGAA 903
QY 261 SerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrAlaAsnPheArgAsp 280
DB 904 TCACACATGGATGATGACAGCCAGAACCGAATATTAATTCATATGCTAATTTTAGGAT 963
QY 281 GluValLeuProArgIleLysArgLeuGlyTyrAspAlaValGlnIleMetAlaIleGln 300
DB 964 GAGGTCTCCAGAAATTAAGGCTTGATACAAAGCACTGCAAGTAAATGGCAATCCAG 1023
QY 301 GluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaProSerSer 320
DB 1024 GAGCATTTCAATATGAGAGCTTTGGGTACATGTTACTTAATTTTGGACCAAGTACG 1083
QY 321 ArgPheGlyThrProGluAspLeuLysSerLeuIleAspArgAlaHisGluLeuGlyLeu 340
DB 1084 CGTTTGGAACTCCAGAGGACTTAAATCCCTGATCATGATGACATGACCTTGTTG 1143
QY 341 LeuValLeuMetAspIleValHisSerHisSerSerAsnAsnThrLeuAspGlyLeuAsn 360
DB 1144 CTGTTCCTTATGAGATTTGTTCTCATGTCATTCATCAATATATACCTTGACGGCTGAT 1203
QY 361 GlyPheAspGlyThrAspThrHisTyrPheHisGlyGlyProArgGlyHisIleTyrPhe 380
DB 1204 GGTTCGATGAGCATGATACCATTTACTTCCACGGTGTGTCCAGCTGGCCATCATGGATG 1263
QY 381 TrpAspSerArgLeuPheAsnTyrGlySerTrpGluValLeuArgPheLeuLeuSerAsn 400
DB 1264 TGGGATTTCTCGTCTATTCAACTATGGAGGTGGGAAGTATGAATCTTCTGTCAAAC 1323
QY 401 AlaArgTyrTrpLeuGluGluTyrLysPheAspGlyPheArgPheAspGlyValThrSer 420
DB 1324 GCGAGATGGTGGCTTGAAAGATATTAAGTTGATGATTTGCAATTTGATGGGGTGACCTCC 1383
QY 421 MetMetTyrThrHisHisGlyLeuGlnMetThrPheThrGlyAsnTyrGlyLysTyrPhe 440
DB 1384 ATGATGATATCTCACCATGATTCATTAATGCAATTAATGCAATTAATGCAATGATATTT 1443
QY 441 GlyPheAlaThrAspValAspAlaValAlaTyrLeuMetLeuValAsnAspLeuIleHis 460
DB 1444 GGAATTCCTGATGATGTGATGCGGTGATTAAGTTCGATGCTGCAAGCATTAATTCAT 1503
QY 461 GlyLeuHisProAspAlaValSerIleGlyGluAspValSerGlyMetProThrPheCys 480
DB 1504 GSACTTCATCTGATGCTGTATTCATTTGATGTAAGATGCAATGCCACATTTTGC 1563
QY 481 IleProValProAspGlyGlyValGlyPheAspTyrArgLeuHisMetAlaValAlaAsp 500
DB 1564 ATCCCTGTCAGATGTGTGGTGTGTTTACATGCTGATGCTGATGCTGATGACAGAT 1623
QY 501 LysTrpIleGlyLeuLeuLysGlnSerAspGluSerTrpLysMetGlyAspIleValHis 520
DB 1624 AAATGATTAACCTCCCAAGCAAGTGAACAATCTTGAAATTAAGGATGATATTTGCAAC 1683
QY 521 ThrLeuThrAsnArgTyrTrpLeuGluLysCysValThrTyrAlaGluSerHisAspGln 540
DB 1684 ACCCTTAACAATTAAGAGGTGCTTGAGAGTGTATCTTATGCAAGAAAGTCATGATCA 1743
QY 541 AlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyrAspPhe 560
DB 1744 GCACTAGTGTGTCACAGACTATGCAATTCGTGTGATGATGATAGAGATATGATATTC 1803
QY 561 MetAlaLeuAspArgProSerThrProArgIleAspArgGlyIleAlaLeuHisTyrPhe 580
DB 1804 ATGGCTTGTAGTAGGCTTCAACTCTCGCATTTGATCTGTGGCATATGCAATTAATAAAG 1863
QY 581 IleArgLeuValThrMetGlyLeuGlyGlyGlyTyrLeuAsnPheMetGlyAsnGlu 600
DB 1864 ATCAGGCTTGTACCAAGAGGTTTAGGTGTGAAGCTATCTTAATTCATGGAAGATGAG 1923
QY 601 PheGlyHisProGluTyrTrpIleAspPheProArgGlyProGlnThrLeuProThrGlyLys 620

Db 1924 TTGGGCAATCCGTGATGATGATGATTTTCCAGAGAGTCCGGAACCTCTTCAACCGGCAAA 1983
|||
Qy 621 ValLeuProGlyAsnAsnAsnSerTyrAspIysCysArgArgArgPheAspLeuGlyAsp 640
|||
Db 1984 GTTCTCCCTGGAAATACAAATAGTATGAAATAATGCCCGCTAGATTGATCTTGAGAGAT 2043
|||
Qy 641 AlaAspPheLeuArgTyrHisGlyMetGlnGluPheAspGlnAlaMetGlnHisLeuGlu 660
|||
Db 2044 GCAGATTTTCTTAGATATCATGATATGCAAGAGTTGATGATGAGCAATGACGATCTTGAG 2103
|||
Qy 661 GlnLysTyrGlyPheMetThrSerGluHisGlnTyrValSerArgLysHisGlnGluAsp 680
|||
Db 2104 GAAAATATGGGTTTATGACATCTGAGCAACAGTATGTTTCAAGAAACATGAGGAAGAT 2163
|||
Qy 681 LysValIleIlePheGluArgGlyAspLeuValPheValPheAsnPheHisTSPSerAsn 700
|||
Db 2164 AAGGATCATCTTGCAGAAAGAGAGATTGGTATTTGTTTCAACTTCCACTGGAGCAAT 2223
|||
Qy 701 SerPheAspTyrArgValGlyCysSerArgProGlyLysTyrLysValAlaLeuAsp 720
|||
Db 2224 AGCTTTTGTGACTACCGTGTGGGTCTTCCAGSCCTGGAGAGTACAAGTGGCTTTAGAC 2283
|||
Qy 721 SerAspAspAlaLeuPheGlyGlyPheSerArgLeuAspHisAspValAspTyrPheThr 740
|||
Db 2284 TCCGACGATGCACTCTTGGTGGATTCAAGAGGCTTGATCATGATGTCGACTCTTACA 2343
|||
Qy 741 ThrGluHisProHisAspAsnArgProArgSerPheSerValTyrThrProSerArgThr 760
|||
Db 2344 ACCGACACATCCGATGACAAACAGCGCGCTCTTCTCGGTGTACACTCCGAGCAGAACT 2403
|||
Qy 761 AlaValIleTyrAlaLeuThrGlu 768
|||
Db 2404 GCGGTGCTATGCTTACAGAG 2427
|||
RESULT 2
ID AAV05639 standard; cDNA to mRNA; 3015 BP.
XX AAV05639;
XX AC
XX 25-MAR-2003 (revised)
DT 01-MAY-1998 (first entry)
XX
XX Rice type IV starch branching enzyme cDNA.
DE
XX
XX Rice; type IV starch branching enzyme; amylopectin synthesis; ds.
KM
XX
XX Oryza sativa.
OS
XX
XX Key Location/Qualifiers
FH CDS 129..2654
FT sig_peptide 129..287
FT mat_peptide 288..2651
FT tag= c
FT product= "type_IV_starch_branching_enzyme"
XX
XX JP10004970-A.
XX
XX
XX 13-JAN-1998.
PD
XX
XX 24-JUN-1996; 96JP-00162983.
PF
XX
XX 24-JUN-1996; 96JP-00162983.
PR
XX
XX (MITS-) MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO.
PA (MITK-) MITSUI TOATSU CHEM INC.
XX
XX
XX MPI: 1998-133625/13.

PT Rice starch branching enzyme gene - synthesises amylopectin to yield high
PT quality starch.
XX
XX
XX Claim 4; Page 5-8; 13pp: Japanese.
XX
XX The present sequence encodes the rice type IV starch branching enzyme,
CC which has the ability to synthesise amylopectin. The quality of starch is
CC improved by the use of the protein. (Updated on 25-MAR-2003 to correct PA
CC field.)
XX
SQ Sequence 3015 BP; 796 A; 606 C; 819 G; 794 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 0 Length: 3015
Score: 3685.00 Matches: 683
Percent Similarity: 85.83% Conservative: 38
Best Local Similarity: 81.31% Mismatches: 47
Query Match: 88.39% Indels: 72
DB: 2 Gaps: 4
US-09-508-377-12 (1-768) x AAV05639 (1-3015)
Qy 1 MetLathrPheAlaValSerGlyValLathrLeuGlyValAlaArgPro-----16
|||
Db 129 ATGGCGTCTGTCGCGGTCTCCGCGGAGCTCGGAGCTCGGAGCGGCGGCGGCGGCGGCGG 188
|||
Qy 17 -----ProAlaAla-----19
|||
Db 189 GCGGCGGAGGAGTGGCGCGCGCGCGCGGATCCGCGGCGGAGACTTGGCTGCTCTTC 248
|||
Qy 19 -----19
|||
Db 249 AGAGGAAGAGACTCTTCTCAAGTGGCGTGTGAGCTGCGGAGTGTCTCTGGGAAGTG 308
|||
Qy 19 -----19
|||
Db 309 CTGTGCTCGGCGGTGGAGCGGACGACTGCTGCTCTCGGAGACGAGACGTGAAACT 368
|||
Qy 20 ---AlaGlnProGlnGluLeuGlnIleProGluAsp-----11GlnGlu 33
|||
Db 369 CAAGAGCAACTGAAAGAAATCTCAATCCTGATGATTAATAAGTAAACCTTTTGAGAG 428
|||
Qy 34 Gln-----ThrAlaGluValAsnMetThrGlyGlyThrAlaGluLysLeu 48
|||
Db 429 GAGGAAGAGATTCAGACGATGCGCAGAGCAGACAGCAATGAAGTGTGTGCTGAACAACTT 488
|||
Qy 49 GluSerSerGluProThrGlnGlyIleValGluThrIleThrAspGlyValThrLysGly 68
|||
Db 489 GAATCTTCAGAAAGTGAATTCAGACATTCAGAAATGTGTACTGAGGCTGTGATCAAGAT 548
|||
Qy 69 ValLysGluLeuValIleGlyLysProAspValIleProLysProGlyAspGlyGln 88
|||
Db 549 GCTGATGAACCACTGTGAGAGATTAACCAACAGATTATCCACCAACAGAGATGGGCA 608
|||
Qy 89 LysIleTyrGlnIleAspProThrLeuLysAspPheArgSerHisLeuAspTyrArgTyr 108
|||
Db 609 AAGATATACCAAAATGACCCCATGCTGGAAGGATTCGGAACCATCTTGACTACCCGATAC 668
|||
Qy 109 SerGluTyrArgArgIleArgAlaIleAspGlnHisGlnGlyLysLeuGluAlaPhe 128
|||
Db 669 AGTGATACCAAGAGATGCTGACACTATTTGACCAACATGAAGTGTGCTTGGATGCAATT 728
|||
Qy 129 SerArgGlyTyrGlnLysLeuGlyPheThrArgSerAlaGlnGlyIleThrTyrArgGlu 148
|||
Db 729 TCTCGTGTATCGAAAGCTTGATTCACCCGACAGGCTGAAGGACTTACCTACCGAGAA 788
|||
Qy 149 TyrAlaProGlyAlaHisSerAlaAlaLeuValGlyAspPheAsnAsnThrPheAsnProAsn 168
|||
Db 789 TGGGCACTGGAGCAGCTGCTCAGCATTAAGTGAAGTCACTTCAACAAATTGGAACCCAAAT 848
|||
Qy 169 AlaAspThrMetThrArgAspAspTyrGlyValIleThrGluIlePheLeuProAsnAsnAla 188
|||

QY 189 AspGlySerProAlaIleProHisGlySerArgValIleIleArgMetAspThrProSer 208
 Db 909 GATGATCCCTGCTATTCCTCATGGCTCAGCGTAAAGATTGGATGATACCATCT 968
 QY 209 GlyValIleAspSerIleSerAlaTrpIleLysPheSerValGlnIleProGlyGluIle 228
 Db 969 GCGGTAAGGATTCAATTCCTCGGATTAAGTTGATGTCGAGCTCCAGGCTGAAATA 1028
 QY 229 ProPheAsnGlyIleTyrTyrAspProProGluGluGluTyrValPheGlnHisPro 248
 Db 1029 CCGTACAAACGGTATATTTATTTATTCACCTGAAGAAAGAAATATGATTTCCAACTCCT 1088
 QY 249 GlnProLysArgProGluSerLeuArgIleTyrGluSerHisIleGlyMetSerSerPro 268
 Db 1089 CAACCTAAACGACCAAAATTCGCTCGCGATATATGAATCATATGATGATAGTACCCG 1148
 QY 269 GluProLysIleAsnSerTyrAlaAsnPheArgAspGluValLeuProArgIleLysArg 288
 Db 1149 GAACCGAAGATTAACACATATCTAATTTAGGATGAGGTGCTACCAAGAAATTAAG 1208
 QY 289 LeuGlyTyrAsnAlaValGlnIleMetAlaIleGlnIleHisSerTyrTyrAlaSerPhe 308
 Db 1209 CTGGGTACATGCTGTACAGATATGCGAATCCAGAGCATCTTATTCGCAAGCTTT 1268
 QY 309 GlyTyrHisValThrAsnPhePheAlaProSerSerArgPheGlyThrProGluAspLeu 328
 Db 1269 GGGTATCATGTTACTACTTCTTTGGCCAGTAGACCTTTCCGAACCCAGAAAGACTTG 1328
 QY 329 LysSerLeuIleAspArgAlaHisGluLeuGlyLeuLeuValLeuMetAspIleValHis 348
 Db 1329 AAATCTCGATTGATTAACCTCAGCGAGCTGTTCTGTACTTATGATATGTTGTCAC 1388
 QY 349 SerHisSerSerAsnAsnThrLeuAspGlyLeuAsnGlyPheAspGlyThrAspThrHis 368
 Db 1389 ACTCATGCTCAACATACCTCGATGCTGATTTGATATGTTGATGCTGATCATCAT 1448
 QY 369 TyrPheHisGlyGlyProArgGlyHisIleTrpMetTrpAspSerArgLeuPheAsnTyr 388
 Db 1449 TACTTCATGATGAGCAACGCGGCTCATCATGATGCGGATTCGCGCTGTTCACTAT 1508
 QY 389 GlySerTrpGluValLeuArgPheLeuLeuSerAsnAlaArgTrpTrpLeuGluGluTyr 408
 Db 1509 GGGAGTTGGGAAGTTTAAGATATTAATTAATCGTCAAGAAAGGAGGCTTGGAAGATAC 1568
 QY 409 LysPheAspGlyPheArgPheAspGlyValThrSerMetMetTyrThrHisIleGlyLeu 428
 Db 1569 AAGTTTGAAGGATTCGATTTGATGGGGTGAACCTCATATGATATCATCATGTTTA 1628
 QY 429 GlnMetThrPheThrGlyAsnTyrGlyGluTyrPheGlyPheAlaThrAspValAspAla 448
 Db 1629 CAGGTGCGCATTTACTGCGCAACTATGCGCAATATTTGGATTTCTACTGATGTTGAGCA 1688
 QY 449 ValValIleTyrLeuMetLeuValAsnAspLeuIleHisGlyLeuHisProAspAlaValSer 468
 Db 1689 GATGTTTACTTGAAGTGTGTTGAACGATCTAATTCATGAGGCTTTATCTCGAGGCTGAGCC 1748
 QY 469 IleGlyGluAspValSerGlyMetProThrPheCysIleProValProAspGlyGlyVal 488
 Db 1749 ATTGGTGAAGATGTCAGCGGAGTCCCACTTTTGTATTTCTGTTCAGATGGTGGT 1808
 QY 489 GlyPheAspTyrArgLeuHisMetAlaValAlaAspLysTrpIleGluLeuLeuLysGln 508
 Db 1809 GGTTTTGAATTCGTTGATGATGCTGATACCGAGCAAAATGATCGAACTCCCAAGCAA 1868
 QY 509 SerArgGluSerTrpLysMetGlyAspIleValHisThrLeuHisAsnArgArgTrpLeu 528
 Db 1869 AATGACGAATATTGAAAATGGGTGATATGTCACACCTTAACGAATAGAGGTGTCA 1928
 QY 529 GluLysCysValThrTyrAlaGluSerHisAspGlnAlaLeuValGlyAspLysThrIle 548
 Db 1929 GAGGAGTGTGTTACTTATGAGAAAGTCAAGCAACCACTAGTGTGTGCAAGACTATT 1988

QY 549 AlaPheTrpLeuMetAspLysAspMetTyrAsnPheMetAlaLeuAspArgProSerThr 568
 Db 1989 GCATTCGTTGATGATGAATGAATGATGATATTTATGAGCTTACAGACACTTCAACA 2048
 QY 569 ProArgTrpLeuAspArgGlyIleAlaLeuHisLysMetIleArgLeuValThrMetGlyLeu 588
 Db 2049 CTTGCAATTGATCGTGGGATGATGATTAATTAATGATTAAGCTTGTACCATGGGCTTA 2108
 QY 589 GlyGlyGluGlyTyrLeuAsnPheMetGlyAsnGluPheGlyHisProGluTrpIleAsp 608
 Db 2109 GAGAGCGAAGCTATCTTAATTTATGAGGAATGATTGGGCACTCGAAATGATAGAT 2168
 QY 609 PheProArgGlyProGlnThrLeuProThrGlyLysValLeuProGlyAsnAsnAsnSer 628
 Db 2169 TTCCAAAGAGCCCGCAAACTTTCCAATGCTCGCTCCCGCTCCGAAACAACCTACCT 2228
 QY 629 TyrAspLysCysArgArgPheAspLeuGlyAspAlaAspPheLeuArgTyrHisGly 648
 Db 2229 TTGATTAATGCCCTCGTAGATTGACCTTGAAGTGAATATCTTAATGATCATGCT 2288
 QY 649 MetGlnGluPheAspGlnAlaMetGlnHisLeuGluGluLysTyrGlyPheMetThrSer 668
 Db 2289 ATGCAGAGTTTGATCAGGCGCATGCAATCTTGAGAAATATGATGATTCATGACATCT 2348
 QY 669 GlnHisGlnTyrValSerArgLysHisGluGluLysPheValIleIlePheGluArgGly 688
 Db 2349 GAGCACGATATATATGTCGCAACACGAGAGGATTAAGTGATATCTTCAGAGAGGA 2408
 QY 689 AspLeuValPheValPheAsnPheHisIleTrpSerAsnSerPhePheAspTyrArgValGly 708
 Db 2409 GATTGGATATTCGTTCACTTCCACGAGATATGATTTTGATCATGCGCGCT 2468
 QY 709 CysSerArgProGlyLysTyrLysValAlaLeuAspSerAspAspAlaLeuPheGlyGly 728
 Db 2469 TGTTTAAGCCTCGAAGATGACAGATGCTGTGACCTGACAGAGTGGCTCTTTGGTGA 2528
 QY 729 PheSerArgLeuAspHisAspValAspTyrPheThrTrpGluHisProHisAspAsnArg 748
 Db 2529 TTCACTGGCTTGAATGATGATGCTGAGTACTTCACTGCTGACTGCGCATACAAACA 2588
 QY 749 ProArgSerPheSerValTyrThrProSerArgThrAlaValIleTyrAlaLeuThrGlu 768
 Db 2589 CCAATGTCATTCCTGGGTGATACCCCAAGAGAACCGCGTGTATGATCATTAACAGAG 2648
 RESULT 3
 ID ABK15494 standard; cDNA; 3039 BP.
 AC ABK15494;
 XX
 DT 08-MAY-2002 (first entry)
 DE Wheat starch branching enzyme IIb cDNA from clone wdk2c_pk009.j17.
 XX
 KM Wheat; starch branching enzyme; starch synthesis; transgenic plant;
 KM wdk2c_pk009.j17; antibody; gene mapping; expressed sequence tag; EST;
 KM gene; ss.
 XX
 OS Triticum aestivum.
 XX
 FH Key Location/Qualifiers
 FT CDS 3..2570
 FT /tag= a
 FT /product= "Starch branching enzyme IIb"
 FT /partial
 FT /note= "No start codon shown. The sequence from
 FT nucleotides 481-3039 is specifically claimed in claim 3
 FT of the specification and is shown as Seq ID. 1"
 XX
 PD 03-JAN-2002

23-FEB-2001, 2001US-00792127.
01-MAR-2000, 2000US-0186098P.
(ALLE/) ALLEN S M.
(BECK/) BECKLES D M.
(BUTL/) BUTLER X H.
(PEAR/) PEARLSTEIN R W.
Allen SM, Beckles DM, Butler XH, Pearlstein RW,
WPI; 2002-178959/23.
P-PSTDB; AAU76219.
Novel isolated polypeptide having starch 11b enzyme activity, useful for
preparing antibodies to the proteins which are used to detect the
polypeptides in situ in cells or in vitro in cell extracts.
Claim 3; Page 17-18; 27pp; English.

This invention relates to the cDNA and protein sequences of a novel wheat starch branching enzyme iib enzyme. Starch branching enzymes are responsible for the formation of alpha 1-6 linkages in amylopectin in the starch synthesis pathway. The nucleotide sequence of the invention is useful for producing a transgenic plant expressing the starch branching enzyme. The protein sequence is useful for preparing antibodies against starch. Branching enzyme iib protein, which are useful for detecting the proteins in situ in cells, or in vitro in cell extracts. The protein is also useful for selecting an isolated polynucleotide that affects the level of expression of a starch branching enzyme iib protein or enzyme activity in a plant cell. All or substantial portion of the nucleotide sequence can be used as probe for genetic and physical mapping of the genes and can be used as markers for traits linked to those genes. This information is useful in plant breeding in order to develop lines with desired phenotypes. A polynucleotide fragment is useful for isolating cDNAs and genes encoding homologous proteins from the same or other plant species. They are also useful as DNA hybridisation probes or as polymerase chain reaction (PCR) amplification primers. The fragments are also useful for creating transgenic plants and may be useful as restriction fragment length polymorphism markers. Nucleic acid probes derived from the cDNA sequence may also be used for physical mapping or for fluorescence in situ hybridisation (FISH) mapping. The present sequence represents the wheat starch branching enzyme iib cDNA from clone wdk2c.pk009.117

Sequence 3039 BP; 836 A; 624 C; 783 G; 796 T; 0 U; 0 Other;

Alignment Scores:

Record No.:	9.57e-309	Length:	3093
Score:	3353.00	Matches:	607
Percent Similarity:	89.27%	Conservative:	75
Local Similarity:	79.45%	Mismatches:	68
Query Match:	80.67%	Indels:	14
		Gaps:	4
			4

S-09-508-377-12 (1-768) x ABK15494 (1-3039)

y 7 SerGlyAlaThrLeuGlyValAlaArgProProAlaAlaIaInPro----- 22
 |||||
 |||||
 b 294 AGTGGGGAAACA-----CCGCTTCCATCGACGCGTCCCGCTTCAATTGAT 338
 |||||
 |||||
 y 23 ---GlnGluGluGlnIleProGluAspIleGlnGlnGlnThrAlaGluValAsmSerThr 42
 |||||
 |||||
 b 339 TCTGATGATCTGAAGTTCCA---TTCATTGATGATTAACA-----ACCTTACAG 386
 |||||
 |||||
 y 42 GlyGlyThrAlaGluLysLeuIleuSerSerGluProThrGlnGlyIleValGluThrIle 61
 |||||
 |||||
 b 387 GATGGAAGTGAAGTACTATTGGCTCTTCAGACACAATACAGTTAGTGAAGAAATTGAT 446
 |||||
 |||||
 y 62 ThrAspGlyValThrIysGlyValLysGlnLeuValValGlyLysProArgValVal 81
 |||||
 |||||
 b 447 GCTGAAGACACGAGCAATATGACAAAGATCATCTACGAGGAGAAATTAACCATCTTG 506
 |||||
 |||||

QY	82	ProLySPProGlyaSPbGlyGlnLysIleTyrGluIleASPProthLeuLysASPPhaArg	101
Db	507	CCACCACCCGGGAATGACAGCAAAATATACAGATTACCAACAGCTCCAGACTTTAAAG	566
QY	102	SerHisLeuAPbPyrArgTyrSerGluTyrArgArgIleArgAlaIleASPGLHis	121
Db	567	TACATCTTGAGTATCCATATAGCCTTACAGGAATACGTTACAGCATTTGATGAACAC	626
QY	122	GluGlyGlyLeuGluAlaPheSerArgGlyTyrGluLysLeuGlyPheThrArgSerAla	141
Db	627	GAAGAGGACATGATGATATTTCCCGCGGTATACAGAAAGTTGGATTATTCGACAGCGCT	686
QY	142	GluGlyIleThrTyrArgGluTyrAlaProGlyAlaHisSerAlaIleuValGlyASP	161
Db	687	GAAGGTATCATTTACGAGAAATGGCGTCCAGCAACATTTGACGATTAAGTTGGAGAC	746
QY	162	PheASPantTPanProASPnaIaASPThMetThrArgASPbPyrGlyValTyrGlu	181
Db	747	TTCAACATTTGGATCCAAATGACGACCAATAGCAAAATAGACCTTGGGTGGGAG	806
QY	182	IlePheLeuProASPnaenIaASpGlySerProAlaIleProHisGlySerArgValLys	201
Db	807	ATTTTTTCGCAAAACAATGACAGATGGTTCGCAACAATTCCTCAGGCTCACGGGTACAG	866
QY	202	IleArgMetAPbTPProSerGlyValLysASPserIleSerAlaTrrPileLysPheSer	221
Db	867	GTGGAATAGGATCTCCATCTGGATGATAAGGATTTCAATTCCTGTTGATCACTACTCC	926
QY	222	ValGlnAlaProGlyGluIleProPheASPnGlyIleTyrTyrASPProGluGluGlu	241
Db	927	GTGCAGACTCCAGAGATATATCCATACATGGAATATATTATGATCTCCCGAAGAGAG	986
QY	242	LysTyrValPheGlnHisProGluProLysArgProGluSerLeuAglIeTyrGluSer	261
Db	987	AAGATGATATTCAGACATCTCCAACTTAAACGACAAATCATTTGCGGATATAGAACA	1046
QY	262	HisIleGlyMetSerSerProGluProLysIleASPserTyrAlaenPheArgASPglu	281
Db	1047	CATGTGGCATGATGATGCCGAGCAACAAAGTCAACACATTCGAACTTCAGGAGTAGC	1106
QY	282	ValLeuProArgIleLysArgLeuGlyTyrASPnaIaValGlnIleMetAlaIleGlnGlu	301
Db	1107	GTGCTTCCAGAAATTAAAGACTTGATGATCAATGCACTGCAAAATTAATGGCAATCCAGAG	1166
QY	302	HisSerTyrTyrAlaSerPheGlyTyrHisValThrASPnhePheAlaProSerSerArg	321
Db	1167	CACTCACAATATGAGAACCTTTGGGTACACATTCACAAATTTCTTTGACCAAGATGCCGT	1226
QY	322	PheGlyThrProGluASPLeuLysSerLeuIleASPArgAlaHisGlyLeuGlyLeuLeu	341
Db	1227	TTTGGGTCCCAAGAACTTTAAATCTTTGATTCATAGACTCACAGGCTTGGCTGGTT	1286
QY	342	ValLeuMetAPbIleValHisSerHisSerSerASPantThrLeuASPbGlyLeuASPnGly	361
Db	1287	GTCTCTCATGATGTTGTTCACAGCTCAGCGCCAAATATATCTTTGGACGGGTGGAATGGT	1346
QY	362	PheASPbGlyThrASPbTPHisTyrPheHisGlyGlyProArgGlyHisSTPmetTyr	381
Db	1347	TTTATAGGCAAGGATACACATTACTTCCATGACCGCTTCAAGGGCCATCACTGGATGGG	1406
QY	382	ASPserArgLeuPheASPnTyrGlySerTrrGluValLeuArgPheLeuLeuSerASPnaIa	401
Db	1407	GATTCGCCGTGCTTTAATCTAATGGGAATAAGAGACTTAAAGTTTTCATCTTCCAATGCA	1466
QY	402	ArgTrrTPbLeuGluGluTyrLysPheASPbGlyPheArgPheASPbGlyValThrSerMet	421
Db	1467	AGATGGTGGCTAGAGGAGTAAATTGATGGTTCGATTCGATGGCGGACCTTCATG	1526
QY	422	MetTyrThrHisGlyLeuGlnMetThrPheThrGlyASPnTyrGlyGluTyrPheGly	441
Db	1527	ATGATATCCATCTGATTTACAGTAACTTTTACAGAAAGCTACATGATATTTTGGC	1586

QY 522 LeuThraenaArgTrpLeuGluYusCyValThrTyAlaGluSerHisAspGlnAla 541
 Db 1952 CTAACAACAGAGAGTGGCTGAGAAAAGTGTGTACTTAAGTCAAGATCAAGCA 2011
 QY 542 LeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysPheValTyrAspPheMet 561
 Db 2012 CTGTGTGAGACAAAGACTATTCATTCGTGTGATGAGACAAAGATATGATATGATTCAGT 2071
 QY 562 AlaLeuAspArgProSerThrProArgIleAspArgGlyIleAlaLeuHisIleValMetIle 581
 Db 2072 GCGCTGAACGAGACCTTCGACGCTTATATGATTCGTGGAATAGCACTGCATTAATAATGATT 2131
 QY 582 ArgLeuValThrMetGlyLeuGluGlyGluGlyTyrLeuAsnPheMetGlyAsnGluPhe 601
 Db 2132 AGACTTATCACAATGGGTCTAGAGAGAGGGTATCTTAACCTTATGGGAATGAGTTC 2191
 QY 602 GlyHisProGluTrpIleAspPheProArgGlyProGluThrLeuProThrGlyLysVal 621
 Db 2192 GGGCATCCTGATGATGATGACTTCCAGAGGCCCAAGTACTTCCAGTGGTAAAGTTC 2251
 QY 622 LeuProGlyAsnAspAsnSerTyrAspLysCysArgArgPheAspLeuGlyAspAla 641
 Db 2252 ATCCAGAAAACAACACGTTACGACAAATGCCGTGCAAGATTAACTTGGGTGATGCA 2311
 QY 642 AspPheLeuArgTyrHisGlyMetGluGluPheAspGlnAlaMetGlnHisLeuGluGlu 661
 Db 2312 GAATTTCTTAGGATCAATGATGATGACAGAGCTTGTGATCAAGCATGACAGCATCTTGAGGAA 2371
 QY 662 LysTyrGlyPheMetThrSerGluHisGlnTyrValSerArgLysHisGluGluAspLys 681
 Db 2372 AAATATGGTTTATGACATCAAGACCAACAGTACGTATCTCGGAAACATGAGAAAGATTAG 2431
 QY 682 ValIleIlePheGluArgGlyAspLeuValPheValPheAsnPheHisTrpSerAsnSer 701
 Db 2432 GTGATTCGTTTGAAGAAAGGAGCTTGTATTTGTTTCACTTCCACGTGAGACTAGTAC 2491
 QY 702 PhePheAspTyrArgValGlyCysSerArgProGlyLysTyrLysValAlaLeuAspSer 721
 Db 2492 TATTTCCGACTACCGGGTGGCTGTTAAAGCCTGGGAATCAAGGTGCTTAAGACTG 2551
 QY 722 AspAspAlaLeuPheGlyGlyPheSerArgLeuAspHisAspValAspTyrPheThrThr 741
 Db 2552 GACGCTGACCTCTTGTGGATTTGTAGAGATCCATCACTGACAGAGCACTTCACTTCT 2611
 QY 742 GluHisProHisAspAsnArgProArgSerPheSerValTyrThrProSerArgThrAla 761
 Db 2612 GACTGCCAACAATGACACAGGCCCATTTCTCTGATGATCACTCTAGACAGAACCTGT 2671
 QY 762 ValValTyrAla 765
 Db 2672 GTGTCTATGCT 2683
 RESULT 6
 ID AAV70961 standard; DNA; 2640 BP.
 AC AAV70961;
 XX 23-AUG-1999 (first entry)
 DE DNA encoding maize branching enzyme II.
 KW Non-glycogen-like polysaccharide production; fermentation;
 KW starch synthase enzyme; glycogen-synthesis enzyme; glycogen synthesis;
 KW non-starch branching gene; amylopectin; amylose; plant-like starch;
 KW maize branching enzyme II; ss.
 OS Zea mays.
 XX MO9844780-A1.
 XX 15-OCT-1998.
 PD

PF 03-APR-1998; 98WO-US006660.
 XX
 PR 04-APR-1997; 97US-0042939P.
 XX
 PA (EXSE-) EXSEED GENETICS LLC.
 XX
 PI Guan H, Keeling PL,
 XX
 DR WPI: 1998-568285/48.
 DR P-PSDB; AAV70961.
 XX
 PT Producing non-glycogen-like polysaccharides in bacteria, fungi or plants
 PT - transformed with genes for enzymes involved in starch or glycogen
 PT synthesis allows fermentative production of starches with engineered
 PT properties.
 XX
 PS Disclosure; Fig 53; 150pp; English.
 XX
 CC The specification describes a method for the production of non-glycogen-
 CC like polysaccharides in a host. The method comprises transforming a host,
 CC suitable for fermentation, with genes encoding starch- or glycogen-
 CC synthesis enzymes, and fermenting the transformants. The specification
 CC also describes how starch transformed with a gene active in glycogen synthesis
 CC and at least one non-starch branching gene, involved in production of
 CC amylopectin or amylose in its original host. The method is used to
 CC produce plant-like starches by fermentation and new starches in plants.
 CC These starches are useful for all food and non-food applications of
 CC starch. The present sequence is used in the course of the invention
 XX
 SQ Sequence 2640 BP; 715 A; 510 C; 686 G; 729 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1,086-307 Length: 2640
 Score: 3351.00 Matches: 609
 Percent Similarity: 87.24% Conservative: 68
 Best Local Similarity: 78.48% Mismatches: 77
 Query Match: 80.38% Indels: 22
 DB: Gaps: 4
 US-09-508-377-12 (1-768) x AAV70961 (1-2640)
 QY 4 PheAlaValSerGlyAlaThrLeuGlyVal-----AlaArgProProAla 18
 Db 108 TTCTTAACCTCGGGGTGCTCGAGTGTGATGTCGGGAGCAAGGCGCATGCGCGGGG 167
 QY 19 AlaAlaGluProGluGluLeuGluIleProGluAspIleGluGluThrAlaGluVal 38
 Db 168 GCCGGCCGACAGAAAGCGGTGATGATGTTCTGAGGCCGCAAGATGAT----- 212
 QY 39 AsnMetThrGlyGlyThrAlaGluLysLeuLysSerGlu----- 52
 Db 213 -----GGCTCGCATCAAGGGCTGACTCGCTCATTCAGTCGAGTGAAGTCTG 260
 QY 53 ProThrGluGlyIleValGluThrIleThrAspGlyValThrLysGlyValLysGluLeu 72
 Db 261 GAGGTACACAGACATTTCTGAAGAGACAACTGCGGTGCT-----GGTGTGCTATGCT 314
 QY 73 ValValGlyGluProArgValValProlLysProGlyAspGlyGlyLysIleTyrGlu 92
 Db 315 CAAGCCTGAACAAGATTGATGATGCTCCCGCCACCAACAGATGACAAAAATATTCGAG 374
 QY 93 IleAspProThrLeuLysAspPheArgSerHisLeuAspTyrArgTyrSerGluTyrArg 112
 Db 375 ATTAGACCCCATGTTGACAGGCTATTAAGATCATCTTGATGATCGGTACAGCTCATAGA 434
 QY 113 ArgIleArgAlaAlaIleAspGlnHisGluGlyGlyLeuGluAlaPheSerArgGlyTyr 132
 Db 435 AGAATCCGTTACAGCATGATGATGAACATGAAAGAGAGCTTGAAAGCTTCTCCGTTGAT 494
 QY 133 GluLysLeuGlyPheThrArgSerArgGluGlyIleThrTyrArgGluThrAlaProGly 152
 Db 495 GAGAGTTTGGATTTAATCCGACCGCGAAGGTATCAATTCAGAAATGGCTCTGCA 554

QY	153	AlaHisSerAlaIaIeuValGlyAspPheAsnMetTrpAsnProAsnIaAspTrpMet	172
DB	555	GCATTTCGCGAGCATGGTGGGTGACTTCAACAATGGATCCAAATGACAGTTCGTATG	614
QY	173	ThrArgAspAspTrpGlyValTrpGluIlePheLeuProAsnAsnIaAspGlySerPro	192
DB	615	ACGAAAAAGAGTTGGTGTGGGAATTTTCTCTCCATGACATGCAATGCTACATCA	674
QY	193	AlaIleProHisGlySerArgValLysIleArgMetAspThrProSerGlyValLysAsp	212
DB	675	CCATATCCCATGATGATCGTGTGTAAGGTGAGATGATCTCCATCAGGAGTAAGAT	734
QY	213	SerIleSerValaTrpIleLysPheSerValGlnAlaProGlyGluIleProPheAsnGly	232
DB	735	TCATATCCAGCCTGGATCAAGTACTGATGTCAGAGCCCGACGAGAAATACATATGATGG	794
QY	233	IleTyrTyrAspProGluGluGluLysTyrValPheGlnHisProGluProLysArg	252
DB	795	ATTATTATATGATCTCTCTGTAAGAGTAAAGTATGTGTTCCAGCATGGCGAACTTAACGA	854
QY	253	ProGluSerLeuArgIleTyrGluSerHisIleGlyMetSerSerProGluProLysIle	272
DB	855	CCMAAATCATTTGGGATATATGAACACATGTGGAAATGATGAGCCCGGAACGAAAGATA	914
QY	273	AsnSerTyrAlaAsnPheArgAspGluValLeuProArgIleLysArgLeuGlyTyrAsn	292
DB	915	AACACATATATAACTTTAGSGATGAGTCTCTCCAGAAATMAAATACTGGATACAT	974
QY	293	AlaValGlnIleMetAlaIleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisVal	312
DB	975	GCAGTGCAATTAATGCGCAATCCAAAGACATCATATTATGGAAGCTTTGATATCCATGTA	1034
QY	313	ThrAsnPhePheAlaProSerSerArgPheGlyThrProGluAspLeuLysSerLeuIle	332
DB	1035	ACTAAATTTTTTGGCCAGAGTACGTTTGGTATCCCAAGAAAGATTGAAGTCTTTGATT	1094
QY	333	AspArgIaHisGluLeuGlyLeuLeuValLeuMetAspIleValHisSerHisSerSer	352
DB	1095	GATAGACACATGAGCTGTGGTTGCTGATGTTCTCATGATGAGTTCATATGATGATGCGTCA	1154
QY	353	AsnAsnThrLeuAspGlyLeuAsnGlyPheAspGlyThrAspThrHisTyrPheHisGly	372
DB	1155	AGTAATATCTCGTAGTGGTGAAGGTGTTGATGTACAGTAACATTAATCTTCAACGT	1214
QY	373	GlyProArgGlyHisHisIleTrpMetTrpAspSerArgLeuPheAsnTyrGlySerTrpGlu	392
DB	1215	GGTCCAGGTGCGCACACTGATGATGGGATTTCTGGCCTATTTAATCTAGGAACCTGGGA	1274
QY	393	ValLeuArgPheLeuLeuSerAsnAlaArgTrpTrpLeuGluGlyTyrLysPheAspGly	412
DB	1275	GTTTTTAAGATTCTCTCTCTCCAAAGCTATGATGTGGCTCGAGAAATTAAGTTGATGAGT	1334
QY	413	PheArgPheAspGlyValaThrSerMetMetTyrThrHisGlyLeuGlnMetThrPhe	432
DB	1335	TTCCGTTTGTATGGTGAACCTCCATGATGTACACTCATCCGGAATTTCAGATGAACATT	1394
QY	433	ThrGlyAsnTyrGlyGluTyrPheGlyPheAlaThrAspValAspAlaValaTyrLeu	452
DB	1395	ACGGGGAACCTCAAGGACTATTGTGGCTTGGCACCATGTAGATGAGTGGTTACTTGG	1454
QY	453	MetIeuValaAsnAspLeuIleHisGlyLeuHisProAspAlaValaSerIleGlyGluAsp	472
DB	1455	ATGCGGTAAATGATCTAATCATGACTGATTTATCTCGAGCGCTGAACCATGGTGAAGAT	1514
QY	473	ValSerGlyMetProThrPheCysIleProValProAspGlyGlyValaGlyPheAspTyr	492
DB	1515	GTTATGTGAATGCCCAATTTGCCCTCTCTGTTCACAGATGGTGGGGTATGATTGACAT	1574
QY	493	ArgLeuHisMetAlaValaAspLysTrpIleGluLeuLeuLysGlnSerAspGluSer	512
DB	1575	CGGATGCAATATGGCTGTGGCTGACAAATGATTCATCTCAAGCAAGTATGAACCT	1634

[illegible]

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FT      /+tag= c
XX      WO9814601-A1.
XX      09-APR-1998.
XX      30-SEP-1997, 97WO-US017555.
XX      PF      30-SEP-1996, 96US-0026855P.
XX      PR      (EXSE-) EXSEED GENETICS LLC.
XX      PA
XX      Keeling P, Guan H;
XX      WPI, 1998-240100/21.
XX      P-PSDB; AAMS6489.
XX      Hybrid polypeptide comprising starch-encapsulating region and protein -
PT      useful for, e.g. producing protein(s) resistant to degradation by stomach
PT      acids.
XX      Example 2, Page 44, 156pp; English.
XX      The sequence is that of the starch branching enzyme II gene. It can be
CC      used in the production of a hybrid polypeptide comprising a starch-
CC      encapsulating region (SER) fused to a payload protein. The hybrid
CC      polypeptide can be used to make modified starches comprising the payload
CC      protein, selected from, e.g. hormones, growth factors, antibodies,
CC      enzymes, dyes, immunoglobulins, etc. The modified starch can also be used
CC      to provide grain feeds enriched in amino acids. By encapsulating the
CC      payload protein in starch, it is more resistant to degradation by stomach
CC      acids.
XX      SQ      Sequence 2725 BP; 727 A; 534 C; 715 G; 749 T; 0 U; 0 Other;

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Alignment Scores:
Pred. No.:      8,09e-307      Length:      2725
Score:          3342.00      Matches:      608
Percent Similarity: 86.98%      Conservative: 67
Best Local Similarity: 78.35%      Mismatches: 79
Query Match:      80.16%      Indels:      22
DB:              Gaps:      4

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US-09-508-377-12 (1-768) x AAV29757 (1-2725)

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QY      4 PheAlaValSerGlyValAlaThrLeuGlyVal-----AlaArgProProAla 18
DB      193 TTCTTAACCTCGGGGTCGTCGAGTGTTCGGGGAGCGACGGGGCCATGCGCGGCG 252
QY      19 AlaAlaGlnProGluGluLeuGlnIleProGluAspIleGluGluGlnThrAlaGluVal 38
DB      253 GCGCGGGCGCAGAGGCGGTGATGCTTCGAGGGCGAGATGAT----- 297
QY      39 AsnMetThrGlyGlyThrAlaGluLysLeuGlnSerSerGlu----- 52
DB      298 -----GGCCTCCGATCAAGGCGTGACTCGGCTCAATTCACGTGAGTGAATG 345
QY      53 ProThrGlnGlyIleValGluThrIleThrAspGlyValThrLysGlyValLysGluLeu 72
DB      346 GAGGTACCAAGACATTTCTGAAGAACAACCTGCGGCT-----GGTGGGCTGATGCT 399
QY      73 ValValGlyGlyLysProArgValAlaProLysProGlyAspGlyGlnLysIleTyrGlu 92
DB      400 CAAGCCTTAACAACAGATTGAGTGGTCCCGCCCAACAAGCATGGAACAAAAATATTCAG 459
QY      93 IleAspProThrLeuLysAspPheArgSerHisLeuAspTyrArgTyrSerGluTyrArg 112
DB      460 ATTGACCCCATGTGTGCAAGGCTTAAGTACCATCTTGAGTATCGGTACAGCTCTATAGA 519
QY      113 ArgGlyLeuAlaAlaIleAspGlnHisGluGlyGlyLeuGluAlaPheSerArgGlyTyr 132
DB      520 AGATATCGTTCAACATTTGATGAACATGAAGAGGCTTGAAGGCTTCTCCCGATGAT 579

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QY      113 GluLysLeuGlyPheThrArgSerAlaGluGlyIleThrTyrArgGluTyrAlaProGly 152
DB      580 GAGAAGTTTGATTAATGCCAGCCGGAGAGGTATCATATGAGAAATGGCTCCCGA 639
QY      153 AlaHisSerAlaAlaLeuValGlyAspPheAsnAsnTyrAspProMetAlaAspThrMet 172
DB      640 GCATTTCTGCAGCATGTGTGGGTGACGTCAACAACATGGAGATCAATGACATCGTATG 699
QY      173 ThrArgAspAspTyrGlyValTyrGluIlePheLeuProAsnAsnAlaAspGlySerPro 192
DB      700 AGCAAAATGAGCTTGTGTGTGGGAAATTTTCTCCCTAACATGCAATGCGATGCACTCA 759
QY      193 AlaIleProHisGlySerArgValLysIleArgMetAspThrProSerGlyValLysAsp 212
DB      760 CCTATTCCTCATGATGATCTGTGTAAAGTGAGAAATGATATCTCATCAGGAGTAAAGAT 819
QY      213 SerIleSerAlaTyrIleLysPheSerValGlnAlaProGlyGluIleProPheAsnGly 232
DB      820 TCAATTCAGCCTGGATGATGATGACTGACAGGCCCGCCGAGAAATACCATATGATGGG 879
QY      233 IleTyrTyrAspProProGluGluGlnLysTyrValPheGlnHisProGlnProLysArg 252
DB      880 ATTTATTTATGATCCCTCCGAGAGAGTAAAGTATGTGTTCAAGCATCCGCACTTAAACGA 939
QY      253 ProGluSerLeuArgIleTyrGluSerHisIleGlyMetSerSerProGluProLysIle 272
DB      940 CCAAAATCATTTGCGGATATATGAACAACATGCGGATGATGATGACCCGGAACCGAAGATA 999
QY      273 AsnSerTyrAlaAsnPheArgAspGluValLeuProArgIleLysArgLeuGlyTyrAsn 292
DB      1000 AACCATATGTAAACTTTAAGGATGAAGTCCCTCCCAAGATTAATAAACTGGATCAAT 1059
QY      293 AlaValGlnIleMetAlaIleGlnGlnHisSerTyrTyrAlaSerPheGlyTyrHisVal 312
DB      1060 GCAGTGCAATATATGCAATTCACAGACATCATATTAATGAAAGCTTTGGATCCATGTA 1119
QY      313 ThrAsnPhePheAlaProSerSerArgPheGlyThrProGluAspLeuLysSerLeuIle 332
DB      1120 ACTAATTTTTTGGCCCAAGTATGCTGTTGGTACCCCAAGATTTGAAGTCTTGATTT 1179
QY      333 AspArgAlaHisGluLeuGlyLeuLeuValLeuMetAspIleValHisSerHisSerSer 352
DB      1180 GATAGAGCAGATGAGCTGTGTGCTAGTTCATGAGATGAGTGTATGATGCTAGTGGCTCA 1239
QY      353 AsnAsnThrLeuAspGlyLeuAsnGlyPheAspGlyThrAspThrHisTyrPheHisGly 372
DB      1240 AGTAATATCTCGATGAGGTGATGATGTTTGAATGATGATGATGATGATGATGATGAT 1299
QY      373 GlyProArgGlyHisHisTyrMetTyrAspSerArgLeuPheAsnTyrGlySerTyrGlu 392
DB      1300 GGTCCAGCATGCGACATCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1359
QY      393 ValLeuArgPheLeuLeuSerAsnAlaArgTyrTyrPheGluGlnLysTyrPheAspGly 412
DB      1360 GTTTAAAGATTTCTCTCTCCATGATGATGATGATGATGATGATGATGATGATGATGAT 1419
QY      413 PheArgPheAspGlyValThrSerSerMetTyrThrHisHisGlyLeuGlnMetThrPhe 432
DB      1420 TTCCGTTTGTATGGGTGATACCTCCATGATGATGATGATGATGATGATGATGATGAT 1479
QY      433 ThrGlyAsnTyrGlyGluTyrPheGlyPheAlaThrAspValAspAlaValLysLeu 452
DB      1480 ACGGGGAACTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1539
QY      453 MetLeuValAsnAspLeuIleHisGlyLeuHisProAspAlaValSerIleGlyLysAsp 472
DB      1540 ATGCTGGTAAATGATCATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1599
QY      473 ValSerGlyMetProThrPheCysIleProValProAspGlyGlyValGlyPheAspTyr 492
DB      1600 GTTAGTGAATGCCATGATTTGGCTTCTGTTCAAGATGGTGGGTAGTTTGAATAT 1659

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Db      1660 CGGATGCATATGGCTGTGGCTGACAAATGGATTGACCTTCTCAAGCAAGTATGAACT 1719
Qy      513 TTPlysmetGlyAspIleValHisThrLeuThrAspArgTrpLeuGluysCysVal 532
Db      1720 TGGAGAGTGGGTGATGATGTGCACACTGACAAATAGAGGTGTGTAGAGAAAGTGTGA 1779
Qy      533 ThrTyralaGluSerHisAspGlnAlaLeuValGlyAspLysThrIleAlaThrPleu 552
Db      1780 ACTTATGCTGAAGACATGATCAACCATTTAGTCGGCGAACAACATTTGCGTTTGCTTG 1839
Qy      553 MetAspLysAspMetTyrAspPheMetAlaLeuAspArgProSerThrProArgIleAsp 572
Db      1840 ATGCAAGAGATATGATGATTCATGGCCCTCGATGACCTTCAACTCCATTCATTCAT 1899
Qy      573 ArgGlyIleAlaLeuHisLysMetIleArgLeuValThrMetGlyLeuGlyGlyGly 592
Db      1900 CGTGGATAGCATTCATTAAGATGATTTGACTTATCACTTATCAATGGCTTTAGAGAGGAG 1959
Qy      593 TyrLeuAspPheMetGlyAsnGluPheGlyHisProGluTrpIleAspPheProArgGly 612
Db      1960 TATCTTATTTTCATGGAAATGATGATTTGGACATCTCGAATGATGATTTTCCAAAGAG 2019
Qy      613 ProGlnThrLeuProThrGlyLysValLeuProGlyAsnAspAsnSerTyrAspLysCys 632
Db      2020 CCGCAAGACTTCCAAAGTGTAGTTTATTCAGGGAATTAACAACAGTTATGCAATGT 2079
Qy      633 ArgArgAspPheAspLeuGlyAspAlaAspPheLeuArgTyrHisGlyMetGlnGluPhe 652
Db      2080 CGTCAAAATTTGACTGGGTGATGACATCTTATGATCATGCTTATTCAGAGGCTT 2139
Qy      653 AspGlnAlaMetGlnHisLeuGluGluLysTyrGlyPheMetThrSerGlnHisGlnTyr 672
Db      2140 GATCAGCGCAATGCAATCATCTTGAGCAAAATATGATTCATGACATCTGATCCAGAT 2199
Qy      673 ValSerArgLysHisGluGluAspLysValIleIlePheGluArgGlyAspLeuValPhe 692
Db      2200 ATTTCCCGGAACAATGAGAGATTAAGATGTTTGTGAAAAGGAGATTTGGATTT 2259
Qy      693 ValPheAspPheHisThrSerAsnSerPheAspTyrArgValGlyCysSerArgPro 712
Db      2260 GTGTTCACTTCCACTGCAACAACACTTTTGTGACTACCGATTTGTTGCAAAAGCT 2319
Qy      713 GlyLysTyrLysValAlaLeuAspSerAspAlaLeuPheGlyGlyPheSerArgLeu 732
Db      2320 GGGGTGTAAAGTGATGCTTGGACTCCGACGCTGACTATTGTTGATTTAGACAGATC 2379
Qy      733 AspHisAspValAspTyrPheThrThrGluHisProHisAspAsnArgProAspSerPhe 752
Db      2380 CATCAACGACCGCACACTTCCCGGCACTGTTCGATGATTAATGGCCATATTCATT 2439
Qy      753 SerValTyrThrProSerArgThrAlaValIleTyrAlaLeuThrGlu 768
Db      2440 TCGGTTTATACCAAGACGAACATGTGTCTATGCTCCAGTGAG 2487

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RESULT 8
AAT69729
ID AAT69729 standard; DNA; 2665 BP.
XX
AC AAT69729;
XX
DT 10-SEP-1997 (first entry)
XX
DE Plasmid pBE240 insert encoding corn starch branching enzyme IIb.
XX
KM Starch branching enzyme IIb, SBEIIb; corn, maize; antisense; amylopectin;
transgenic plant; pBE240; ss.
XX
OS Zea mays.
XX
Key Location/Qualifiers
FH 79..2478
FT CDS /tag= a

```

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XX      MO9722703-A2.
PN      26-JUN-1997.
XX      12-DEC-1996; 96MO-US019678.
XX      20-DEC-1995; 95US-0009113P.
XX      (DUPO) DU PONT DE NEMOURS & CO E. I.
PI      Hubbard NL, Klein TM, Broglie KE;
XX      WPI; 1997-341694/31.
XX      P-PSDB; AAW19212.
DR      Transgenic corn in which grain derived starch fine structure is
PT      controlled - specifically branch chain distribution of amylopectin,
PT      useful in preparation of chickened foodstuff.
XX      Example 1; Page 50-53; 92pp; English.
XX      A cDNA insert (AAT69729) in plasmid clone pBE240 comprises a 2.7 kb EcoRI
CC      -XhoI fragment isolated from a corn cDNA library. It includes an open
CC      reading frame encoding starch branching enzyme IIb (SBEIIb) (AAW19212).
CC      The insert was used as a starting point in the assembly of DNA constructs
CC      (see also AAT69730, AAT69736-37) designed to achieve suppression of
CC      SBEIIb expression in transgenic corn plants, and thereby to produce novel
CC      starches that have properties beneficial in food and industrial
XX      applications
XX      SQ Sequence 2665 BP; 700 A; 525 C; 705 G; 735 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 9,766-307 Length: 2665
Score: 3341.00 Matches: 608
Percent Similarity: 86.98% Conservative: 67
Best Local Similarity: 78.35% Mismatches: 79
Query Match: 80.14% Indels: 22
DB: Gaps: 4
US-09-508-377-12 (1-768) x AAT69729 (1-2665)
Qy      4 PheAlaValSerGlyAlaThrLeuGlyVal-----AlaArgProProAla 18
Db      181 TTCTTAACCTGGGGTGTCTCGAGTTGATGTTCCGGGAGCAACGGGCGCATGCGCGGG 240
Qy      19 AlaAlaGlnProGluGluGlnIleProGluAspIleGluGluGlnThrAlaGluVal 38
Db      241 GCGCGCGCCAGGAAGCGGTATGTCTCTCAAGGCGCAATGAT----- 285
Qy      39 AsnMetThrGlyGlyThrAlaGluLysLeuGluSerGlu----- 52
Db      286 -----GGCTCGATCAAGGCGTCACTCGCTCAATTCAGTCGATGAAC 333
Qy      53 ProThrGlnGlyIleValGluThrIleThrAspGlyValThrLysGlyValLysGluLeu 72
Db      334 GAGGTACCAAGCATTTCTGAAGAGACAACGTCGCTGCT-----GGTGTGCTATGCT 387
Qy      73 ValValGlyGluLysProArgValValProLysProGlyAspGlyGlnLysIleTyrGlu 92
Db      388 CAAGCCTTGAACAGAGTTCAGTGTGCTCCGCCCAACCAACGATGACAAATATTCGCG 447
Qy      93 IleAspProThrLeuLysAspPheArgSerHisLeuAspTyrArgTyrSerGluTyrArg 112
Db      448 ATTAACCCCATGTGCAAGGCTATTAAGTACCATCTTGTAGTACGCTCTATAGA 507
Qy      113 ArgIleArgAlaAlaIleAspGlnHisGluGluGlyLysGluAlaPheSerArgGlyTyr 132
Db      508 AGATCCGTTCAAGCATGTGATGAACATGAAGAGGCTTGAAGCCTTCCCGTGTAT 567
Qy      133 GluLysLeuGlyPheThrArgSerAlaGluGlyIleThrTyrArgGluTyrAlaProGly 152

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Db 568 GAGAACTTGGATTAAATCCAGCCGGAAGGATACATATCGAATAGGGCTCCCTGGA 627
 Qy 153 AAlhSeraIaAlaLeuValGlyAaPheAsnAsnTyrAsnProAsnAlaAspThrMet 172
 Db 628 GCATTTTCGAGCAGCATGTTGGTGTGATCTTCACACATCGGGATCCAAATGACAGATCGATG 687
 Qy 173 ThraGAspAspTyrGlyValTyrGluIlePheLeuProAsnAlaAspGlySerPro 192
 Db 688 AGCAAAATAGAGTTGGTGTGGGAAATTTTCTGCTTAACATGACATGAGATGGATCA 747
 Qy 193 AlaIleProHisGlySerArgValLysIleArgMetAspThrProSerGlyValLysAsp 212
 Db 748 CCTATTCCTCCAGGATCTGTGTAAAGGTGAGATGATCTCCATCAGGAGATTAAGAT 807
 Qy 213 SerIleSerAlaTyrIleLysPheSerValGlnAlaProGlyGluIleProPheAsnGly 232
 Db 808 TCAATTCAGCCTCGATCAAGTACTCAGTGCAGGCCCAAGAAATACCATATGATGGG 867
 Qy 233 IleTyrTyrAspProProGluGluGlyLysTyrValPheGlnHisProGluInProLysArg 252
 Db 868 ATTATATGATCCCTCGTGAAGAGGTAAAGTATGTGTTCCAGCATGCGCAACCTAAACGA 927
 Qy 253 ProGluSerLeuArgIleTyrGluSerHisIleGlyMetSerSerProGluProLysIle 272
 Db 928 CCAAAATCATGGGATATATGAACACATGTCGAAATGAGTACCCGGAACCGAAGATA 987
 Qy 273 AsnSerTyrAlaAsnPheArgAspGluValLeuProArgIleLysArgLeuGlyTyrAsn 292
 Db 988 AACACATAGTAACTTTAGGATGAGTACTCCCAAGATTAATAAACTTGGATACAT 1047
 Qy 293 AlaValGlnIleLeuValIleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisVal 312
 Db 1048 GCAGTCAATATATGCAATCCAAAGACACTCATATATGAAAGCTTGGATACCATGTA 1107
 Qy 313 ThrAsnPhePheAlaProSerSerArgPheGlyThrProGluAspLeuLysSerLeuIle 332
 Db 1108 ACTAAATTTTTTGGCCCAATAGTCGTTTGGTACCCCAAGAAATTTGAACTTTGATTT 1167
 Qy 333 AspArgAlaHisIleGluLeuGlyLeuLeuValLeuMetAspIleValHisSerHisSerSer 352
 Db 1168 GATAGAGCACAATAGCTGGTTTGTCTAGTCTCATGATGTGCTTCAATGACAGCCGCA 1227
 Qy 353 AsnAsnThrLeuAspGlyLeuAsnGlyPheAspGlyThrAspThrHisTyrPheHisGly 372
 Db 1228 AGTAATATCTGTGATGGTGTGAATGTTTGTGATGTGATGATACATTAATCTTACACGT 1287
 Qy 373 GlyProArgGlyHisHisTyrMetTyrAspSerArgLeuPheAsnTyrGlySerTyrGlu 392
 Db 1288 GGTCCACGTGGCCATCCTGATGTGGATTCGACCTATTTAATGATGGAACTGGGAA 1347
 Qy 393 ValLeuArgPheLeuLeuSerAsnAlaArgTyrTyrLeuGluGluGlyPheAspGly 412
 Db 1348 GTTTTAAGATTTCTTCTCTCCATGCTAGATGTGGCTCGAGAAATATAAGTTTATGCT 1407
 Qy 413 PheArgPheAspGlyValHisSerMetMetTyrThrHisIleGlyLeuGlnMetThrPhe 432
 Db 1408 TTCCTGTTTGTGATGGTGCACCTCCATGATGTACATCCACCGGATTTCAAGTACATTT 1467
 Qy 433 ThrGlyAsnTyrGlyGluTyrPheGlyPheAlaThrAspValAspAlaValValTyrLeu 452
 Db 1468 ACCGGGAACCTCAATGAGTATTTTGGCTTGGCACCGAATGAGATGAGTGGTTTAACTTG 1527
 Qy 453 MetLeuValAsnAspLeuIleHisIleGlyLeuHisProAspAlaValSerIleGlyGluAsp 472
 Db 1528 ATGCTGTGAATGATCTTAATTCATGAGATTTAATCTGAGGCTGTAACCATTTGCTGAAGAT 1587
 Qy 473 ValSerGlyMetProThrPheCysIleProValProAspGlyGlyValGlyPheAspTyr 492
 Db 1588 GTTAGTGAATGAGCTTACATTTGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1647
 Qy 493 ArgLeuHisMetAlaValAlaAspLysTyrIleGluLeuLeuLysGlnSerAspGluSer 512
 Db 1648 CGGATGATATGCTGTGGCTGACAAATGAGATTTGACTTTCTCAAGCAAACTGATGAACCT 1707

Qy 513 TrrPlyMetGlyAspIleValHisThrLeuThrAsnArgArgTrrPleuGluLysCysVal 532
 Db 1708 TGGAAAGATGGGTGATATTTGTGCACACATGACAAATAGAGGTGTTTAAAGAAATGTGTA 1767
 Qy 533 ThrTyrAlaGluSerHisAspGlnAlaLeuValGlyAspLysThrIleAlaPheTrrPleu 552
 Db 1768 ACTTATGCTGAAGTCAATGATCAAGCATTAATGTCGCGACAGACATTAATGCGTTTGTGTTG 1827
 Qy 553 MetAspLysAspMetTyrAspPheMetAlaLeuAspArgProSerThrProArgIleAsp 572
 Db 1828 ATGACAAAGATATGATGATTTTCAATGACCTCGATGATGACCTTCAACTCCATGATGAT 1887
 Qy 573 ArgGlyIleAlaLeuHisIleLysMetIleArgLeuValThrMetGlyLeuGluGlyGlu 592
 Db 1888 CGTGGGATGACATTAATGAATGATTAATGATTAATCAATGAGTTTAAAGAGAGAGGCG 1947
 Qy 593 TyrLeuAsnPheMetGlyAsnGluPheGlyHisProGluTrrIleAspPheProArgGly 612
 Db 1948 TATCTTAATTTCAATGAGAAATGAGTTTGGACATCTCGAATGATGATTTTCCAAAGAGT 2007
 Qy 613 ProGlnThrLeuProThrGlyLysValLeuProGlyAsnAsnAsnSerTyrAspLysCys 632
 Db 2008 CCGCAAGACTTCCAAAGTGTAAATTTTCCAGGGAATTAACAACGTTATATGACAAATGT 2067
 Qy 633 ArgArgArgPheAspLeuGlyAspAlaAspPheLeuArgTyrHisGlyMetGlnGluPhe 652
 Db 2068 CGTGGAAATTTGACCTGGGTGATGACAGCTATCTTAGATATCATGATATGCAAGACTTT 2127
 Qy 653 AspGlnAlaMetGlnHisLeuGluGluGluLysValIleIlePheGluArgGlyAspLeuValPhe 672
 Db 2128 GATCAGGAAATGCAACATCTTGAAGCAAAATATGATTCATGACATCTGATCAACGATAT 2187
 Qy 673 ValSerArgLysHisIleGluGluAspLysValIleIlePheGluArgGlyAspLeuValPhe 692
 Db 2188 ATTTCCCGGAAACATGAGGAGATTAAGTATTTGTTCCGAAAGGAGATTTGGTATTT 2247
 Qy 693 ValPheAsnPheHisTrrPserAsnSerPhePheAspTyrArgValGlyCysSerArgPro 712
 Db 2248 GTGTTCACCTTCCACTGCAACAACAGCTAATTTGATCCGATATGTTGTTTCGAAAGCTT 2307
 Qy 713 GlyLysTyrLysValAlaLeuAspSerAspAlaLeuPheGlyGlyPheSerArgLeu 732
 Db 2308 GGGGTGTATAGGTGCTTGTGACTCCGACGCTGACATTTTGTGGATTTAGCAGGATC 2367
 Qy 733 AspHisAspValAspTyrPheThrThrGluHisProHisAspAsnArgProArgSerPhe 752
 Db 2368 CATCAACGACCGAGACTTACCGCGGCACTGTCGATGATATAGGCCATATATTCATCC 2427
 Qy 753 SerValTyrThrProSerArgThrAlaValValTyrAlaLeuThrGlu 768
 Db 2428 TCGGTTTATACCAAGCAAGACATGTGTGTATGCTCCAGTGAG 2475

RESULT 9
 ADA71289
 ID ADA71289 standard, DNA: 2655 BP.
 AC ADA71289;
 XX
 XX 20-NOV-2003 (first entry)
 DE
 XX Rice gene, SEQ ID 4612.
 XX
 XX Plant; bacterial infection; fungal infection; viral infection; rice;
 XX gene; de.
 OS
 XX Oryza sativa.
 XX
 XX WO2003000898-A1.
 XX
 XX 03-JAN-2003.
 PD
 XX 22-JUN-2001; 2001WO-18001105.

```

XX 22-JUN-2001, 2001WO-IB001105.
XX
XX (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
XX Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
XX Katsagiri F, Quan S, Tao Y, Whitcham S, Xie Z, Zhu T, Zou G;
XX
XX WPI; 2003-175290/17.
XX
XX Identifying at least one gene involved in plant resistance or response to
XX pathogenic infection for conferring resistance or tolerance to a plant to
XX bacterial, fungal or viral infection by determining or detecting plant
XX gene expression.
XX
XX Claim 6; SEQ ID NO 4612; 899bp; English.
XX
XX The present invention relates to a method (M1) for identifying genes
XX involved in plant resistance or response to pathogenic infection. M1
XX comprises identifying a gene whose expression is significantly altered in
XX the incompatible interaction of plant gene expression relative to
XX expression of the gene in an uninfected plant, in a mutant plant that
XX does not express a gene associated with response to pathogenic infection,
XX or in a corresponding incompatible or compatible interaction. (M1) is
XX useful for conferring resistance to resistance or tolerance to a plant to
XX bacterial, fungal or viral infection. The present sequence was used to
XX illustrate the invention.
XX
XX Sequence 2655 BP; 714 A; 529 C; 680 G; 732 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 2,096-306 Length: 2655
XX Score: 3337.50 Matches: 646
XX Percent Similarity: 77.09% Conservative: 44
XX Best Local Similarity: 72.18% Mismatches: 68
XX Query Match: 80.06% Indels: 139
XX DB: Gaps: 8
XX
US-09-508-377-12 (1-768) x ADA71289 (1-2655)
QY 1 MetAlaThrPheAlaValSerGlyAlaThrLeuGlyValAlaArgPro-----16
Db 1 ATGGCGTCGTTGCGCGGTCCGGCGGAGGCTCGGGGTGCGGGGGGGGGCGGCGGCG 60
QY 17 -----ProAlaAla-----19
Db 61 GGCGCGCGCGCGGGGTGGCGCGCGCGCGATCCCGCGGGGTGAGATTGCCGTGGTG 120
QY 19 -----19
Db 121 CTCTTCAGAGAGAGAGACTCTCTTCTCACTGCGGCTTGTAGCTGCGGGGTCTCTGGG 180
QY 19 -----19
Db 191 AAGGTGCTGTGCTGCGGTGGGAGAGAGAGACTTGTGCTCTCTGCGGAGACAGAGTG 240
QY 20 -----AlaGlnProGluGluLeuGlnIleProGluAspIleGluGluGlnThrAla 36
Db 241 GAAACTCAAGAGAGAACTGAGAGATCTGAGATACCTGATGATATATATATATATATATAT 300
QY 37 GValAlaMetThrGlyThrAlaGluLeuGluSerSerGluProThrGlnGly 56
Db 301 GAGAGAGAGAGAGAGAAATTCACAGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
QY 57 ILeValGluThrIleThrAspGlyValThrLeuGlyValIleGluLeuValIleGlyGlu 76
Db 361 ATTGAGGAGAAATGATGATGAGGCTGATCAAGATGATGATGATGATGATGATGATGAT 420
QY 77 LysProIleValValProIleProGlyAspGlyGlnIleValIleValIleValIleVal 96
Db 421 AAACCAAGGATATCCACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
QY 97 LeuIleValAspPheArgSerHisLeuAspIleValIleValIleValIleValIleVal 107

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Db 481 CTGAGAGAGATTTGGAGAACCATCTTGACTACCGCAAAATTAATTCGATATCTGGCCTTT 540
QY 108 -----TyrSerGluTyrArgGlyIleArgAlaIle 117
Db 541 TGTGGGAAACCTACTCTGTAACTTGATATATCTTT-TTGGTAAATTAATTAATTCGCA 599
QY 118 Ile-----AspGlnHisGluGly 124
Db 600 TTACTACAGAAATGCTCAATATTTACTTGATATCAATATCAATATCAATATCAATATCAT 659
QY 125 LeuGluAlaPheSerArgGlyTyrGluLeuGluIlePheThrArgSerAlaGluGlyIle 144
Db 660 TATTCGCTCTTCC-----AGCGTGAAGGCATT 689
QY 145 ThrTyrArgGlu-TTAlaProGlyAlaHisSerAlaAlaLeuValGlyAspPheAsnAs 164
Db 690 ACCTACCGAGAAATGGGCACCTGGAGACAGCTGCGAGCATTAAGTGAAGTCACTTCAACA 749
QY 164 nTProAsnProAsnAlaAspThrMetThrArgAspAspTyrGlyValTPGluIlePheIe 184
Db 750 TTGGAACCCAAATGCAATACTATGACAGAAATGAGATGCTTTGGAGATTTCCT 809
QY 184 uProAsnAsnAlaAspGlySerProAlaIleProHisGlySerArgValIleArgGlye 204
Db 810 GCCTTAACATGCTGATGATGATCCCTGCTATCTCATGCTCAAGTGAAGATTGCGAT 869
QY 204 tAspThrProSerGlyValIleAspSerIleSerAlaThrIleLeuPheSerValGlnAla 224
Db 870 GATATACCAATCTGGCGGTAAAGATTCAATTCCTGCTGAATTAAGTTGCTGTCAGAGC 929
QY 224 aProGlyGluIleProPheAsnGlyIle-----TyrTyrAspProProGlu 239
Db 930 TCCAGGTAATATCCGATACCAAGGATAT-TTCCATTTTAACCTTATTTTCCATTCCTTA 988
QY 239 u-----GluIleValTyrValPheGlnHisPro-GlnProIleArgP 253
Db 989 TGTTGTTATACGCACTGACGAGAAATATATGATTCACACATCCTCAACCTTAACGAC 1048
QY 253 roGluSerLeuArgIleTyrGluSerHisIleGlyMetSerSerProGluProIleAla 273
Db 1049 CAATTCGCTGGGATATGATGATCAATATGATGATAGTACCCGAGACCAAGATTA 1108
QY 273 snSerTyrAlaAsnPheArgAspGluValLeuProArgIleLysArgLeuGlyTyrAsn 293
Db 1109 ACATATATGCTAATTTTGGATAGGTGCTACCAAGAAATTAAGATTCGTTGATCAAG 1168
QY 293 lValGlnIleMetAlaIleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValT 313
Db 1169 CTGTACAGATATATGCAATCCAGAGACACTTTATTAAGCAAGCTTTGGGTATCATGTA 1228
QY 313 hPheAsnPheAlaProSerSerArgPheGlyThrProGluAspLeuLysSerLeuIleA 333
Db 1229 CTAACTTCTTGGCCCAAGTACCGCTTTCGGAACCCAGAGAACTGAATCTTGATTTG 1288
QY 333 sPAsnAlaHisGluLeuGlyLeuLeuValLeuMetAspIleValHisSerHisSerSerA 353
Db 1289 ATTAAGCTACAGAGCTTGTTGCTGTGATCTATGATGATGATGATGATGATGATGATGAT 1348
QY 353 snAsnThrLeuAspGlyLeuAsnGlyPheAspGlyThrAspThrHisTyrPheHisGlyG 373
Db 1349 ACAATACCCCTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1408
QY 373 lYProArgGlyHisHisSerMetThrAspSerArgLeuPheAsnTyrGlySerTyrGly 393
Db 1409 GACCAAGGAGGATCACTGAGATGAGGATCTTCGCTGTTCAACATGAGAGAGAGAGAG 1468
QY 393 alleuArgPheLeuLeuSerAsnAlaArgTyrTyrLeuGluGluTyrIleValPheAspGly 413
Db 1469 TTTTAAGTATTTATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1528
QY 413 hArgPheAspGlyValThrSerMetTyrThrHisHisGlyLeuGlnMetThrPheT 433

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Db 1529 TTGATTTGATGGGTGACCTCCATGATGTAATCTCATCTCATGTTTACAGGTGGCAATT 1588
QY 433 hgclyAsnTyrGlyGluTyrPheGlyPheAlaThrAspValAspAlaValAlaTyrLeuM 453
Db 1589 CTGGCACTATGGCGAATATTTTGGATTGCTCTACTGATGTTGATGCGATGCTTACTTGA 1648
QY 433 ctleuValasnAspLeuIleHisGlyLeuHisProAspAlaValSerIleGlyGluAspV 473
Db 1649 TCGTGTGCAACGATCTAATTCATGAGCTTATCTCTGAGCGCTGATGACCATTTGGTAAGATG 1708
QY 473 aISerGlyMetProThrPheCysIleProValProAspGlyValGlyPheAspTyrA 493
Db 1709 TCAGCGGAGATGCCACATTTTGTATTCCTGTTCAGATGGTGGTGGTGGTGGTGGTGGTATC 1768
QY 493 tglLeuHisMetAlaValAlaAspLysTrpIleGluLeuLeuLysGlnSerAspGluSerT 513
Db 1769 GTTTGATATGGCTGTACCGGACAAATGATCGAATCTCTCAAGCAAAAGTACGAATATTT 1828
QY 513 tPLysMetGlyAspIleValHisThrLeuThrAsnArgArgTrpLeuGluLysCysValT 533
Db 1829 GCAAAATGGGTGATATCGTGACACACCTTAAGATAGAGTGGTGCAGAGAAGTGTGTTA 1888
QY 533 hTTrAlaGluSerHisAspGlnAlaLeuValGlyAspLysTrpIleAlaPheTrpLeuM 553
Db 1889 CTTATGCAAAAGTCAATGACCAAGCACTAGTGGTGCACAAAGCTATTGCAATTCGTGTTGA 1948
QY 553 eTAspLys----- 555
Db 1949 TGGATTAAGTAAATCATTTGTAGTTCACAAATCGACCGGATATCTCAATCTTTCATGTC 2008
QY 556 --AspMetTyrAspPheMetAlaLeuAspArgProSerThrProArgIleAspArgGlyT 575
Db 2009 AGGATATGATGATTTTATGCTGCTAGACAGACCTTCAACACTCGCATGATGCTGGGA 2068
QY 575 leAlaLeuHisLysMetIleHisGlyLeuValThMetGlyLeuGlyGlyGlyTyrIleuA 595
Db 2069 TAGCATTAATATAAAAGATTAGGCTTGTCACCATGGCTTAGAGAGGGAGGCTATCTTA 2128
QY 595 snPheMetGlyAsnGluPheGlyHisProGluTrpIleAspPheProArgGlyProGlnT 615
Db 2129 ATTTTCATGGAATATGATTTGGGCATCTCGAATGATAGTATGATTTCCCAAGGCCCGAAA 2188
QY 615 hIleuProThrGlyLysValIleuProGlyAsnAsnAsnSerTyrAspLysCysArgArg 635
Db 2189 GCTTCCCAATAGGCTGCTGCTCCCAAGAAACAATACATGATTGATTAATGCGCTGCTGA 2248
QY 635 tGPheAspLeuGlyAspAlaAspPheLeuArgTyrHisGlyMetGlnGluPheAspGlnA 655
Db 2249 GATTTCACCTTGGAGATGACGATTAATCTTAGATATCATGATATGACAGAGTTGATAGG 2308
QY 655 lAmetGlnHisLeuGluGluLysTyrGlyPheMetThrSerGlnHisGlnTyrValSerA 675
Db 2309 CCAATGACGATCTTGGAGAAATAATGATTCATGACATCTGAGCACCAAGTATATATATGCG 2368
QY 675 tglLysHisGluGluAspLysValIleIlePheGluArgGlyAspLeuValPheValPheA 695
Db 2369 GCAAAACACAGAGAGATTAAGTATCATCTTCAGAGAGAGAGATTTGGTATTCGCTGTTCA 2428
QY 695 snPheHisTrpSerAsnSerPhePheAspTyrArgValGlyCysSerArgProGlyLysT 715
Db 2429 ACTTCACACGAGTAAATACATTTTGCATATGCGCGGTGTTTAAACCTCGGAAGAT 2488
QY 715 yLysValAlaLeuAspSerAspAspAlaLeuPheGlyGlyPheSerArgLeuAspHisA 735
Db 2489 ACAAAGATGTGTGGCTACAGACGATGGCTCTTTGGTGAATTCAGTCGGCTTGATCATG 2548
QY 735 sPValAspTyrPheThrGlnHisProHisAspAsnArgProArgSerPheSerValT 755
Db 2549 ATGCTGAGACTTCACTGCTGACCTGGCGGATGACAAACAGACCATGTTCAATTCGCGTGT 2608
QY 755 yTThrProSerArgThrAlaValAlaValTyrAlaLeuThrGlnI 768
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RESULT 10
AAV38720
ID AAV38720 standard; DNA; 3090 BP.
XX
XX
AC AAV38720;
XX
XX 21-SEP-1998 (first entry)
DE Full length cassava tuber cDNA in pS1146.
XX
XX Starch branching enzyme; SBE; cassava; ss.
XX
XX Manihot esculenta.
OS
FH Key Location/Qualifiers
FT misc_feature 35..2760
FT /tag= a
FT /note= "these nucleotides are SBE II sequence, the
FT remainder are derived from the plasmid"
FT CDS 131..2677
FT /*tag= b
FT /product= "SBE II"
XX
XX W09820145-A2.
XX
XX 14-MAY-1998.
XX
XX 04-NOV-1997; 97WO-GB003032.
XX
XX 05-NOV-1996; 96GB-00023095.
XX
XX (NATTT ) NAT STARCH & CHEM INVESTMENT HOLDING COR.
XX
XX Jobling SA, Safford R;
XX
XX WPI; 1998-286958/25.
XX
XX P-PSDB; AAM62600.
XX
XX Starch branching gene from cassava - useful for producing altered plants
XX giving modified starch.
XX
XX Claim 2; Fig 13; 67pp; English.
XX
XX
XX The present sequence encodes starch branching enzyme (SBE) II. It was
XX isolated from cassava tubers. The products can be used for producing
XX plants having altered starch quantities and qualities. They can also be
XX used for producing altered plants such as cassava, banana, potato, pea,
XX tomato, maize, wheat, barley, oat, sweet potato and rice plants
XX
XX
SQ Sequence 3090 BP; 877 A; 578 C; 721 G; 914 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 5.4e-302 Length: 3090
Score: 3292.00 Matches: 595
Percent Similarity: 86.49% Conservative: 71
Best Local Similarity: 77.27% Mismatches: 72
Query Match: 78.96% Indels: 32
DB: Gaps: 4
US-09-508-377-12 (1-768) x AAV38720 (1-3090)
QY 23 GluGluLeuGlnIleProGluAsp-----IleGluGlnThrAlaGluVal 38
Db 332 GAGAAAGGCTCTTGTTCCTGATGATCAGATGATGATGCTCTTCTTCAACATATCAATT 391
QY 39 AsnMetThrGly-----GlyThrAlaGluLysLeu--- 48
Db 392 GAAACCACTGGCACAGTTTGGAGAGATCCAGATTCTTGTGATGACAGAGTCTTGTG 451
QY 49 -----GlySerSerGluProThrGlnGlyIleVal 58
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QY 59 GIUThrlleThrAspGlyValThrIysGlyValIysGluLeuValValIglIuIysPro 78
Db 512 GAGACAAATTAGCATGGAAAAAGTGA-----TCTAAACCA 547
QY 79 ArgValValProIysProGlyAspGlyGlnIleTyrgluIleAspProThrIeulys 98
Db 548 AGGTCATCTCCCTCCACCTCGCAGTGGGCGAGAAATATGACATAGATCCAGCTTGGA 607
QY 99 AspheIysSerHisLeuAspTyrArgTyrSerGluTyrArgArgIleArgAlaIle 118
Db 608 GGTTCCGTCAGACATCTTACTACCATCTTCACAGTACCAAAAGCTGCGTAGAGAAATT 667
QY 119 AspGlnHisGluIglIyLeuGluAlaPheSerArgIleTyrgluIleuIysLeuIysPheThr 138
Db 668 GACAAGTATGAAAGTGGTGGTGGATGCTCTCTCGGATTTGAAAAGTTGGTTCTTA 727
QY 139 ArgSerAlaGluIglIyLeuThrTyrArgIleTyrAlaProGlyAlaHisSerAlaIleu 158
Db 728 CGCAGTGAACACGAAATACTTATAGGGAATGGGCCTGAGCTACGCGGCTGCACCT 787
QY 159 ValGlyAspPheAsnThrPheAsnProAsnAlaAspThrMetThrArgAspAspTyrGly 178
Db 788 ATTGAGATTTCAACATGGAACTCTAATGCAAGATGTCATACCTCGGATAGATTGGT 847
QY 179 ValTyrGluIlePheLeuProAsnAsnAlaAspGlySerProAlaIleProHisGlySer 198
Db 848 GTCTGGAGATTTTGTGGCAATAACGAGATGGTTCACCAACATCTCTAGTTT 907
QY 199 ArgValIleIleArgMetAspThrProSerGlyValIysAspSerIleSerAlaTyrIle 218
Db 908 CGAGTAAAGATCGCATGATGATCTCCATCTGCACCAAAAGATTCAATCTCTGAGATC 967
QY 219 LysPheSerValGlnAlaProGlyGluIleProPheAsnGlyIleTyrgluIleAspPro 238
Db 968 AAGTTCTCAGTTCAAGCCTGCTGTAAATCCATACATGCAATATCTATGATCCACA 1027
QY 239 GluIglIuIysTyrValPheGlnHisProGlnIleProIysArgProGlnSerLeuArgIle 258
Db 1028 AAGGAGGAGAAATGATGTCTCAACATCTCTCAGCAAAAGACCAAAATCACTTAGATT 1087
QY 259 TyrGlnSerHisIleGlyMetSerSerProGluProIysIleAsnSerTyrIleAsnPro 278
Db 1088 TATGATCTCATGTGGAGATGATGATGAGCCAAATATTAACACATATCCCACTT 1147
QY 279 ArgAspGluValLeuProArgIleIysArgLeuGlyIleTyrAsnAlaValGlnIleMetAla 298
Db 1148 AGAGATGATATCTCTCTCGCATCAAAAAGCTTGCGTCAATGCTGTCAGATCAGGT 1207
QY 299 IleGlnGluHisSerTyrTyrAlaSerPheGlyIleTyrHisValThrAsnPheAsnPro 318
Db 1208 ATTCAAAGACATTTCTATATGCTAGTTTGGTACCAATGTCACAAACTTTTTCACCT 1267
QY 319 SerSerArgPheGlyThrProGluAspLeuIysSerLeuIleAspArgAlaHisGluLeu 338
Db 1268 AGCAGCCGATTTGGAACCTCGATGATTTGAAGTCTTTATATGATTAAGCTCATAGTTA 1327
QY 339 GlyLeuLeuValLeuMetAspIleValHisSerHisSerSerAsnAsnThrLeuAspGly 358
Db 1328 GGGCGCTGTGTTCTCATGATATTGTTCTATGCTCAATGCTCAATAATAATGCTGATGGG 1387
QY 359 LeuAsnGlyPheAspGlyThrAspThrHisTyrPheHisGlyIleProArgGlyHisHis 378
Db 1388 CTGAACATCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1447
QY 379 TyrMetTyrAspSerArgLeuPheAsnTyrGlySerTyrGluValLeuArgPheLeuLeu 398
Db 1448 TGGTGTGGAGCTCTCGCTTTTCAACTATGAGAGCTGGAGAGCTTAAGATTCTTCTT 1507
QY 399 SerAsnAlaArgTyrTyrLeuGluIglIuIysPheAspGlyPheArgPheAspGlyVal 418
Db 1507

QY 419 ThrSerMetTyrThrHisIleGlyLeuGlnMetThrPheThrGlyAsnTyrGlyGlu 438
Db 1568 ACTCCATGATATTAACCTCCATGGGTGGCAGGATGCTTTTACCTGGCAACTCAATGAG 1627
QY 439 TyrPheGlyPheAlaThrAspValAspAlaValIleTyrLeuMetLeuValAsnAspLeu 458
Db 1628 TACTTGGATATGCAACTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1687
QY 459 IleHisGlyLeuHisProAspAlaValSerIleGlyIleAspValSerGlyMetProThr 478
Db 1688 ATTCACGGCTCTTCCCTGAGGCTGTACCATTTGGAGATGTTAGCGGAAAGCCAAACA 1747
QY 479 PheCysIleProValProAspGlyValGlyPheAspTyrArgLeuHisMetAlaVal 498
Db 1748 TTTTGATTTCCAGTGAAGATGCTGTTGATTTGATTCGCTCCACATGGCCATT 1807
QY 499 AlaAspIysTyrIleGlyLeuLeuIysGlnSerAspGlySerTyrIysMetGlyAspIle 518
Db 1808 GCCGATTAATGGATGAGATCTTAAAGAGAGATGAGAGCTGGAAAAATGGGTGCACATT 1867
QY 519 ValHisThrLeuThrAsnArgArgTyrLeuGluIysCysValThrTyrAlaGlnSerHis 538
Db 1868 GTGATACACTCACCAACAGAGGTGGTGGAAAAATGTTGCTTATGCTGAAAGTCAAT 1927
QY 539 AspGlnAlaLeuValGlyAspIysThrIleAlaPheTyrLeuMetAspIysAspMetTyr 558
Db 1928 GACCAAGCTCTGTTGGTGAACAAAATATGATTTGGCTGATGACAAAGACATGTAC 1987
QY 559 AspheMetAlaLeuAspArgProSerThrProGlyIleAspArgGlyIleAlaLeuHis 578
Db 1988 GACTTCATGCGCTCGTGAACAGACATCTCTCTTATAGATCGTGAATATACATTTGCAC 2047
QY 579 LysMetIleArgLeuValThrMetGlyLeuGlyIglIuIysGluIleAsnPheMetGly 598
Db 2048 AAAATGATCAGCTTATTAACATGGGCTTAGGCGGAGAAAGATTTGAAATTTTAGGA 2107
QY 599 AsnGluPheGlyHisProGluTyrIleAspPheProArgGlyProGlnThrLeuProThr 618
Db 2108 AATGATTTGGACATCTGAGAGATGATTTTCCAGAGGAGATGCATCTGCCCAAT 2167
QY 619 GlyIysValLeuProGlyAsnAsnAsnSerTyrAspIysCysArgArgPheAspLeu 638
Db 2168 GGTAAAGTATTCAGGAGAACCAACACATTTGATTAATGCGGTGATGATTTGATCTTA 2227
QY 639 GlyAspAlaAspPheLeuArgTyrHisGlyMetGlnIlePheAspGlnAlaMetGlnHis 658
Db 2228 GGTATGACAGATATCTAAGATATCATGAATGCAAGATTTGATCAGGCATGCAACAT 2287
QY 659 LeuGluGluIysTyrGlyPheMetThrSerGlnHisGlnIleTyrValSerArgIysHisGlu 678
Db 2288 CTGGAAGAGCCTATGTTCTATGACTCTGTGACACCGATATATACACGGAAGATGA 2347
QY 679 GluAspIysValIleIlePheGluArgGlyAspLeuValPheValPheAsnPheHisTyr 698
Db 2348 GGAATGCGATCATTTGCTTTGAGAGGGAACCTGTTTTTGTATCAACTTATTGG 2407
QY 699 SerAsnSerPhePheAspTyrArgValGlyCysSerArgProGlyIleTyrIleValAla 718
Db 2408 ACTAACACCTATTCAGATTACGAGATGCTGCTTCAAGTCAAGAAAGTAAAGATGTT 2467
QY 719 LeuAspSerAspAspAlaLeuPheGlyIlePheSerArgLeuAspHisAspValAspTyr 738
Db 2468 TTGACTCGCATGATGCTGTTGTTGAGAGCTTCAACAGGCTTATGATGATGATGATGAT 2527
QY 739 PheThrThrGluHisProHisAspAsnArgProArgSerPheSerValTyrThrProSer 758
Db 2528 TTCACTTTCAGGAGGTGATGATTAACCGGCTCGCTCTCATGATGATGATGATGATGAT 2587
QY 759 ArgThrAlaValValTyrAlaLeuThrGlu 768
Db 2588 AGGACAGAGTGTCTATGCTTTAGTAGAA 2617


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Db 1378 CATATGAGACTCTGCTGGATTGATTTACTGGAACTACACCGAATCTTGGATTGGAAACT 1437
QY 445 AspValAspAlaValAlaValTyrLeuMetLeuValAsnAspLeuIleHisGlyLeuHisPro 464
Db 1438 GATGTGGATGCTGGAATTAATCATCTGCTGGTTATGATATGATCATGGCTTACCT 1497
QY 465 AspAlaValSerIleGlyGluAspValSerGlyMetProThrPheCysIleProValPro 484
Db 1498 GAAGCGATACCGTGTGGAAAGATGTATGATGATCCAAACATCTGATTTCTGTCCTCA 1557
QY 485 AspGlyGlyValGlyPheAspTyrArgLeuHisMetAlaValAlaAspIleValIleHisThrLeuThrAsn 504
Db 1558 GATGGTGGCTGGATTTGACTTACCTTATCAGTGGCCATAGCTGATAGAGATAGAA 1617
QY 505 LeuLeuGlyGlnSerAspGlnSerTyrPlySerMetGlyAspIleValIleHisThrLeuThrAsn 524
Db 1618 ATGCTCAAGAAAGAGATGAAGACTGGCAAAATGGCGCATCATATTACACACTTACCAAC 1677
QY 525 ArgArgTyrPleuGlnGlyCysValThrTyrAlaGlnSerHisAspGlnAlaValGly 544
Db 1678 AGAAGGTGTGAGAAAGTATCTCTTATGCTGAAGTCAAGATCAAGCTCTTGTGT 1737
QY 545 AspPlyThrIleAlaPheTyrPleuMetAspPlyAspMetTyrAspPheMetAlaLeuAsp 564
Db 1738 GATAAACAAATTTGCTTCTGTTATGACAAAGATATGATTTCAATGGCAGTAAAC 1797
QY 565 ArgProSerThrProArgIleAspArgGlyIleAlaLeuHisLeuMetIleArgLeuVal 584
Db 1798 AGACCATCAACTCCCTTATCATATGAGAGATAGCTTTCACAAATGATTTAGGCTTAA 1857
QY 585 ThrMetGlyLeuGlyGlyGlyGlyTyrLeuAsnPheMetGlyAspGlnPheGlyHisPro 604
Db 1858 ACTATGGGATTAAGGGGTGAAGGTTACTTAATTTATGGAAACCAATTCGAGACCA 1917
QY 605 GluTyrPleuAspPheProArgGlyProGlnThrLeuProThrGlyLeuValLeuProGly 624
Db 1918 GAAATGATGATTTTCCAGAGGCGAGCGAGCGCTTTCGATGGTACCGTATCTTGGC 1977
QY 625 AsnAsnAsnSerTyrAspPlyCysArgArgArgPheAspLeuGlyAspAlaAspPheLeu 644
Db 1978 AACATATTCAGTATGACAAATGCGCGCCAGATTGATCTTGGGATGCAATATATCTC 2037
QY 645 ArgTyrHisGlyMetGlnGlnPheAspGlnAlaMetGlnHisLeuGlnGlyTyrGly 664
Db 2038 AGATACCGCGGACTCAAAATTTGATTCAGGCATGCAACATCTTGAAGGAATTCGGT 2097
QY 665 PheMetThrSerGlnHisGlnTyrValSerArgLysHisGlnGluAspLysValIleIle 684
Db 2098 TTTATGACTTCGAGAGCCAAATTCATATCAGAAAGACGAAACAGATAGATATCGTA 2157
QY 685 PheGlnArgGlyAspLeuValPheValPheAsnPheHisTyrSerAsnSerPhePheAsp 704
Db 2158 TTGAAAAGAGGATCTGCTCTTGTCTTAACTTCACTGAGCAAGCAAGCTACTTGGAT 2217
QY 705 TyrArgValGlyCysSerArgProGlyLysTyrTyrValAlaLeuAspSerAspAspAla 724
Db 2218 TACCCCATGTTGCTCCAAAGCTGGAATAATTAATGATTTGGCTGAGCAAGATCT 2277
QY 725 LeuPheGlyGlyPheSerArgLeuAspHisAspValAspTyrPheThrThrGlnHisPro 744
Db 2278 CTCCTTTGGTGAATTCATAGCTCGATCGAAGCAGAGTACTTCACTTATGATGGCTTA 2337
QY 745 HisAspAsnArgProArgSerPheSerValTyrThrProSerArgThrAlaValValTyr 764
Db 2338 TACGACGACGACCCGCTCTCTCATGCTGTATGACCCGTGTAACCCGCTGGTTAT 2397
QY 765 AlaLeu 766
Db 2398 GCTTTA 2403

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RESULT 12
ADA68438
ID ADA68438 standard; DNA; 2418 BP.

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XX AC ADA68438;
XX AC
XX 20-NOV-2003 (first entry)
XX DE Arabidopsis thaliana gene, SEQ ID 672.
XX DE
XX KW Plant; bacterial infection; fungal infection; viral infection; ds.
XX OS Arabidopsis thaliana.
XX PN NC003000898-A1.
XX PD 03-JAN-2003.
XX PF 22-JUN-2001; 2001MO-IB001105.
XX PR 22-JUN-2001; 2001MO-IB001105.
XX PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
XX PI Katagiri F, Qian S, Tao Y, Whitman S, Xie Z, Zhu T, Zou G;
XX DR WPI; 2003-175290/17.
XX PT Identifying at least one gene involved in plant resistance or response to
XX PT pathogenic infection for conferring resistance or tolerance to a plant to
XX PT bacterial, fungal or viral infection by determining or detecting plant
XX PT gene expression.
XX PS Claim 6; SEQ ID NO 672; 899pp; English.
XX CC The present invention relates to a method (M1) for identifying genes
XX CC involved in plant resistance or response to pathogenic infection. M1
XX CC comprises identifying a gene whose expression is significantly altered in
XX CC the incompatible interaction of plant gene expression relative to
XX CC expression of the gene in an uninfected plant, in a mutant plant that
XX CC does not express a gene associated with response to pathogenic infection,
XX CC or in a corresponding incompatible or compatible interaction. (M1) is
XX CC useful for conferring resistance to resistance or tolerance to a plant to
XX CC bacterial, fungal or viral infection. The present sequence was used to
XX CC illustrate the invention.
XX SQ Sequence 2418 BP; 692 A; 482 C; 556 G; 688 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6,46e-299 Length: 2418
Score: 3258.00 Matches: 584
Percent Similarity: 86.48% Conserved: 75
Best Local Similarity: 76.64% Mismatches: 71
Query Match: 78.15% Indels: 32
DB: 7 Gaps: 4

US-09-508-377-12 (1-768) x ADA68438 (1-2418)
QY 18 AlaAlaIleGlnPheProGlnGluLeuGlnIleProGlu----- 29
Db 175 GCTATCTCTGCTCTGAGAAAGTCTTACTGATATCTTGTATGATGATGATCCAGAGT 234
QY 30 -----AspIleGlnGlnGlnThrAlaGlnValAsnMetThrGlyThr 44
Db 235 TTTTCAAGATATTTGATCTAGAAAGTCAACAAATGAATAT----- 276
QY 45 AlaGlnLysLeuGlnSerSerGlnProThrGlnGlyIleValGlnThrIleThrAspGly 64
Db 277 ACTAGGACAGTAAAGACAGAACCAACCAATGAAGTT----- 315
QY 65 ValThrLysGlyValLysGluLeuValAlaGlyGlnLysProArgValAlaProLysPro 84
Db 316 -----GTCAGAGAGAGA-----GGGTGAAGACCAAGATATGTTCCCAACCG 357
QY 85 GlyAspGlyGlnLysIleTyrGlnIleAspProThrLeuLysAspPheArgSerHisLeu 104

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XX Full length cassava tuber CDNA in pSJ107.
 XX Starch branching enzyme; SBE; cassava; ss.
 XX Manihot esculenta.
 XX
 XX Key Location/Qualifiers
 XX CDS 21..2531
 XX FT /*tag= a
 XX FT /product= "SBE II"
 XX
 PN WO9820145-A2.
 XX
 PD 14-MAY-1998.
 XX
 PF 04-NOV-1997; 97WO-GB003032.
 XX
 PR 05-NOV-1996; 96GB-00023095.
 XX
 PA (NATT) NAT STARCH & CHEM INVESTMENT HOLDING COR.
 XX
 PI Jobling SA, Safford R;
 XX
 DR WPI; 1998-286958/25.
 XX
 DR P-PSDB; AAM62599.
 XX
 PT Search branching gene from cassava - useful for producing altered plants
 XX giving modified starch.
 PS
 PS Claim 2; Fig 4; 67p; English.
 XX
 CC The present sequence encodes starch branching enzyme (SBE) II. It was
 CC isolated from cassava tubers. The products can be used for producing
 CC plants having altered starch quantities and qualities. They can also be
 CC used for producing altered plants such as cassava, banana, potato, pea,
 CC tomato, maize, wheat, barley, oat, sweet potato and rice plants
 XX
 SQ Sequence 2913 BP; 818 A; 549 C; 680 G; 866 T; 0 U; 0 Other:
 XX
 Alignment Scores:
 Pred. No.: 3.09e-297 Length: 2913
 Score: 3241.50 Matches: 582
 Percent Similarity: 87.53% Conservative: 78
 Best Local Similarity: 77.19% Mismatches: 83
 Query Match: 77.75% Indels: 11
 DB: 2 Gaps: 2

QY 135 LeuGlyPheThrArgSerAlaGluGlyIleThrTyrArgGluTrpAlaProGlyValHis 154
 DB 591 TTGTGTTTCTCAGCAGTGAACAGAAATTAATTATAGAGAGTGGGACAGAGCTAACG 650
 QY 155 SerAlaAlaLeuValGlyAspPheAsnAspTrpAsnProAsnAlaAspTrpMetThrArg 174
 DB 651 TGGGCTGCAATGGATTGAGATTTCATTAATCGAAATCCTAATGACAGATGTCATACCTAG 710
 QY 175 AspAspTyrGlyValTrpGluIlePheLeuProAsnAlaAspGlySerProAlaIle 194
 DB 711 AATGAGTGTGTGTCTGGAGATCTTTTCCAAATTAATGCAAGTGGTTCACCAACAAAT 770
 QY 195 ProHisGlySerArgValIleArgMetAspThrProSerGlyValIleAspSerIle 214
 DB 771 CCCCATGTTCTCGAGTAAAGATACGATGATATCTCATCTGGCAACAAAGATTCTAT 830
 QY 215 SerAlaTrpIleLysPheSerValGlnAlaProGlyGluIleProPheAsnGlyIleTyr 234
 DB 831 CCTGCTTGATCAAGTTCTCACTTCAAGCACACAGTGAACCTCCATATTAATGGCATATAC 890
 QY 235 TyrAspProProGluGluGlyTyrValPheGlnHisProGlnProLysArgProGlu 254
 DB 891 TATGATCTCCGAGAGAGAGAGATGTGTCTCAAAAATCCTCAGCCAAAGACCAAA 950
 QY 255 SerLeuArgIleTyrGluSerHisIleGlyMetSerSerProGluProLysIleAsnSer 274
 DB 951 TCACCTCGGATTTATGATGCGACAGTGAATGATGATGACGAGCAGATATTAAACACA 1010
 QY 275 TyrAlaAsnPheArgAspGluValLeuProArgIleLysArgLeuGlyTyrAsnAlaVal 294
 DB 1011 TATGCCAACTTTAGAGTGAATGTGTCTTCCTGCACTCAAAAAGCTTGGCTACATGCTGTT 1070
 QY 295 GlnIleMetAlaIleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsn 314
 DB 1071 CACCTATGCTATTTCAGAGCATTCATATTATGCTAGTTGGATACAGTCAACAAAC 1130
 QY 315 PhePheAlaProSerSerArgPheGlyThrProGluAspLeuLysSerLeuIleAspArg 334
 DB 1131 TTTTATGACACTAGACAGCCGATTTGGAATCTCGATGATTTAAAGTCTCTAATATATAA 1190
 QY 335 AlaHisGluLeuGlyLeuLeuValLeuMetAspIleValHisSerHisSerSerAsn 354
 DB 1191 GCTCACCAGATTAGTCTTCTGTGTTCTCATGATATGTGTCATAGCAGTCAACTAAT 1250
 QY 355 ThrLeuAspGlyLeuAsnGlyPheAspGlyThrAspThrHisTyrPheHisGlyPro 374
 DB 1251 ACGTTGATGGCTGAATATGTTGATGTCGATGTCACACTTTCACCTCGAGACA 1310
 QY 375 ArgGlyHisIleTrpMetTrpAspSerArgLeuPheAsnTyrGlySerTrpGluValLeu 394
 DB 1311 CGGGCTATCATGATGATGGGACTCGCTTTTCAACTATGGAGCTGGAGGTTCTTA 1370
 QY 395 ArgPheLeuLeuSerAsnAlaArgTrpTrpLeuGluGluTyrLysPheAspGlyPheArg 414
 DB 1371 AGTTTCTTCTTCAATATGCAAGGTGGTGGTGAAGTGCACAAATTTGATGGTTCACA 1430
 QY 415 PheAspGlyValThrSerMetMetTyrThrHisIleGlyLeuGlnMetThrPheThrGly 434
 DB 1431 TTGATGGGGTGAATTCATATGATGATACCCATCATGATGGACGTGATTTTACCGGCG 1490
 QY 435 AsnTyrGlyGluTyrPheGlyPheAlaThrAspValAlaAspAlaValIleTrpLeuMetLeu 454
 DB 1491 AACTACATGAATACCTTGGATATGCAACTATATGATGATGCTGGTTATTTATGATGCTG 1550
 QY 455 ValAsnProLeuIleHisIleGlyLeuHisIleProAspAlaValSerIleGlyGluAspValSer 474
 DB 1551 TTGATATATATGATTCATGCTCTCTCCCAAGGCTGTCACCATTTGGTCAAAATGTTAT 1610
 QY 475 GlyMetProThrPheCysIleProValProAspGlyValGlyPheAspTyrArgLeu 494
 DB 1611 GGATGCCAACAGTTTGATTCCTGGTTGAAGTGTGTGTGGCTTTGATATATGCTCTC 1670

QY 495 HisMetAlaValAlaAspIleTrpIleGluLeuLeuGlnSerAspGluSerTrpIle 514
 Db 1671 CACATGGCGTGTGGCTGAATAAGGCTTGAGATTATTCAGAGAGAGATGAAGATTGGAAA 1730
 QY 515 MetGlyAspIleValHisThrLeuThrAsnArgArgTrpLeuGlnIleValThrTyr 534
 Db 1731 ATGGGTGACATTGTACATATGCTGACCAACAGCGGTGTGGAAAAAGTGTCTTCTAT 1790
 QY 535 AlaGluSerHisAspGlnAlaLeuValGlyAspIleThrIleAlaPheTrpLeuMetAsp 554
 Db 1791 GGTGAAGTCATGACACAGCGCCCTGTGGTGAACAAACATTCATCTTGGCTGATGAC 1850
 QY 555 LysAspMetTyrAspPheMetAlaLeuAspArgProSerThrProArgIleAspArgGly 574
 Db 1851 AAGGATATGATGACTTCATGGCTCTGACAGACATCTACTCTCATAGATCGTGA 1910
 QY 575 IleAlaLeuHisGlyMetIleArgLeuValThrMetGlyLeuGlyGlyGlyTyrLeu 594
 Db 1911 GTAGCATTCACAAATGATCAGGCTTATTCATGGATTAAGCGGAGAGAGATATTG 1970
 QY 595 AsnPheMetGlyAsnGluPheGlyHisProGluTrpIleAspPheProArgGlyProGln 614
 Db 1971 AATTTTATGGGAAATGAATTTGGACACCCGAGTGAATTGTTCCAAAGAGTGATCTA 2030
 QY 615 ThrLeuProThrGlyLysValLeuProGlyAsnAsnAsnSerTyrAspIleGlyArg 634
 Db 2031 CATCTTCCAGTGTGTAATTTGTTCTCGGGAACAAATTACGTTATGATTAATGCGGCGT 2090
 QY 635 ArgPheAspLeuGlyAspAlaAspPheLeuArgTyrHisGlyMetGlnIlePheAspGln 654
 Db 2091 AGGTTTGAATCTAGGCAATTCAAACATCTGAGATATCATGAAATGCAAGATTGATCA 2150
 QY 655 AlaMetGlnHisLeuGluGluIleValTyrGlyPheMetThrSerGluHisGlnTyrValSer 674
 Db 2151 GCAATTCAGCATCTTGAAGAGCCTATGTTTCATGACTTCTGAGCACCAATACATATCA 2210
 QY 675 ArgGlyHisGluGluAspLysValIleIlePheGluArgGlyAspLeuValPheValPhe 694
 Db 2211 CGGAAGGATGAAGAGATCGATCATGTTCTTCGAGAGGGGAAACCTCGTTTGTATTC 2270
 QY 695 AsnPheHisThrSerAsnSerPhePheAspTyrArgValGlyCysSerArgProGlyLys 714
 Db 2271 AATTTTCATTTGACCTGACGACTATCGGATTCGAGATTGCGCTCTTAAAGCCAGAAAG 2330
 QY 715 TyrLysValAlaLeuAspSerAspAlaLeuPheGlyGlyPheSerArgLeuAspHis 734
 Db 2331 TACAGATAGTCTTGATTCAGATGATCCTTTGTTGAGGCTTTGGCAGGCTTATCAT 2390
 QY 735 AspValAspTyrPheThrThrGluHisAspHisAspAsnArgProArgSerPheSerVal 754
 Db 2391 GATGACAGACACTTCAGCTTGAAGGCTGTGAGATTAACGGGCTCGATCCTTCATGCTG 2450
 QY 755 TyrThrProSerArgThrAlaValAlaTyrAlaLeuThrGlu 768
 Db 2451 TACACCACTGTGAACAGCAGTGTCTATGCTTATGATGAG 2492
 RESULT 14
 ID AAT17267 standard; DNA; 2531 BP.
 AAT17267;
 AC AAT17267;
 DT 03-MAR-1997 (first entry)
 DE Class A starch branching enzyme (direct sequencing).
 KW Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;
 OS amylose; viscosity; potato; ss.
 OS Solanum tuberosum.
 XX
 XX W09634968-42.
 XX

PD 07-NOV-1996.
 XX
 PF 03-MAY-1996; 96WO-GB001075.
 XX
 PR 05-MAY-1995; 95GB-00009229.
 PR 10-APR-1996; 96GB-00007409.
 XX
 PA (NAT) NAT STARCH & CHEM INVESTMENT HOLDING COR.
 XX
 PI Cooke D, Debet M, Gidley MJ, Jobling SA, Safford R,
 PI Sidebottom CM, Westcott RJ;
 XX
 DR WP1: 1996-506170/50.
 DR P-PSDB: AAR93804.
 XX
 PT New potato plant starch having high amylose content - also class A starch
 PT branching enzyme and corresp. DNA to alter the viscosity of starch; for
 PT use in food, biodegradable products, adhesives, etc.
 XX
 PS Example 1; Fig 9; 142pp; English.
 XX
 CC Class A starch branching enzyme (SBE) has been obtained from potatoes. In
 CC class A SBE mols., a flexible N-terminal domain, is found, which is not
 CC found in class B mols. This sequence was obtained by direct sequencing of
 CC PCR fragments amplified from first strand cDNA. Nucleotides which could
 CC not be unambiguously assigned are indicated using standard IUPAC notation
 XX
 XX Sequence 2531 BP; 735 A; 458 C; 599 G; 723 T; 0 U; 16 Other;
 SQ
 Alignment Scores:
 Pred. No.: 4,266-293 Length: 2531
 Score: 3197.00 Matches: 586
 Percent Similarity: 82.53% Conservative: 80
 Best Local Similarity: 72.61% Mismatches: 93
 Query Match: 76.69% Indels: 48
 DB: Gaps: 6
 US-09-508-377-12 (1-768) x AAT17267 (1-2531)
 QY 2 AlaThrPheAlaValSerGlyAlaThrIleu-----GlyValAlaArgProPheAla 19
 Db 92 TCTACAGTTGCAAGCATCCGGGAAAGTCTTGCTGCTGGAAYCCAGATGATGCTCTCA 151
 QY 20 AlaGlnProGluGluLeuGlnIleProGlu----- 29
 Db 152 TCTTCAACAGACCAATTTGAGTTCCTGAGACATCTCCGAAATTTCCCGACATCAACT 211
 QY 30 AspIleGluGluGlnThrAlaGlu----- 37
 Db 212 GATGAGAGTACTGCAACATGAGACACGCTACGAGATTAAACTGAGAACATGACGTT 271
 QY 38 -----ValAsnMetThrGlyGlyThrAlaGlu----- 46
 Db 272 GAGCGCTGAGAGATCTTACAGGAAGTGTGAAGAGCTGAGATTGCTTCATGACATCA 331
 QY 47 -----LysLeuGluSerSerGluProThrGlnGlyIleValGluThrIle 61
 Db 332 CTACAAAGAGGTGTAACTGGAGAGGTAAACATTAAATCTTCTGAAAGACAAATT 391
 QY 62 ThrAspGlyValThrLysGlyValLysGluLeuValAlaGlyLysProArgValAla 81
 Db 392 ATGTATGANTCGATAGAG-----ATCAGAGAG-----AGGGGATC 427
 QY 82 ProLysProGlyAspGlyGlnLysIleTyrGluIleAspProThrIleuLysAspPheArg 101
 Db 428 CCTCCACCTGACCTTGCTGACAGAGATTATGAATTAAGACCCCTTTTGACAAACTATCGT 487
 QY 102 SerHisLeuAspTyrArgTyrSerGluTyrArgArgIleArgAlaIleAspGlnHis 121
 Db 488 CAACACCTTGATTAACAGGATATTCACGTCACAGAACTGAGGAGGCAATGACAGATAT 547
 QY 122 GluGlyGlyLeuGluAlaPheSerArgGlyTyrGluLysLeuGlyPheThrArgSerAla 141

Key Location/Qualifiers
CDS 3..2552
FT /*tag= a
FT /product= "SBE II"
FT /partial
FT /note= "No start codon shown"
XX GB2160521-A.
XX PD 26-SEP-2001.
XX PF 20-MAR-2000; 2000GB-00006733.
XX PR 20-MAR-2000; 2000GB-00006733.
XX PA (DANI-) DANISCO AS.
XX PI Poulsen P, Sorensen IS;
XX DR WPI: 2001-650142/75.
XX P-PSDB; AAU80169.
XX PT New transformed plants with reduced endogenous starch branching enzyme
XX PT and heterologous glucan branching enzyme activities, useful for producing
XX PT starch with improved properties, which is in the food, paper and chemical
XX PT industries.
XX PS Example 1; Page 31-35; 61pp; English.
XX The invention relates to a transformed organism, preferably a transformed
XX plant, having a reduced endogenous starch branching enzyme (SBE)
XX activity, and having a heterologous glucan branching enzyme (GBE)
XX activity. The reduced SBE activity is effected via expression of a
XX nucleotide sequence that is antisense to at least part of a SBE exon.
XX Also included are a method of producing starch with altered
XX characteristics comprising (a) providing a plant having reduced
XX endogenous SBE activity, and having heterologous GBE activity (b)
XX propagating the plant of (a) and optionally (c) obtaining starch from the
XX plant; starch obtainable from the transformed plant; and a nucleic acid
XX construct system capable of directing the expression of all or part of
XX one or more antisense SBE exons and optionally one or more heterologous
XX GBE. The transformed plants are useful for producing starch with modified
XX and improved properties, which is an important raw material and used in
XX the food, paper and chemical industries. The present sequence encodes
XX Potato SBE II, used to make transgenic plants of the invention
SQ Sequence 2563 BP; 749 A; 462 C; 614 G; 738 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4.34e-293 Length: 2563
Score: 3197.00 Matches: 586
Percent Similarity: 82.78% Conservative: 82
Best Local Similarity: 72.61% Mismatches: 91
Query Match: 76.69% Indels: 48
Gaps: 6

US-09-508-377-12 (1-768) x ABK50301 (1-2563)

QY 2 AlaThrPheAlaValSerGlyAlaThrLeu-----GlyValAlaArgProProAlaAla 19
DB 114 TTTACAGCTTGCAGCATCGGGGAAAGTCCTTGTGCTCGGAAACCCAGAGTGTAGCTCTCA 173
QY 20 AlaGlnProGlnGluLeuGlnInleProGlu----- 29
DB 174 TCTCTCAACAGCAACCAATTGAGTCACTGAGACATCTCCAGAAATTTCCCGACATCAACT 233
QY 30 AspIleGluGlnInleThrAlaGlu----- 37
DB 224 GATGTAGATGATTCACCAATGGAACGCTGAGCCAGATTAAACTGAGAAAGATGACGTT 293
QY 38 -----ValAsnMetThrGlyGlyThrAlaGlu----- 46

QY 47 -----LysLeuGlnSerSerGluProThrGlnGlyIleValGluThrIle 61
DB 354 CTACAGAGAGGTGTAAACTGAGAGAGCTTAAACATTAAATACCTTTGAGAGGACAAATT 413
QY 62 ThrAspGlyValThrLysGlyValLysGluLeuValIleGlyLysProArgValIle 81
DB 414 ATTGATGATCTGATAGG---ATCAGAGG-----AGGGGCATC 449
QY 82 ProLysProGlyAspGlyGlnLysIleTyrgluIleAspProThrLeuLysAspPheArg 101
DB 450 CCTCCACCTGAGACTTGTCAGAGATTATGAAATAGACCCCTTTTGACAAACTATCGT 509
QY 102 SerHisLeuAspTyrgTyrgTyrgSerGluTyrgArgGlyLeuArgAlaIleAspGlnHis 121
DB 510 CACACCTTGATTCAGGTTATTCACAGTACAGAAACTGAGGAGGCAATGTGCAAGTAT 569
QY 122 GluGlyGlyLeuGluAlaPheSerArgGlyTyrgLysLeuGlyPheThrArgSerAla 141
DB 570 GAGGTTGTTGAAAGCTTTTCTGCTGTTTGAAGAAATAGGCTTCACTGCTAGTGTCT 629
QY 142 GluGlyIleThrTyrgArgGluThrAlaProGlyAlaHisSerAlaIleLeuValGlyAsp 161
DB 630 ACAGGTACACTTACCGTAGAGGCTCCTGCTGCCAGTCAAGTCCCTCATTTGAGAT 689
QY 162 PheAsnAsnTPasnProAsnAlaAspThrMetThrArgAspAspTyrgIleValITrgGlu 181
DB 690 TTCAACAATTGGAGCGCAAAATGCTGACATTATGACTCGCAATGAATTTGGTCTCGGAG 749
QY 182 IlePheLeuProAsnAsnAlaAspGlySerProAlaIleProHisGlySerArgValLys 201
DB 750 ATTTTTCGCAAAATATAGTGATGCTCTCTGCATTTCCATAGGCTCCAGAGTGAAG 809
QY 202 IleArgMetAspThrProSerGlyValLysAspSerIleSerAlaITrgIleLysPheSer 221
DB 810 ATAGGTATGAGACATCCATCAGGTGTTAAGATTCATTCCTGCTGATCAACTACTCT 869
QY 222 ValGlnAlaProGlyGlnIleProPheAsnGlyIleTyrgTyrgAspProGluGluGlu 241
DB 870 TTACAGCTTCCTGATGAATTCATATGAGATATATATGATCCACCCGAAGAGAG 929
QY 242 LysTyrgValPheGlnHisProGlnProLysArgProGluSerLeuArgIleTyrgIleSer 261
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QY 262 HisIleGlyMetSerSerProGluProLysIleAsnSerTyrgAlaAsnPheArgAspGlu 281
DB 990 CATATTTGGAATGAGTAGTCCGGAACCTTAAATTTAATCTCATCGTGAATTTTGAAGATGA 1049
QY 282 ValLeuProArgIleLysArgLeuGlyTyrgAsnAlaValGlnIleMetAlaIleGlnGlu 301
DB 1050 GTTCTTCTCCCAAAAACCTGGGTGACGTGCGGTGCATAATTAATGCTATTCAAGAG 1109
QY 302 HisSerTyrgTyrgAlaSerPheGlyTyrgHisValThrAsnPhePheAlaProSerSerArg 321
DB 1110 CATCTTATTTATGCTAGTTGTTGTTATCATGTCACAAATTTTTCACACAGACACCCGT 1169
QY 322 PheGlyThrProGluAspLeuLysSerLeuIleAspArgAlaHisGluLeuGlyLeu 341
DB 1170 TTTGGAATCCCGAGACCTTAAGCTTTGATGTATTAAGCTCATGAGCTAGGAATTTGT 1229
QY 342 ValLeuMetAspIleValHisSerHisSerSerAsnAsnThrLeuAspGlyLeuAsnGly 361
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QY 382 AspSerArgLeuPheAsnTyrgTyrgTyrgTyrgTyrgValIleValPheLeuLeuSerAla 401
DB 1350 GATTCGCGCTTCTTAATCTATGAGAACTGGAGGTACTTAGGATCTTCTCCAAATGCG 1409

Tue Apr 20 10:02:28 2004

us-09-508-377-12.rge

Page 1

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 17, 2004, 18:30:19 / Search time 5304 Seconds
(without alignments)
6275.914 Million cell updates/sec

Title: US-09-508-377-12

Sequence: 4169
1 MATPAVSGATLGVARPPAAA.....PRSFVTPSPRAVYVALTE 768

Scoring table:

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09508377.GCEN 1.1.3296 @runat.15042004.084305.2304 -NCPU=6 -ICPU=3
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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15: em_ba:*
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17: em_hum:*
18: em_in:*
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41: em_hcg_other:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4169	100.0	2726	AF338432	AF338432 Trilicium
2	4119.5	98.8	2970	AF286319	AF286319 Trilicium
3	4113.5	98.7	2970	TASBA2	Y11282 T. aestivum
4	4080.5	97.9	2549	BT008928	BT008928 Trilicium
5	4031.5	96.7	2853	AR340173	AR340173 Sequence
6	4031.5	96.7	2853	TAU66376	U66376 Trilicium ae
7	3938	94.5	2554	AF064560	AF064560 Hordeum ae
8	3685	88.4	3015	E14723	E14723 Rice mRNA f
9	3685	88.4	3015	AB023498	AB023498 Oryza sat
10	3667	88.0	2364	E14724	E14724 Rice mRNA f
11	3588.5	86.1	2446	AR427891	AR427891 Zea mays at
12	3588.5	86.1	2795	ZMU65948	U65948 Zea mays at
13	3362	80.6	2918	R1CBCE3	D16201 Oryza sativ
14	3362	80.6	2919	AR304540	E08183 Gene of stea
15	3351.5	80.4	2664	AF427892	AF427892 Hordeum b
16	3351	80.3	2720	AF064561	AF064561 Hordeum v
17	3348.5	80.3	3549	PSSBERGEN	X80009 P. sativum m
18	3346	80.2	2640	BD071188	BD071188 Plant 11k
19	3342	80.2	2725	AR106495	AR106495 Sequence
20	3342	80.2	2725	MZEGJUCTRN	L08065 Corn starch
21	3341	80.1	2665	AR368850	AR368850 Sequence
22	3337.5	80.1	2655	AX654742	AX654742 Sequence
23	3337.5	79.3	3360	AB029548	AB029548 Phaseolus
24	3307.5	79.0	3090	AX92164	AX92164 Sequence 30
25	3292	79.0	2418	AX506177	AX506177 Sequence
26	3258	78.1	2418	AX651816	AX651816 Sequence
27	3258	78.1	2542	ATU22428	U22428 Arabidopsis
28	3257.5	78.1	3123	AB071286	AB071286 Ipomoea b
29	3257.5	77.8	2913	AX92162	AX92162 Sequence 28
30	3241.5	77.2	2517	AB042937	AB042937 Ipomoea b
31	3219	76.9	2493	STSBERI	AJ000004 Solanum t
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33	3197	76.7	2529	AS8167	AS8167 Sequence 17
34	3196	76.6	2523	STU011889	AJ011889 Solanum t
35	3194	76.6	2955	STU011885	AJ011885 Solanum t
36	3192	76.5	2578	AS8169	AS8169 Sequence 19
37	3189	76.5	3074	AR123355	AR123355 Sequence
38	3189	76.5	3074	AR241392	AR241392 Sequence
39	3189	76.5	2982	STU011888	AJ011888 Solanum t
40	3180	75.3	2576	AX755372	AX755372 Sequence
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RESULT 1

ALIGNMENTS

AF338432
LOCUS AF338432 2726 bp mRNA linear PLN 27-MAR-2001
DEFINITION Triticum aestivum starch branching enzyme I1a variant mRNA,
complete cds.
ACCESSION AF338432
VERSION AF338432.1 GI:13447951
KEYWORDS
SOURCE
ORGANISM
Triticum aestivum (bread wheat)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
REFERENCE
AUTHORS Rahman, S., Regina, A., Li, Z., Abraham, S. and Morell, M.K.,
Kosar, Hashem, B., Abraham, S. and Morell, M.K.,
Comparison of starch-branching enzyme genes reveals evolutionary
relationships among isoforms. Characterization of a gene for
starch-branching enzyme I1a from the wheat genome donor Aegilops
tauschii
TITLE Plant Physiol. 125 (3), 1314-1324 (2001)
JOURNAL
MEDLINE 21140316
PubMed 11244112
REFERENCE 2 (bases 1 to 2726)
AUTHORS Rahman, S., Regina, A., Li, Z., Abraham, S. and Morell, M.K.
TITLE Direct Submision
JOURNAL Submitted (18-JUN-2001) Plant Industry, CSIRO, Clunies Ross,
Canberra, ACT 2601, Australia
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KFVQAPGEIPFNQIYYDPPEEKVFPQHPQPKRESLRITESHGMSPEKISAWI
NFRDEVLPRIKRIYNAVOIAIOHSHSYAFSGYVNFPASSFPGPEDIKSIDR
AHEGLVIMDIIVSHSSNNTLDGNGFDGDIHFHGGPRGHMMMSRLPNYSWE
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ORIGIN
Alignment Scores:
Pred. No.: 3.72e-315 Length: 2726
Score: 4169.00 Matches: 768
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0
US-09-508-377-12 (1-768) x AF338432 (1-2726)

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QY 21 GlnProglugluLeuGlnIleProgluAspIleGluGluGlnIleThAlaGluValaIaIaIa 40
Db 184 CAACTGAAGATTAACGATACCTGAAGACATCGAGGAGCAACCGGCTGAATAAATG 243
QY 41 ThrgIyglYthraIaGluIyLeuGluIySerGluIuProThrgIyglYleValaIuIthr 60

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Db 304 ATCACTAGTGTGTAAACCAAGAGATTAAAGAACTACGTCTGGGGAGAAACCCGGAATT 363
QY 81 ValProIySPProgluYAspGlyGlnIyIleTyGluIleAspProThrLeuIyAspPhe 100
Db 364 GTCCCAAAACCAAGAGATGGCGAAGAAATATACAGAGTTTACCAACGCTGAAGATT 423
QY 101 ArgSerHisLeuAspIyArgIySerGlyTyArgIyGluIleArgAlaIaIleAspGln 120
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QY 121 HisGluGlyGlyLeuGluIaIaPheSerArgGlyTyGlyIuIySGluIyPheThArgSer 140
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QY 141 AlaGluGlyIleThTyArgGluIuTPAlaProGlyValaHisSerAlaIaIeValaGly 160
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QY 161 AspPheAsnAsnTPAsnProAsnAlaAspIyThMetThraArgAspPheTyGlyValTTP 180
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QY 221 SerValGlnAlaProgluGlyIuIleProPheAsnGlyIleTyTyAspProProgluIu 240
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RESULT 2
 AF286319
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 DEFINITION
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 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Triticum aestivum (bread wheat)
 Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.
 1 (bases 1 to 2970)
 McCue, K.F., Hurkman, W.J., Tanaka, C.K. and Anderson, O.D.
 Starch Branching Enzymes Sbe1 and Sbe2 from Wheat (Triticum aestivum cv. Cheyenne): Molecular Characterization, Developmental Expression, and Homolog Assignment by Differential PCR
 Plant Mol. Biol. Rep. 20 (2), 191-192 (2002)
 2 (bases 1 to 2970)
 McCue, K.F. and Anderson, O.D.
 Direct Submision
 Submitted (11-JUL-2000) United States Department of Agriculture, Agricultural Research Service, 800 Buchanan Street, Albany, CA 94710-1105, USA
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ORIGIN
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 Query Match: 98.81% Gaps: 55
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US-09-508-377-12 (1-768) x AF286319 (1-2970)

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LOCUS	RESULT 3
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DEFINITION	2970 bp mRNA linear
ACCESSION	T1282
VERSION	Y1282.1
KEYWORDS	GI:1865343
	1,4-alpha-glucan branching enzyme; sbe2 gene; starch branching enzyme II.

Alignment Scores:	
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Best Local Similarity:	92.95%
Query Match:	96.67%
DB:	8
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	Mismatches: 3
	Indels: 35
	Gaps: 1

ORGANISM
Triticum aestivum (wheat)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticeae; Triticum.
1

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

Nair, R. B., Baga, M., Scoles, G. J., Kartha, K. K. and Chibbar, R. N.
Isolation, characterization and expression analysis of a starch
branching enzyme II cDNA from wheat
Plant Sci.
2 (bases 1 to 2970)
Chibbar, R. N.
Direct Submission
Submitted (14-FEB-1997) R. N. Chibbar, Plant Biotechnology

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RESULT 4
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 accession BT008928
 version BT008928.1 GI:32128479
 keywords FLI CDNA.
 SOURCE Triticum aestivum (bread wheat)
 ORGANISM Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Triticum.
 1 (bases 1 to 2549)
 REFERENCE
 Tingey,S.V., Wolters,P., Powell,W., Dolan,M., Miao,G.-H.,
 Carlier,N.R., Hanafey,M.K. and Hailey,C.F.
 Direct Submision
 Submitted (20-JUN-2003) Crop Genetics, E. I. DuPont de Nemours and
 Company, 1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104,
 USA

FEATURES
 location/Qualifiers

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D	b	1842	ATTCTGTGTTATGATTAAGATATAGTATGATTTATGAGCTCTGATAGAGCCCTTCAACCC	1901
Q	y	569	cArgIleAspArgGlyIleAlaLeuHisSHLeuMetIleArgLeuValaThrMetGlyLeuGly	589
D	b	1902	TCCGATTCATCGTGGCATGACATTCATCAATAAATGATCAGCGCTTGCCACCAAGGATTAGG	1961
Q	y	589	yGlyGlyGlyTyrglyLeuAsnPheMetGlyAsnGlyPheGlyHisAspGlyTrpTrpIleAspPh	609
D	b	1962	TGGGAAAGCATATCTTAACCTCATGGGAAATGAGATTTGGCATCCTGATGATGATGATTT	2021
Q	y	609	eProArgGlyProGlnThrLeuProThrGlyLysValLeuProGlyAsnAsnAsnSerTyrgl	629
D	b	2022	TCCAAAGGGCCCAAACTCTTCCACCGCGAAAGTTCTCCCTGAAATTAACAATATTA	2081
Q	y	629	rAspTyrglyCysArgArgArgPheAspLeuGlyAspAlaAspPheLeuArgTyrglySHSGlyMe	649
D	b	2142	GCAAGAGTTGCATCAGCGCAATGACAGCATCTTGAAGAAAAATATGGGTTTATGACATCTGA	2201
Q	y	669	uHisGlnTyrglyValSerArgLysSHSGlyGluAspTyrglyAlaIleIlePheGlyAspGlyLys	689
D	b	2202	GCACACAGATATGTTTCACGGAAACATGAGGAAGATTAAGGTGATCATCTTCCAAAGAGGAGA	2261
Q	y	689	pLeuValPheValPheAsnPheHisSHTrpSerAsnSerPhePheAspTyrglyArgValaGlyCys	709

	Db	2262	TTTGATATTGTTTTCACCTCCAGCCTGGACCATTAGCTTTTTTGACTACGCGTGTGGGCTG	2231
	Oy	709	SSEarGPrrooLYLstYrlyrsValAlaleuasPSeAspaSPalAleubheglglyph	729
	Db	2322	TTCCAAGCTGTGGAAACAAGGCGCTTGAGCTCCGACGAAGCACTCTTGGTGATT	2381
	Oy	729	eSefArGLeasPhisAaspValAapYrrPheTrThGluiHIsProhisASpasnaGpr	749
	Db	2382	CAGCAGGCTGCATCATATGTCGACTACTTCACCAACGGAACATCCGATGACACAGGCC	2441
	Oy	749	CaRSeePheSerValYrThrProSeerArgThralAlaValYrZnAlaleuThrglu	768
	Db	2442	GCGCTCTTTCGCTGTGACACTCCGACAGACAGCTGCGGTGCTGATGCTCCCTTACAGAG	2499
RESULT 6				
LOCUS	TAU66376	2853 bp	mRNA	linear
DEFINITION	Triticum aestivum 1,4-alpha-D-glucan			
ACCESSION	U66376			
VERSION	U66376.1			
KEYWORDS	GI:1620661			
SOURCE				
ORGANISM	Triticum aestivum (bread wheat)			
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta, Liliopsida, Poales; Poaceae; Poideaee; Triticeae; Triticum. 1 (bases 1 to 2853) Kroegeer,C., Loerz,H. and Luetticke,S. Direct Submission Submitted (08-AUG-1996) University of Hamburg, Institute of General Botany, Centre of Applied Molecular Biology, AMP II, Ohnhorststr. 18, Hamburg 22609, Germany Location,Qualifiers 1..2853 /organism="Triticum aestivum" /mol_type="mRNA" /cultivar="T.A. Florida" /db_xref="taxon:4565" /tissue_type="kernels 21 DAP" 313..2502 /EC_number="2.4.1.18" /note="branching enzyme" /codon_start=1 /product="1,4-alpha-D-glucan 6-alpha-D-(1,4-alpha-D-glucanotransferase" /protein_id="AA817086.1" /db_xref="GI:1620662"			
FEATURES				
source				
CDS				
ORIGIN				
Alignment Scores:				
Pred. No.:	2.05e-304	Length:	2853	
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Percent Similarity:	92.56%	Conservative:	9	
Best Local Similarity:	91.46%	Mismatches:	9	
Query Match:	96.70%	Indels:	52	
	8	Gaps:	1	

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 DB 42 ATGGCGACGTTTCGGGCGGTCCGGCGGCACTCGGTGTGGCGGGCGGCGGTGGAGT 101
 QY 16 ----- 16
 DB 102 GCGCGGGCGGCTCGAGCGGAGGGCGGGCGGACTTGGCCGTGCTCTCAGGAA 161
 QY 16 ----- 16
 DB 162 GAAGGACTCTCTCGCGCGCTCTGAGCGCGGCGCTCTCCAGGAAAGCTCTGGTGC 221
 QY 17 -----ProAlaAlaagInProGluGluLeuGlnIleProG 29
 DB 222 TGACGGGAGAGGAGCGACGACTGGCAAGTCCGGCGCACTCGAAGAAATTACAGATACCTGA 281
 QY 29 uAspIleGluGluGlnThrAlaGluValAsnMetThrGlyGlyThrAlaGluLeuG 49
 DB 282 AGATATCCAGAGCAACGGCGGAAGTGAACATGACAGGGGCGACTGCGAGAAAACCTTCA 341
 QY 49 uSerSerGluProThrGlnGlyIleValGluThrIleThrAspGlyValThrLeuGlyVa 69
 DB 342 ATCTTCGAACCGGCACTCGGGCGATTGTGAAACAATCACTGATGGTGTAAACCAAGAGT 401
 QY 69 lLysGluLeuValAlaGlyGluLeuProArgValAlaProLysProGlyAspGlyGlnLy 89
 DB 402 TAAAGAACTACTCGTGGGGGAGAAACCGCGAGTGTCCCAAAACAGAGATGGGCGAGA 461
 QY 89 sIleTyrGluIleAspProThrLeuLysAspPheArgSerHisLeuAspTyrArgTyrSe 109
 DB 462 AATATACAGAGATTGACCAACACTGAAAGATTTTCGAGCCACTCTGACTACCGAATACG 521
 QY 109 rGluTyrArgArgGlyLeaArgAlaAlaIleAspGlnHisGluGlyValLeuGlnAlaPheSe 129
 DB 522 CGAATACAGAGAAATTCGTGCTGCTATTGACCAACAGAGAGTGGATGGAAAGCATTTTC 581
 QY 129 rArgGlyTyrGluLysLeuGlyPheThrArgSerAlaGluGlyIleThrTyrArgGlyLur 149
 DB 582 TCGTGGTTATGAAGAAGCTTGATTTACCCGCGAGTGTGAAGATACCTACCGAAGAG 641
 QY 149 rAlaProGlyAlaHisSerAlaAlaLeuValGlyLysPheAsnAspTrpAsnProAsnAl 169
 DB 642 GGCTCTTGAGCGGCACTTCGCGAGCTTAGTAGTGACTTCAACAATGGAAATCCAAATGC 701
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 DB 702 AGATGCTATGACCAAGATGATTAATGTTGTTGGGAGATTTCTCTCCATCAACCTGA 761
 QY 189 rGlySerProAlaIleProHisGlySerArgValLysIleArgMetAspThrProSerG 209
 DB 762 TGGATCCCAAGCTATTCCTCATGCGCTCAGCTGAAGTAAGATACGATACCTCAATCCG 821
 QY 209 yValLysAspSerIleSerAlaTrpIleLysPheSerValGlnAlaProGlyGluIlePr 229
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 QY 229 oPheAsnGlyIleTyrTyrAspProProGluGluGluLysTyrValPheGlnHisProG 249
 DB 882 TTTCATGGCATATTTATGATCCACTGAAGGAGGAAGTATGTCTTCCAACTCTCA 941
 QY 249 nProLysArgProGluSerLeuArgIleTyrGluSerHisIleGlyMetSerSerProG 269
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 DB 1002 ACCGAAGATTAATTTATGTCTAAATTTTAAAGATGGGTGGCCAAAGATTTAAAGGCT 1061
 QY 289 uGlyTyrAsnAlaValGlnIleMetAlaIleGlnGluHisSerTyrTyrAlaSerPheG 309
 DB 1062 TGGATACATGACGTGCGATTAATGGCAATCCAGAGCATTCATCTATGCAAGCTTTGG 1121

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 QY 429 nMetThrPheThrGlyAsnTyrGlyGlyTyrPheGlyPheAlaThrAspValaAspAlaVa 449
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 DB 1602 TGGTGAAGATGACAGGAATGCTCATATTTGGATCCCTGTCCAGATGGTGGTGG 1661
 QY 489 yPheAspTyrArgLeuHisMetAlaValAlaAspLysTrpIleGluLeuLysGlnSe 509
 DB 1662 TTTTGAATCCGCGCTGTGATGGCTGAGAGAAATGATTAACCTCCCAAGCAAG 1721
 QY 509 rAspGluSerTrpLysMetGlyAspIleValHisThrLeuThrAsnArgArgTrpLeuG 529
 DB 1722 TGAAGATCTTGAAATAGGCGCATATTTGACACCCCTTAACAATAAAGTGGCTTGA 1781
 QY 529 uLysCysValThrTyrAlaGluSerHisAspGlnAlaLeuValGlyAspLysThrIleAl 549
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 DB 1902 TCGCATTTGATCGGCGATAGCATTTACATTAATATATCAGGCTTGACACATGGGTTAG 1961
 QY 589 yGlyGluGlyTyrLeuAsnPheMetGlyAsnGluPheGlyHisProGluTrpIleAspPh 609
 DB 1962 TGGTGAAGCTATCTTAATCTTCAATGGGAATGAAGTTTGGGCATCTGATGATGATTT 2021
 QY 609 eProArgGlyProGlnThrLeuProThrArgLysValLeuProGlyAsnAsnAsnSerTy 629
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 QY 629 rAspLysCysArgArgArgPheAspLeuGlyAspAlaAspPheLeuArgTyrHisGlyMe 649
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Db	2202	GCACGAGTATGTTTCCAGCGAAACATGAGAGATAGTATGATCTTTCGAAAGAGAGA	2261
Qy	689	PleuValPheValPheAsnPheHisIleTrpSerAsnSerPhePheAspTyrArgValGlyCys	709
Db	2262	TTTGGTATTTCTTTTCAACTTCCACTGAGCATATGCTTTTGTGACTACCGCTTGGGGT	2321
Qy	709	sSerArgProGlyIleTyrIleValAlaLeuAspSerAspAspAlaLeuPheGlyGlyPhe	729
Db	2322	TTCCAGAGCTGGGAGATGACAGGTGGCTTGGACTCCGACATGACATCTTTGGTGGATT	2381
Qy	729	eSerArgLeuAspHisAspValAspTyrPheThrThrGluHisProHisAspAsnArgPro	749
Db	2382	CAGCAGGCTTATATCATGATGCTGACTTCCACACCGAATCCGATGACACAGGCC	2441
Qy	749	CArGSerPheSerValTyrThrProSerArgThrAlaValTyrAlaLeuThrGlu	768
Db	2442	CGCGCTCTTCTCGGTGATACCTCCAGACGAGACTGGGTGCTGATGCCCTTACAGAG	2499
RESULT 7			
AF064560		2554 bp mRNA linear PLN 03-NOV-1998	
LOCUS		Hordeum vulgare cultivar Bomi starch branching enzyme Iia (SbeIIa)	
DEFINITION		mRNA, nuclear gene encoding plastid protein, complete cds.	
ACCESSION		AF064560	
VERSION		AF064560.1 GI:3822019	
KEYWORDS			
SOURCE		Hordeum vulgare subsp. vulgare	
ORGANISM		Hordeum vulgare subsp. vulgare	
		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
		Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;	
		Poidea; Triticeae; Hordeum.	
REFERENCE		1 (bases 1 to 2554)	
AUTHORS		Sun, C., Sathish, P., Ahlandsberg, S. and Jansson, C.	
TITLE		The two genes encoding starch-branching enzymes Iia and Iib are	
		differentially expressed in barley	
JOURNAL		Plant Physiol. 118 (1), 37-49 (1998)	
MEDLINE		98404232	
PUBMED		9733524	
REFERENCE		2 (bases 1 to 2554)	
AUTHORS		Sun, C., Sathish, P., Ahlandsberg, S. and Jansson, C.	
TITLE		Direct Submission	
JOURNAL		Submitted (11-MAY-1998) Stockholm University, Biochemistry,	
		Stockholm S-10691, Sweden	
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		FGPEWIDPPEPGQTLPTGKVLPGNNNSYDKRRARFDLGDADFLRYGQDFDQMGH	
		LEKXGFMTSEHQYVSRKEEDKVIIPERGDIVFVFHMSNKKDYRVCCKSKYKX	
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gene			
CDS			

Alignment Scores:			
Pred. No.:	3,44e-297	Length:	2554
Score:	3938.00	Matches:	722
Percent Similarity:	99.05%	Conservative:	6
Best local Similarity:	98.23%	Mismatches:	7
Query Match:	94.46%	Indels:	0
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Qy	54	ThRGInGlyIleValGluThrIleThrAspGlyValThrIleGlyValIleGluVal	73
Db	64	ACTCAGGATTTGGGAAACATCATGATGCTGAACCAAGAGTTAAAGAACTAGTC	123
Qy	74	ValGlyGluLysProArgValValProLysProGlyAspGlyGluIleTyrGluIle	93
Db	124	GTGGGGGAGAAACCGCAAGTTGTCCAAACCAAGAGATGGGCAAAATATACAGATT	183
Qy	94	ASPProThrLeuLysAspPheArgSerHisLeuAspTyrArgTyrSerGluTyrArgArg	113
Db	184	GACCCAAAGCTGAAAGATTTTCCAGCCATCTTGACTACGATACAGGAAATACAGAGA	243
Qy	114	IleArgAlaIleAspGlnHisGluGlyGlyLeuGluAlaPheSerArgGlyTyrGlu	133
Db	244	ATTGCTGCTGATATGACCAACATGAAGTGATGAAAGTTTTCGTGTTATGAA	303
Qy	134	LysLeuGlyPheThrArgSerArgGluGlyIleThrTyrArgGluTyrAlaProGlyAla	153
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Qy	194	IleProHisGlySerArgValLysIleArgMetAspThrProSerGlyValLysAspSer	213
Db	484	ATTCTCATGCTCACCGTAAAGATGAGATGATCTCCATCTGGTGTGAAGATTTCA	543
Qy	214	IleSerAlaTyrIleLysPheSerValGlnAlaProGlyGluIleProPheAsnGlyIle	233
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Qy	314	AsnPhePheAlaProSerSerArgPheGlyThrProGluAspLeuLysSerLeuIleAsp	333
Db	844	AATTTTGTGACCAAGTAGCGTTTGGAACTCCAGAGACTTAAATCTTGAATGAT	903
Qy	334	ArgAlaHisGluLeuGlyLeuLeuValIleMetAspIleValHisSerHisSerSerAsn	353

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 VERSION E14723.1 GI:5709406
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 ORGANSIM
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 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Euphorbiaceae; Oryzae; Oryza.
 1 (bases 1 to 3015)
 REFERENCE
 AUTHORS Baba, T., Kawasaki, T. and Ichikawa, N.
 TITLE NEW RICE GENE FOR STARCH-BRANCHING ENZYME
 JOURNAL Patent: JP 1998004970-A 1 13-JAN-1998;
 MITSUI SHOKUBUTSU BIO KENKUSHO:KK, MITSUI PETROCHEM IND LTD
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 PN JP 1998004970-A/1
 PD 13-JAN-1998
 PF 24-JUN-1996 JP 1996162983
 PI BABA TADASHI, KAWASAKI TSUTOMU, ICHIKAWA NORIO PC
 C12N15/09, A01H5/00, C07H21/04, C12N6/10, C12N9/10, (C12N15/09, PC
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 FT /organism='Oryza sativa'
 FT /cultivar='Nihonbare'
 FT /clone_id='Rice Immature Seed Lambda gIII FT
 FT cDNA library'
 FT /clone_type='Immature seed'
 FT /clone_gpb41'
 FT CDS 129..2654
 FT /product='branching enzyme-4' FT sig_peptide
 FT 129..287.
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 source 1..3015
 Location/Qualifiers
 /organism='Oryza sativa'
 /mol_type='genomic DNA'
 /db_xref='taxon:4550'
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 Score: 3685.00 Matches: 683
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 Best Local Similarity: 81.31% Mismatches: 47
 Query Match: 88.39% Indels: 72
 DB: Gaps: 4
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QY 17 -----ProAla1A----- 19
Db 189 GCGCGCGGGGTGCGCCGCGCGGATCCGGCGGGGTGGAATTGCCGTGGTCTTTC 248
QY 19 ----- 19
Db 249 AGAGAGAGACCTCTTCTCAGCTGGCGGTGTGAGCTGCGGGGTGCTCTCTGGGAAGTGTG 308
QY 19 ----- 19
Db 309 CTGGTGGCTGGCGGTGGAGGACGACCTTGTCTCTCTGGGAAACGACGCTGGAACCT 368
QY 20 ---AlaGlnProGlnGluLeuGlnIleProGlnAsp-----IleGlnGln 33
Db 369 CAAGAGCAACCTGAAGAACTCTCAGATACCTGATGATATAAGTAAACCTTTTGAGAGAG 428
QY 34 Gln-----ThraGluValAsnMetThrGlyGlyThrAlaGluValLeu 48
Db 429 GAGGAAGAGATTCAGACGTGGCAGAGCAAGCATMAAGTTGTGGCTGAAAGCAAACTT 488
QY 49 GluSerSerGluProThrGlnGlyIleValGluThrIleThrAspGlyValThrIleGly 68
Db 489 GAATCTTCAAGAGTATTCAGACATTTGAGGAAATGTGACTGAGGGTGTGATCAAAAGAT 548
QY 69 ValIleGluLeuValGlyGluIleProAspGlyValProIleProGlyAspGlyGln 88
Db 549 GCTGATGAACCACTGTGGAGGATTAACCAAGATTATCCACCAAGAGATGGGACG 608
QY 89 LysIleIleGlyGluIleAspProThrIleuIleuIleuIleuIleuIleuIleuIleu 108
Db 609 AAGATATCAACCAATTCACCAATTCGTCGAGATTTCCGAAACCATCTTACATCCCATATC 668
QY 109 SerGluIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 128
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Db 729 TCTCGTGGTTCAGAAAGGCTTGAATTCACCCGACGCTGAAGGCACTTACCTACCGAGAA 788
QY 149 ThrAlaProGlyAlaHisSerIleAlaIleuValGlyAspPheAsnAsnIleuProAsn 168
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QY 169 AlaAspThrMetThrArgAspAspIleuIleuIleuIleuIleuIleuIleuIleu 188
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QY 189 AspGlySerProAlaIleProHisGlySerArgValIleArgMetAspThrProSer 208
Db 909 GATGATATCCCTGCTATTCCTCATGGCTCAGCGTGAAGATTCGATGATACCAATCATCT 968
QY 209 GlyValIleAspSerIleSerIleIleIleIleIleIleIleIleIleIleIleIleIle 228
Db 969 GCGGTAAGGATTCATTCCTGCTGCGATTAAGTTGATGAGGCTCCAGGTTGAAATA 1028
QY 229 ProPheAsnGlyIleThrIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 248
Db 1029 CCGTAACCAAGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1088
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QY 549 AlaPheIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 568
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 LOCUS AB023498 Oryza sativa mRNA for starch branching enzyme rbe4, complete cds.
 DEFINITION AB023498.1 GI:5689137
 ACCESSION AB023498.1
 VERSION 1
 KEYWORDS starch branching enzyme rbe4.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (sites)
 Mizuno K., Tachibana M., Kobayashi E., Kawasaki T., Funane K.,
 Kobayashi M. and Baba T.
 Molecular cloning and expression analysis of a novel member of
 starch branching enzyme isoform in developing rice seeds
 Unpublished
 2 (bases 1 to 3015)
 Mizuno K. and Baba T.
 Direct Submission
 Submitted (09-FEB-1999) Kouichi Mizuno, University of Tsukuba,
 Institute of Agricultural and Forest Engineering, 1-1-1 Tennoudai,
 Tsukuba, Ibaraki 305-8572, Japan
 (E-mail: koum@tsakura.cc.tsukuba.ac.jp, Tel: 81-298-53-4656,
 Fax: 81-298-55-2203)
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ORIGIN
 Alignment Scores:
 Pred. No.: 2,24e-277 Length: 3015
 Score: 3685.00 Matches: 683
 Percent Similarity: 85.83% Conservative: 38
 Best Local Similarity: 81.31% Mismatches: 47
 Query Match: 88.39% Indels: 72
 DB: 8 Gaps: 4
 US-09-508-377-12 (1-768) x AB023498 (1-3015)
 Oy 1 MetAlaThrPheAlaValAlaSerGlyAlaThrLeuGlyValAlaArgPro----- 16
 Db 129 ATGGCGTCGTCGCGGTGTCGGCGCGAGGCTCGGGGTCGTGCGCGCGGCGCGCGC 188
 Oy 17 -----ProAlaAla----- 19
 Db 189 GCGGCGGGGGTGGCCCGCGCGCGATCCGGCGGGGTGCACTTGCCGTGGTCTTC 248
 Oy 19 ----- 19
 Db 249 AGAGAGAGAGACTCTTCTCAAGTGGCGTTGAGCTGCGCGGGTCTCTCGGAAGTG 308
 Oy 19 ----- 19
 Db 309 CTGGTGCCTGCGCGGTGGAGAGCAGCACTTGCTCTCTCGGMAACAGACTGAAACT 368
 Oy 20 ---AlaGlnProGluGluLeuGlnIleProGluAsp-----IleGluGlu 33
 Db 369 CAAGAGCACTGAAAGATCTCAGATCTGATGATTAATAAAGTAAACCTTTGAGAG 428
 Oy 34 Gln-----ThrAlaGluValAsnMetThrGlyGlyThrAlaGluLysLeu 48
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 Db 669 AGTGATATCAAGAGATGCTGACAGTATTCACCAAGAGAGTGGCTTGATGCTTT 728
 Oy 129 SerArgGlyTyrGluLysLeuGlyPheThrArgSerAlaGluGlyIleThrTyrArgGlu 148
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 Oy 169 AlaAspThrMetThrArgAspAspTyrGlyValIleTrpGluIlePheLeuProAsnAla 188
 Db 849 GAGGATACATATACCAAGAAATAGTAGTGTGGAGATTTCCCTGCTTAACAATGCT 908
 Oy 189 AspGlySerProAlaIleProHisGlySerArgValLysIleArgMetAspThrProSer 208
 Db 909 GATGATCCCCCTGCTATCTCTCATGCTCAGCGTAAAGTTGAGATGATGATACCATCT 968
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FEATURES

Location/Qualifiers

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Score:	3667.00	Matches:	668
Percent Similarity:	93.01%	Conservative:	37
Best Local Similarity:	88.13%	Mismatches:	43
Query Match:	87.96%	Indels:	10
DB:	6	Gaps:	2
US-09-508-377-12 (1-768) x E14724 (1-2364)			
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DB	148	GAGATTCCAGCAGTGGCAGAGCAAGCATTAAGTTGTGGCTGAAGACAACTTGAATCT	207
QY	51	SerGluProthrglnGlyIleValGluThrIleThraSPGlyValThrlGlyValIlys	70
DB	208	TCAGAAATGATTCAAGACATTGAGAAATGTGACTGAGGTGTGATCAAAATGCTGAT	267
QY	71	GlulValValGlyGlyLeuProArgValValProlysProGlyASPGLYLeuIysIle	90
DB	268	GAACCAATGTGGAGATTAACCAAGCATTTCCACACAGAGATGGGCAAGAATA	327
QY	91	TyrGluIleASPProThrlLeuLysASPpheArgSerHisLeuASPThrlArgIysSerGlu	110
DB	328	TACCAAAATTCGACCAATGCTGGAAGGATTTGGAAACCATCTTGATCCGATACAGTGA	387
QY	111	TyrArgArgIleArgAlaIleASPGLNHisGluGlyGlyLeuGluValasmeSerArg	130
DB	388	TACAGAGAAATGCTGAGCTATTGACCAATGAAGGTGCTTGATGCAATTTCTCTGT	447
QY	131	GlyTyrGlyLysLeuGlyPheThraArgSerHisGluGlyIleThrlTyrArgIleTrrPa	150
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QY	171	ThrlMetThraSPASPThrlGlyValTrrGluIlePheLeuProAsnAlaASPGLY	190
DB	568	ACTATGACCAAGAAATGAGTATGGTGTGGAGATTTCCCTGCTCAACATCTGATGA	627
QY	191	SerProAlaIleProHisGlySerArgValIysIleArgMetASPThraSPSerGlyVal	210
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QY	211	LysASPserIleSerHisLeuIleLysPheSerValGlnAlaProGlyGluIleProPhe	230
DB	688	AAGGATTCATTCCTGCTGATTAAGTTGCTGTGCAAGGCTCCAGGTGAATACCGTAC	747
QY	231	AsnGlyIleTrrTyrASPProGluGluGlyValPheGlnHisProGlnPro	250
DB	748	AACGCTATATATATGATCCACTGAAGAAATATATGATTCACACATCTCAACT	807
QY	251	LysArgProGluSerLeuArgIleTrrGlySerHisIleGlyMetSerSerProGluPro	270
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QY	271	LysIleAsnSerTrrAlaAsnPheArgASPGLYValIleProArgIleLysArgLeuGly	290
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QY	311	HisValThraSPphePheAlaProSerSerArgPheGlyThrlProGluASPLeuSer	330
DB	988	CATGTTACTTAACCTTCTTTCGCGCAAGTACCGTTCGGAACCCACAGACTTGAATCT	1047
QY	331	LeuIleASPArgAlaHisGluLeuGlyLeuLeuValIleuMetAspIleValHisSerHis	350
DB	1048	CTGATGATTAAGAGCTCACAGCTTGTTGCTTGTACTTATGATATGTTTCAAGTCAT	1107
QY	351	SerSerAsnAsnThrlLeuASPGLYLeuAsnGlyPheASPGLYThraSPThrlHisTrrPhe	370
DB	1108	GCATCAACATACCTCGATGGTGTGAATGTTTGTATGATGATACATTAATCTTC	1167
QY	371	HisGlyGlyProArgGlyHisHisTrrMetTrrASPserArgLeuPheAsnTrrGlySer	390
DB	1168	CATGTGGACCAACGGGATCATCATGAGATGGAAATTCCTCGCTTCAACTATGAGAGT	1227
QY	391	TrrGluValIleuArgPheLeuLeuSerAsnAlaArgTrrPrrLeuGluGluTrrLysPhe	410
DB	1228	TGGAAATTTTAAGATATTTTACTGTGCAATCCAGGTGTGCTTGAAGAAATGAAATTT	1287
QY	411	ASPGLYPheArgPheASPGLYValThrlSerMetMetTrrHisHisGlyLeuGlnMet	430
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QY	471	GluSPValSerGlyMetProThrlPheCysIleProValProASPGLYValGlyPhe	490
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QY	511	GluSerTrrLysMetGlyAspIleValHisThrlLeuThraSPArgTrrPrrLeuGly	530
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QY	551	TrrLeuMetAspLysASPmetTrrASPpheMetAlaLeuASPArgProSerThrlProArg	570
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QY	571	IleASPArgGlyIleAlaLeuHisIlysmetIleArgLeuValThrlMetGlyLeuGly	590
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QY	591	GluGlyTrrLeuAsnPheMetGlyAsnGluPheGlyHisProGluTrrPrrIleASPphePro	610
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QY	611	ArgGlyProGlnThrlLeuProthrglnGlyValIleuProGlyIleAsnAsnSerTrrASP	630
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QY	631	LysCysArgArgPheASPLeuGlyASPAlaASPpheLeuArgTrrHisGlyMetGln	650
DB	1948	AAATGCGTGTGATTTGACCTTGGAGATGCAGATATATCTAGATATCATGATGACAA	2007
QY	651	GluPheASPGLNAlaMetGlnHisLeuGluGluLysTrrGlyPheMetThrlSerGlnHis	670

Db	208	GAGTTTATCATGCGCGTACGACGACATCTTGAGAGAAAATATGATTCATGACATCTGAGAC	2067
Qy	671	GlnTyValSerArgLysIleGluAspLysValIleIlePheGluArgGlyAspLeu	690
Db	2068	CAGATATATGCGCCCAACACGAGAGAGATTAAGATTCATCTTCGAGAGAGAGATTGG	2127
Qy	691	ValPheValPheAsnPheHisTyrSerAsnSerPhePheAspTyrArgValGlyCysSer	710
Db	2128	GTAATCGTGGTCAACTTCACCTGAGTAATATGCTATTGACTATCGCGTGGTTGTTA	2187
Qy	711	ArgProGlyLysTyrLysValAlaLeuAspSerAspAlaLeuPheGlyLysPheSer	730
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Qy	731	ArgLeuAspHisAspValAspTyrPheThrThrGluHisProHisAspAsnArgProArg	750
Db	2248	CGGCTTATCATGATGCTGAGATTAATCTTCACTGCTGACGCGCGCATGACACAGACCAT	2307
Qy	751	SerPheSerValTyrThrProSerArgThrAlaValValTyrAlaLeuThrGlu	768
Db	2308	TCATTCTCGGTGACACCCCAAGACAGAACCCGCTGCTATGACATTACAGAG	2361
RESULT 11			
LOCUS	AR427891	2446 bp	DNA linear PAT 18-DEC-2003
DEFINITION	Sequence 9 from patent US 6639126.		
ACCESSION	AR427891		
VERSION	AR427891.1	GI:40186911	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 2446)		
AUTHORS	Sewale,V.J.H. and Singletary,G.W.		
TITLE	Production of modified polysaccharides		
JOURNAL	Patent: US 6639126-A 9/28-OCT-2003;		
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Db	113	CTTCTCTCCGAGAGCCGGTCGTGAGACATCACTGAGAACTACAGATTAAGCTGAA---	169
Qy	31	IleGluGluGlnThrAlaGluValAsnMetThrGlyGlyThrAlaGluLysLeuGluSer	50
Db	170	-----GCGAAACTG-----ACTGTGAGAGAG--ACATCC	196
Qy	51	SerGluProThrGln-----	55
Db	197	TCCCTACCAACTCAAAACACATCAGACGTGCTGAGCAAGCTCAGAGATTGAGGCTGAG	256
Qy	56	-----GlyIleValGluThrIleThrAsp	63
Db	257	GAGAGCGCTGAGCTCTCAGAAAGTATGAGATTGAGAGTACTGGTGAACCAAAATTGAT	316
Qy	64	GlyValThrLysGlyValLysGluLeuValAlaGlyGluLysProArgValAlaProLys	83
Db	317	GGTCCAGGACATCAAGCCAAAGCAACCACTCGTGGAGAGAAACACAGATTATCCACCA	376
Qy	84	ProGlyAspGlyGluLysIleTyrGluIleAspProThrIleLysAspPheArgSerHis	103
Db	377	CGAGAGATGGCCCAACAAATATATGAGATTGACCAATGTTGAGAGGTTTCGGCGTCA	436
Qy	104	LeuAspTyrArgTyrSerGluTyrArgArgIleArgAlaAlaIleAspGlnHisGluGly	123
Db	437	CTTGACATCCGATACAGTGAATTAATTAAGATTTAGCTGGCTATTTGATCAACATGAAG	496
Qy	124	GlyLeuGluAlaPheSerArgGlyTyrGluLysLeuGlyPheThrArgSerAlaGluGly	143
Db	497	GGTTTGATCATTTTCAACCGCGTTCGAAAGAGTTTGATTTACTCCACGCGCTGAAGGT	556
Qy	144	IleThrTyrArgGluTyrAlaProGlyAlaHisSerAlaAlaLeuValGlyAspPheAsn	163
Db	557	ATCATTAACAGAGAAATGGGCTCTCGAGCACTCTGACACATTAATTAAGGTGACTTCA	616
Qy	164	AsnTyrAsnProAsnAlaAspThrMetThrArgAspAspTyrGlyValTyrGluIlePhe	183
Db	617	AACCTGAACCAATATGCTGATGCTATGATGCGCAAGAAATAGATACGCGTTGGAGATTT	676
Qy	184	LeuProAsnAlaAspArgLysSerProAlaIleProHisGlySerArgValLysIleArg	203
Db	677	CTGCTTAACATGCTGATGTTCCCTCGATATTCCTATGATGCTCACCGTGAACATACG	736
Qy	204	MetAspThrProSerGlyValLysAspSerIleSerAlaThrIleLysPheSerValGln	223
Db	737	ATGACACACCATCTGGTGTTAAGATTCATTCCTCGATCAAGATTTCCTGTGAG	796
Qy	224	AlaProGlyGluIleProPheAsnGlyIleTyrTyrAspProProGluGluGluLysTyr	243
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Db	857	GTATTCAACACCTCACTAAGCGGCCCAAGTCACTGGAGATTAATTAATTAATTAAT	916
Qy	264	GlyMetSerSerProGluProLysIleAsnSerTyrAlaAsnPheArgAspGluValLeu	283
Db	917	GGAATGAGTACCGCCGAGCAACAAAGTAAACAAATCTAATCTTCAACAGATGAGTCTT	976
Qy	284	ProArgIleLysArgLeuGlyTyrAsnAlaValGlnIleMetAlaIleGlnGluHisSer	303
Db	977	CCAGATTTAAAAAGCTTGATACACACGATACACATTAATTAATTAATTAATTAATTA	1036
Qy	304	TyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaProSerSerArgPheGly	323
Db	1037	TATATACAAAGCTTTGGGTACATGTTACGAATTTTTCGCCCAAGTAGCCGTTTGGG	1096
Qy	324	ThrProGluAspLeuLysSerLeuIleAspArgAlaHisGluLeuGlyLeuLeuValLeu	343
Db	1097	ACTCCAGAGACCTTAATATCTTATTAATTAATTAATTAATTAATTAATTAATTAAT	1156
Qy	344	MetAspIleValHisSerHisSerSerAsnAsnThrLeuAspGlyLeuAsnGlyPheAsp	363
Db	1157	ATGATATTTGCTCATATCATCTTCAATCAAAATTAATTAATTAATTAATTAATTAAT	1216
Qy	364	GlyThrAspThrHisTyrPheHisGlyGlyProArgGlyHisHisTyrMetTyrAspSer	383
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Db      1457 ACTGATGTTGATGACAGTAGTTTACCTAAAGCTGTAACGATCTTATTGCGGCTTAT 1516
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QY      484 ProAspGlyValGlyPheAspTyrArgLeuHisMetAlaValAlaAspIleStrpIle 503
Db      1577 CAAGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1636
QY      504 GluLeuLeuLeuGlnSerAspGlnSerTrpIleMetGlyAspIleValHisThrLeuThr 523
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QY      544 GlyAspIleThrIleAlaPheTrpLeuMetAspIleAspMetTyrAspPheMetAlaLeu 563
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QY      664 GlyPheMetThrSerGlnHisGlnTyrValSerArgLysHisGlnGluAspIleValIle 683
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QY      684 IlePheGlnArgGlyAspLeuValPheValPheAsnPheHisTrpSerAsnSerPhePhe 703
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QY      724 AlaLeuPheGlyGlyPheSerArgLeuAspHisAspValAspTyrPheThrThrGlnHis 743
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QY      744 ProHisAspAsnArgProArgSerPheSerValTyrThrProSerArgThrAlaValVal 763
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RESULT 12
LOCUS   ZM065948          2795 bp    mRNA    linear    PLN 21-AUG-1997
DEFINITION   Zea mays starch branching enzyme I1a (Sbe2a) mRNA, partial cds.
ACCESSION   U65948
VERSION     U65948.1   GI:2340107

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SOURCE      Zea mays
ORGANISM    Zea mays
REFERENCE   1 (bases 1 to 2795)
AUTHORS     Gao,M., Fisher,D.K., Kim,K.N., Shannon,J.C. and Guiltinan,M.J.
TITLE       Independent genetic control of maize starch-branching enzymes I1a
            and I1b: Isolation and characterization of a Sbe2a cDNA
JOURNAL     Plant Physiol. 114 (1), 69-78 (1997)
MEDLINE     97303618
PUBMED      9159942
REFERENCE   2 (bases 1 to 2795)
AUTHORS     Gao,M., Fisher,D.K., Kim,K.N., Shannon,J.C. and Guiltinan,M.J.
TITLE       Direct Substitution
JOURNAL     Submitted (02-AUG-1996) Hort./Biotech. Inst., Penn State University,
            519 Marik, University Park, PA 16802, USA
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Pred. No.:      6,71e-270
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Best Local Similarity: 84.65%
Query Match:    86.08%
DB:             8
Length:         2795
Matches:        662
Conservative:   32
Mismatches:    49
Indels:         39
Gaps:          4
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QY      31 IleGluGlnGlnThrAlaGluValAsnMetThrIleGlyThrAlaGluValLeuGluSer 50
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QY      51 SerGluProThrGln----- 55

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Qy 397 LeuLeuSerAsnAlaArgTTPLeuGluGluTyrLysPheAspGlyPheArgPheAsp 416
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Qy 617 ProThrGlyLysValLeuProGlyLysAsnAsnSerTyrAspLysCysArgArgArgPhe 636
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RESULT 14
E08183
LOCUS E08183 2919 bp RNA linear PAT 29-SEP-1997
DEFINITION Gene of starch-branching enzyme.
ACCESSION E08183
VERSION E08183.1 GI:2176304
KEYWORDS JP 1994261767-A/1.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Euphorbiaceae; Oryzaceae; Oryza.
1 (bases 1 to 2919)
REFERENCE
Baba,T. and Shimada,H.
NEW RICE PLANT STARCH-BRANCHED ENZYMIC GENE
Patent: JP 1994261767-A 1 20-SEP-1994;
MITSUI GIYOUSAI SHOKUBUTSU BIO KENKYUSHO:KK
OS Oryza sativa (rice plant)
PN JP 1994261767-A/1
PD 20-SEP-1994
PF 22-OCT-1993 JP 1993265171
PR 29-OCT-1992 JP 92P 291719
PI BABA TADASHI, SHIMADA HIROAKI
PC C12N15/54,A01H5/00,C12N5/10,C12P19/16//A23U1/10,C12N5/10; CC
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FT 5'UTR /clone='PRB33'
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FEATURES
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Alignment Scores:
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Score: 3362.00 Matched: 602
Percent Similarity: 89.10% Conserved: 68
Best Local Similarity: 80.05% Mismatches: 72
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 QY 577 LeuHisLysMetIleArgLeuValThrMetGlyLeuGlyGlyGlyTyTyLeuAsnPhe 596
 Db 2027 TTGCATTAATAATGATTTAGACTTATCACAAATGGGTAGAGAGAGAGGCTATCTTAACCTT 2086
 QY 597 MetGlyAsnGluPheGlyHisProGluTrrIleAspPheProArgGlyProGluThrLeu 616
 Db 2087 ATGGAAATGATGTTGGACATCTGATGATGATTAATTTTCCAAGCTCCCAACTACTT 2146
 QY 617 ProThrGlyLysValLeuProGlyAsnAsnAsnSerTyraAspLysCysArgArgPhe 636
 Db 2147 CCAATGCTTAATTCATCCACAGGAATACAAACAGTATGATTAATGCCGTGAAAGATT 2206
 QY 637 AspLeuGlyAspAlaAspPheLeuArgTyHisGlyMetGlnGluPheAspGlnAlaMet 656
 Db 2207 GACCTGGGTATCGGACTATCTTAAGTATCGTGGCATGTAGAGTTTGACCGCGCATG 2266
 QY 657 GlnHisLeuGluGluLysTyrgLyuPheMetThrSergLuuHisGlnTyValSerArgLys 676
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 Db 2327 CATGAGAGATTAAGATTAATTTGAGAAAGGAGATCGTGAATTTGTGTTCAACTTC 2386
 QY 697 HisTrrPheSerSerPhePheAspTyraGlyCysSerArgProGlyLysTyrys 716
 Db 2387 CATTTGAGTAAACGTAATTTGATACCGTGTGTGTGTTTAAACCGAGAAATTAATG 2446
 QY 717 ValAlaLeuAspSerAspAspAlaLeuPheGlyGlyPheSerArgLeuAspHisAspVal 736
 Db 2447 GTGTCTTGAGTCAAGATGCTGACCTCTTGTGTGATTTGGCAAGATCATACACTGCA 2506
 QY 737 AspTyrrPheThrThrGlnHisProHisAspAsnArgProArgSerPheSerValTyThr 756
 Db 2507 GAGCACTTCACTCGCGATTTGTTCAATGACAAACGGCCCTACTCGTTCTCATGTTATCT 2566
 QY 757 ProSerArgThrAlaValAlaTyraAlaLeuThrGlu 768
 Db 2567 CTTAGCAAACTCGGTGTGTATGCTTCAACGGCA 2602

RESULT 15

LOCUS AY304540 2664 bp mRNA linear PLN 24-JUN-2003
 DEFINITION Sorghum bicolor starch branching enzyme IIB (sbeIIb) mRNA, complete cds; nuclear gene for plastid product.
 ACCESSION AY304540
 VERSION AY304540.1 GI:32186929
 KEYWORDS
 SOURCE
 ORGANISM
 Sorghum bicolor (sorghum)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.
 1 (bases 1 to 2664)
 Mutisya,J., Sabish,P., Sun,C., Andersson,L., Ahlandsberg,S., Baguma,Y., Palmqvist,S., Ochiambo,B., Amen,P. and Jansson,C.
 Starch branching enzymes in sorghum (Sorghum bicolor) and barley (Hordeum vulgare): Comparative analyses of enzyme structure and gene expression
 J. Plant Physiol. (2003) In press
 2 (bases 1 to 2664)
 Jansson,C. and Mutisya,J.
 Direct Submission
 Submitted (23-MAY-2003) Plant Biology & Forestry Genetics, SU, Uppsala SE-75007, Sweden
 FEATURES
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Alignment Scores:
 Pred. No.: 1,866-251 Length: 2664
 Score: 3351.50 Matches: 609
 Percent Similarity: 84.92% Conservative: 78
 Best Local Similarity: 75.28% Mismatches: 75
 Query Match: 80.39% Indels: 47
 DB: 8 Gaps: 4

US-09-508-377-12 (1-768) x AY304540 (1-2664)

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 Db 54 ATGCGCGCGCTTCCGGCTCTGGAGCGCGCTCGTGGGCGCGTAAAGGCTCCCGCACTC 113
 QY 14 ----- 14

QY 15 -----ArgProProAlaAla 20
 Db 174 GGGGGTCTAGAGTTGGAGCTTCCGGACCGGCGCATGCCGCGCGCGCGCTG 233
 QY 21 GlnProGlnIuLeuGlnIleProGlnAspIleGlnIuGlnThraA---GluValAsn 39
 Db 234 TCCAGAGAGCGGTGCGTGTCTGAGACGAGAACGACGCGCTCGCATCGAAGCTGAC 293
 QY 40 MetThGlyGlyThraGlnIuGlyLeuGluSerSerGluProThnGlnGlyIleValGlu 59
 Db 294 TCGGCTCAGTTCAGTGCAGTGAAGTGAAGTACGACGTTACTGAA-----GAG 344
 QY 60 ThrIleThraSpGlyValThnIleGlyValIleGluLeuValIleGlyIuLysProArg 79
 Db 345 ACCATGGCGCATGCC-----GGCGTGCCTGATGCTCAAGCTTGAACGAGATTGCA 395
 QY 80 ValValProLysProGlnIuAspGlyGlnLysIleGlyGluIleAspProThnIleLysAsp 99
 Db 396 GTGATCCCAACCAACCGACGATGACAAATAATATTCAGATTGACCCCATGCTGCAAGGC 455
 QY 100 PheArgSerHisLeuAspIleArgIleSerGluThraArgArgIleArgAlaIleAsp 119
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 QY 120 GlnHisGlnIuGlyIleGlnIuAlaPheSerArgIleGlyIuLysLeuGlyPheThraArg 139
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 QY 140 SerAlaGlnIuGlyIleThraArgGlnIuThraProGlnIuAlaHisSerAlaIleVal 159
 Db 576 AGCGCGGAGAGTACCATTCGAAATGGGCTCTGAGACACTTTCGACCATTTGGG 635
 QY 160 GlnAspPheLeuAsnIleThraProAsnAlaAspThnMetThraArgAspIleGlyVal 179
 Db 636 GGCACCTTCAACAACCTGGATCCAAATGCAAGCCTTATGAGCAAAATGAGTTGGTGT 695
 QY 180 TrpGlnIlePheLeuProAsnAsnAlaAspIleSerProAlaIleProHisGlySerArg 199
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 QY 200 ValIleSerIleArgValAspThnProSerGlyValIleAspSerIleSerAlaIleLys 219
 Db 756 GTAAAGGTGAAATGATATCTCATCAAGGATTAAGATTCATTCCTGCGATGCAAG 815
 QY 220 PheSerValGlnAlaProGlnIuGlnIleProPheAsnGlyIleThraArgAspProGln 239
 Db 816 TACTCAGTACGGCTCCAGGAAATACCAATGAGTGGCTTATATATATCTCTCTGA 875
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 Db 1056 CAAGAGCATCATATATAGGAAGCTTGGATTCATGATATATTTTGGACCAAGT 1115
 QY 320 SerArgPheGlyThnProGlnAspLeuLysSerLeuIleAspArgAlaHisGluLeuGly 339
 Db 1116 AGTCGTTTGGATCCGAAAGATTGAAGCTTAATGATTAAGACACATGAGCTTGT 1175
 QY 340 LeuIleuValIleuMetAspIleValHisSerHisSerSerAsnAsnThraLeuAspGlyLeu 359
 Db 1235 ----- 1235

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QY 380 MetTrpAspSerArgLeuPheasnTyrGlySerTrpGluValLeuArgPheLeuSer 399
Db 1296 ATGGGAGATTCTCGCTTATTCACATGGAACCTGGGAAGTTTAAGATTCTCTCTCC 1355
QY 400 AsnAlaArgTrpTrpLeuGluGluTyrLysPheaspGlyPheArgPheaspGlyValThr 419
Db 1356 AATGCTAATGCTGCTGAGGAAATTAAGTTGATGTTGCTTCGCTTATGATGTTGAC 1415
QY 420 SerMetMetTyrThrHisHisGlyLeuGlnMetTrpPheThrGlyAsnTyrGlyGluTyr 439
Db 1416 TCCATGATGATACCTACCCGATTCACAGTAACATTTACGGGAGCTTCATAGAT 1475
QY 440 PheGlyPheAlaThrAspValAspAlaValTyrLeuMetLeuValAsnAspLeuIle 459
Db 1476 TTGGCTTTGCCACCGATGATGATGCAAGTGTTCCTGATGCTCGTAATGATCTAATT 1535
QY 460 HisGlyLeuHisProAspAlaValSerIleGlyGluAspValSerGlyMetProThrPhe 479
Db 1536 CATGACCTTTATCCTGAGGCTTAACCATTTGTTGAAGATGTTAGTGAATGCCCTCATTT 1595
QY 480 CysIleProValProAspGlyGlyValGlyPheaspTyrArgLeuHisMetAlaValAla 499
Db 1596 GCCCTTCCTGTCACAGATGAGTGGGAGTTTGATTCGATCGATCGACATGGCTGTGGCT 1655
QY 500 AspIleTrpIleGluLeuLeuLysGlnSerAspGluSerTrpLysMetGlyAspIleVal 519
Db 1656 GACAAATGATTTGATTTCTCAGCAAGTGATGAAGCTTGGAGAGTGGTGATTTGTG 1715
QY 520 HisThrLeuThrAsnArgArgTrpLeuGluLysCysValThrTyrAlaGluSerHisAsp 539
Db 1716 CACACACTAACAAATAGAAAGTGTGGAGAACTGTGAATCTTATGCTGAAGTCAATGAT 1775
QY 540 GlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyrAsp 559
Db 1776 CAAGCATTTAGTGTGACAGACTATTTGATTTGTTGATGACAGCAAGATATGAT 1835
QY 560 PheMetAlaLeuAspArgProSerThrProArgIleAspArgGlyIleAlaLeuHisLys 579
Db 1836 TTCAATGGCCCTTGATGACCTGCACTCCTACCATTTGATCGTGAGATGACATTAAG 1895
QY 580 MetIleArgLeuValThrMetGlyLeuGlyGlyGlyTyrLeuAsnPheMetGlyAsn 599
Db 1896 ATGATTAACCTATCAACAATGCTTATGAGAGGAGGAGGCTATCTTAATTCATGGGAAAT 1955
QY 600 GluPheGlyHisProGluTrpIleAspPheProArgGlyProGlnThrLeuProThrGly 619
Db 1956 GAGTTTGACATCTCGAATGATGATGATTTTCCAAAGGATCCCAAGACTTCCAAAGTGT 2015
QY 620 LysValLeuProGlyAsnAsnAsnSerTyrAspLysCysArgArgArgPheAspLeuGly 639
Db 2016 AAGTTCAATTCAGGGGATATAAACAAGTTATGACAAATGCCGTGAAGATTGACCTGGGT 2075
QY 640 AspAlaAspPheLeuArgTyrHisGlyMetGlnGluPheaspGlnAlaMetGlnHisLeu 659
Db 2076 GATGCGGACTATCTAGGTATCGTGTATGCAAGATTGATCAGGCAATGACCAACATCTT 2135
QY 660 AspIleValIleIlePheGluArgGlyAspLeuValPheValPheAsnPheHisTrpSer 679
Db 2136 GAGCAAAATATGATTCATGACATCCGATCCACCAATATTTCTCGAAAACATGAGAG 2195
QY 680 AspLysValIleIlePheGluArgGlyAspLeuValPheValPheAsnPheHisTrpSer 699
Db 2196 GATAAGATGATGTTGTTGAAAAAGGAGATTGTTGTTGTTGTTCAACTCCACTGTAA 2255
QY 700 AsnSerPhePheAspTyrArgValGlyCysSerArgProGlyLysTyrLysValAlaLeu 719
Db 2256 AACAGCTATTTGACTACCGATATGTTGTGTGAAAACTGGGATGTATTAAGTGTCTTG 2315

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Search completed: April 17, 2004, 21:39:52
Job time : 5397 secs

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Db 2316 GACTCGGACCCCTGGACCTATTGTTGATTTGGAGAGATCCATCAAGCAGAGCACTTC 2375
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QY 760 ThrAlaValValTyrAlaLeuThrGlu 768
Db 2436 ACCTGCGTGTCTATGCTCCAGTGGAG 2462

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 15, 2004, 08:35:15 ; Search time 61 Seconds
(without alignments)
3557.319 Million cell updates/sec

Title: US-09-508-377-12
Perfect score: 4169
Sequence: 1 MATFVSGATLGVANRPPAAA.....PRSFVYTPSRVAVTALTE 768

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues
Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:.*
1: geneseqp1980s:.*
2: geneseqp1990s:.*
3: geneseqp2000s:.*
4: geneseqp2001s:.*
5: geneseqp2002s:.*
6: geneseqp2003as:.*
7: geneseqp2003bs:.*
8: geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4169	100.0	768	2	AAV06917 Starch br
2	3685	88.4	841	2	AAW41763 Rice type
3	3588.5	86.1	814	6	AAE33549 Maize BEI
4	3363	80.7	855	5	AAU76219 Wheat sta
5	3362	80.6	825	2	AAE60811 Rice star
6	3351	80.4	871	2	AAW70895 Maize bra
7	3342	80.2	799	2	AAW56489 Zea mays
8	3341	80.1	799	2	AAW19212 Corn star
9	3292	79.0	848	2	AAW62600 Starch br
10	3241.5	77.8	836	2	AAW62599 Cassava s
11	3197	76.7	842	2	AAE33804 Class A s
12	3197	76.7	849	4	AAU80169 Potato st
13	3193	76.6	878	2	AAW19113 Potato st
14	3189	76.5	847	2	AAW06400 Class A s
15	3155	75.7	858	3	AAE39092 Arabidops
16	3144	75.4	721	3	AAE39093 Arabidops
17	3135	75.2	882	2	AAW06399 Class A s
18	3080	73.9	767	7	ADCO8219 Rice prot
19	3074	73.7	693	3	AAE39094 Arabidops
20	2900	69.6	592	3	AAV84410 Amino aci
21	2900	69.6	758	3	AAV84408 Amino aci
22	2879.5	69.1	888	3	AAV84416 Consensus
23	2227	53.4	481	2	AAW62650 Starch br
24	2166.5	52.0	820	2	AAE33228 Rice star

26	2156.5	51.7	906	2	AAW69300 Potato cl
27	2156.5	51.7	906	2	AAW71290 Potato st
28	2155	51.7	762	7	ADCO8305 Rice prot
29	2146.5	51.5	833	3	AAV32466 Maize sta
30	2146	51.5	751	2	AAE33582 Branching
31	2146	51.5	759	2	AAW70896 Maize bra
32	2146	51.5	822	2	AAW56490 Zea mays
33	2146	51.5	822	6	AAE33548 Maize BEI
34	2146	51.5	844	2	AAW19213 Corn star
35	2140	51.3	702	4	AAE90803 Human she
36	2140	51.3	702	6	ABP71504 Amino aci
37	2134.5	51.2	807	2	AAV06916 wSBE I-D4
38	2064	49.5	834	7	ADCO7804 Rice prot
39	2060	49.4	686	3	AAE49603 Glycogen
40	1965	47.1	665	4	ABE60350 Drosophila
41	1960	47.0	1101	4	AAE82299 Wheat sta
42	1870	44.9	760	4	AAU80171 Red alga
43	1642	39.4	546	6	AAE33547 Potato BE
44	1552	37.2	368	3	AAE15423 Arabidops
45	1547	37.1	367	3	AAE15424 Arabidops

ALIGNMENTS

RESULT 1
ID AAY06917 standard; protein; 768 AA.
XX
XX AAY06917;
AC
XX 17-OCT-2003 (revised)
DT
DT 05-JUL-1999 (first entry)
XX
DE Starch branching enzyme II (SBE II) amino acid sequence.
XX
KW Starch biosynthetic pathway; cereal plant; enzyme; SBE; SSS; DBE; GBSS;
KW starch branching enzyme; starch soluble synthase; debbranching enzyme;
KW endosperm; wheat; barley; granule-bound synthase; glutenin; starch;
KW grain softness protein I; bacterial isoamylase; glycogen synthase;
KW wSBE I-D4 gene.
XX
OS Aegilops tauschii.
XX
XX WO9914314-A1.
XX
XX 25-MAR-1999.
PD
XX 11-SEP-1998; 98WO-AU000743.
PF
XX 12-SEP-1997; 97AU-00009108.
PR
PR 20-MAR-1998; 98AU-00002509.
XX
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
PA (AUSU) UNITV AUSTRALIAN NAT.
PA (GOOD-) GOODMAN FIELDS LTD.
PA (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.
PI Li Z, Morell M, Rahman S;
XX WPI; 1999-229525/19.
DR
XX New isolated cereal plant enzyme genes used for, e.g. expression of
PT antisease sequences of granule bound synthase.
XX
XX Disclosure; Page 83-85; 171pp; English.
XX The invention relates to a novel enzyme of starch biosynthetic pathway in
CC a cereal plant, where the enzyme is selected from starch branching enzyme
CC (SBE) I, SBE II, starch soluble synthase (SSS) I, and debbranching enzyme
CC (DBE), with the proviso that the enzyme is not SSS I of rice, or SBE I of
CC rice or maize. The methods and products can be used for targeting

CC such as wheat or barley. They can be used for the expression of e.g.
 CC antisense sequences of granule-bound synthase (GBS), SBE II, low mol.
 CC wt. glucenin, grain softness protein 1, bacterial isomylase, bacterial
 CC glycogen synthase, and wheat high mol. wt. glucenin Bx1. They can be
 CC used for modifying the characteristics of starch produced by a plant. The
 CC present sequence represents the SBE II protein sequence. (updated on 17-
 CC OCT-2003 to standardise OS field)

XX Sequence 768 AA;

Query Match 100.0%; Score 4169; DB 2; Length 768;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 768; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATFAVSATLGVARPPAAQPELQIPEDIEBQTAENVMTGTAELSEPTQGIYET 60
 DB 1 MATFAVSATLGVARPPAAQPELQIPEDIEBQTAENVMTGTAELSEPTQGIYET 60
 QY 61 ITDGVTKGVKELVYGEKRVVPEKPGDQKIYEIDPTLKDFRSHLDYRSEYRIRAIIDQ 120
 DB 61 ITDGVTKGVKELVYGEKRVVPEKPGDQKIYEIDPTLKDFRSHLDYRSEYRIRAIIDQ 120
 QY 121 HEGGLAFAFRGYEKLGTTRAEAGITTRERAPGASALVGDFFNNMNPADMTEDDYGW 180
 DB 121 HEGGLAFAFRGYEKLGTTRAEAGITTRERAPGASALVGDFFNNMNPADMTEDDYGW 180
 QY 181 ERLPNNADSPAIPIHSGRVKIRMDTSGVYDSISAMIKFSVQAPGEIPIFYDPEE 240
 DB 181 ERLPNNADSPAIPIHSGRVKIRMDTSGVYDSISAMIKFSVQAPGEIPIFYDPEE 240
 QY 241 ERYVFGHPQKPRESLRIYESHISMSSPEPKINSYANFRDVLPRIKLGNVAQVMAIQ 300
 DB 241 ERYVFGHPQKPRESLRIYESHISMSSPEPKINSYANFRDVLPRIKLGNVAQVMAIQ 300
 QY 301 EHSYVASFQHVNTNFAPSSRFCTPEDLKSILDRANHELGLVMDIVSHSSNNTLDGLN 360
 DB 301 EHSYVASFQHVNTNFAPSSRFCTPEDLKSILDRANHELGLVMDIVSHSSNNTLDGLN 360
 QY 361 GFPGCTDHYHGGPRGHMMWDSRLFNYSWEVLRFLSNARWMLLEEKYFGRFDGVT 420
 DB 361 GFPGCTDHYHGGPRGHMMWDSRLFNYSWEVLRFLSNARWMLLEEKYFGRFDGVT 420
 QY 421 MMYTHHGLQMTFTGNNGYEGFATDVAVYVLMVNDIIGHLPDASIGEDVSGMPFC 480
 DB 421 MMYTHHGLQMTFTGNNGYEGFATDVAVYVLMVNDIIGHLPDASIGEDVSGMPFC 480
 QY 481 IVPDGVGVGDYRLHMAVADKWIELLKQSDSMKMGDIVHTLTKRMLEKCVTAESHQ 540
 DB 481 IVPDGVGVGDYRLHMAVADKWIELLKQSDSMKMGDIVHTLTKRMLEKCVTAESHQ 540
 QY 541 ALVGDKTIAMFLMDKMDYDFMALDRPSTPRIDRGIALHKMIRLVTMGSGBYLNFANE 600
 DB 541 ALVGDKTIAMFLMDKMDYDFMALDRPSTPRIDRGIALHKMIRLVTMGSGBYLNFANE 600
 QY 601 FGHPEWIDPRGPQTLPTGKVLPGNNNSYDKCRREFDGDADFLRHYGQEQEDQMOHLE 660
 DB 601 FGHPEWIDPRGPQTLPTGKVLPGNNNSYDKCRREFDGDADFLRHYGQEQEDQMOHLE 660
 QY 661 EKGGMFSEHQYVRKHEEDKVIIFERGDVLFVNFHNSNFFEDRVGCSRGKXKVALD 720
 DB 661 EKGGMFSEHQYVRKHEEDKVIIFERGDVLFVNFHNSNFFEDRVGCSRGKXKVALD 720
 QY 721 SDDALFCGFSRLDHDVDYFTEHHPDNRPRSFVYTPERTAVVVALTE 768
 DB 721 SDDALFCGFSRLDHDVDYFTEHHPDNRPRSFVYTPERTAVVVALTE 768

RESULT 2
 AA41763
 ID AA41763 standard; protein; 841 AA.

XX
 AC
 XX
 AA41763;
 XX

DT 25-MAR-2003 (revised)
 DT 01-MAY-1998 (first entry)
 XX Rice type IV starch branching enzyme.
 DE Rice type IV starch branching enzyme; amylopectin synthesis.
 XX Rice; type IV starch branching enzyme; amylopectin synthesis.
 XX Oryza sativa.
 OS Oryza sativa.
 PN JP10004970-A.
 XX 13-JAN-1998.
 PD 24-JUN-1996; 96JP-00162983.
 PF 24-JUN-1996; 96JP-00162983.
 PR 24-JUN-1996; 96JP-00162983.
 PA (MITSU) MITSU GYOSAI SHOKUBUTSU BIO KENKYUSHO.
 PA (MITK) MITSU TOATSU CHEM INC.
 DR WPI; 1998-133625/13.
 DR N-PSDB; AAV05639.
 XX Rice starch branching enzyme gene - synthesises amylopectin to yield high
 PT quality starch.
 PS Claim 1; Page 5-8; 13pp; Japanese.
 XX The present sequence is the rice type IV starch branching enzyme, which
 CC has the ability to synthesise amylopectin. The quality of starch is
 CC improved by the use of the protein. (updated on 25-MAR-2003 to correct PA
 CC field.)
 CC Sequence 841 AA;

Query Match 88.4%; Score 3685; DB 2; Length 841;
 Best Local Similarity 88.1%; Pred. No. 0;
 Matches 668; Conservative 37; Mismatches 43; Indels 10; Gaps 2;

QY 21 QPEELQIPED-----IEEQ-----TAEVMTGTAEKLSSEPTQGIYETITDGVTKVK 70
 DB 83 QPEEQIPDDNKVKPFESEELPAVAFASIKVYAEKLSSEVYQIIEENVTEGVIRKAD 142
 QY 71 ELVGEKPRVVPKPGDQKIYEIDPTLKDFRSHLDYRSEYRIRAIIDQHEGLAFAFR 130
 DB 143 EPTVEDKPRVIPPQGGQKIYIDPWLBEGRNHLDRYSEYKMRRAIDQHEGLAFAFR 202
 QY 131 GYEXKGFTRSAGITTYREWAPGASALVGDFFNNMNPADMTEDDYGWEIFLPNNADG 190
 DB 203 GYEXKGFTRSAGITTYREWAPGASALVGDFFNNMNPADMTEDDYGWEIFLPNNADG 262
 QY 191 SPALPHSGRVKIRMDTPSGVKSISAMIKFSVQAPGEIPIFYDPEEKKYFQHPQ 250
 DB 263 SPALPHSGRVKIRMDTPSGVKSISAMIKFSVQAPGEIPIFYDPEEKKYFQHPQ 322
 QY 251 KRPESLRITESHITGSSPEPKINSYANFRDVLPRIKLGNVAQVMAIOEHSYASFGY 310
 DB 323 KRPNSLRITESHITGSSPEPKINTYANFRDEVLPRIKLGYNVQVMAIOEHSYASFGY 382
 QY 311 HTNFPAPSRFGTPEDLKSILDRANHELGLVMDIVSHSSNNTLDGLNGFDGTDHYF 370
 DB 383 HTNFPAPSRFGTPEDLKSILDRANHELGLVMDIVSHSSNNTLDGLNGFDGTDHYF 442
 QY 371 HCGPRGHMMWDSRLFNYSWEVLRFLSNARWMLLEEKYFGRFDGVTSMYTHHGLQV 430
 DB 443 HCGPRGHMMWDSRLFNYSWEVLRFLSNARWMLLEEKYFGRFDGVTSMYTHHGLQV 502
 QY 431 TPTGNNGYEGFATDVAVYVLMVNDIIGHLPDASIGEDVSGMPFCIPVDGGVGF 490
 DB 503 APTGNNGYEGFATDVAVYVLMVNDIIGHLPDASIGEDVSGMPFCIPVDGGVGF 562
 QY 491 DYRLHMAVADKWIELLKQSDSMKMGDIVHTLTKRMLEKCVTAESHQDALVGDKTIAP 550

Db 563 DYRLHMAVPDDKRIELLKQSDDEYKMGDIYHTLTNRBMSKCYTAAASHDQALVGDKTIAF 622
 Qy 551 WLMDXDMTDFMALDRPSTPRIDRGIALHKMIRLVTMGLGEGYLTNFMNGEFGHPEDIDP 610
 Db 623 WLMDXDMTDFMALDRPSTPRIDRGIALHKMIRLVTMGLGEGYLTNFMNGEFGHPEDIDP 682
 Qy 611 RGPQLLPFGKULPGNNNSYDKCRRRFDLDADLRYHGMQEPDOAQHLEKYGEMTSEH 670
 Db 683 RGPQLLPFGKULPGNNNSYDKCRRRFDLDADLRYHGMQEPDOAQHLEKYGEMTSEH 742
 Qy 671 QYVSRKHEEDKXIIIFERGLVVFNFHMSNSFEDYRGVCSRPQKYKVALDSDALFEGGFS 730
 Db 743 QYISRKHEEDKXIIIFERGLVVFNFHMSNSYFDYRGVCSRPQKYKVALDSDALFEGGFS 802
 Qy 731 RLDDVDVFTTEHPHNDPRPSFSVYTPSRATVAVYALTE 768
 Db 803 RLDDVDVFTTEHPHNDPRPSFSVYTPSRATVAVYALTE 840

RESULT 3
 AAE33549 standard; protein; 814 AA.

AC AAE33549;
 XX 16-APR-2003 (first entry)
 XX Maize BEII protein #2.
 DE Transgenic; amylose; branching enzyme; BE; R1 protein; starch; maize;
 KM enzyme.
 XX Zea mays.
 OS WO2002101059-A2.
 PN 19-DEC-2002.
 FD 07-JUN-2002; 2002WO-EP006265.
 PF 12-JUN-2001; 2001DE-01028363.
 PR (PARB) BAYER CROPS SCIENCE GMBH.
 XX Uwer U, Froberg C, Pilling J, Landshuetz V;
 PI WPI; 2003-148812/14.
 DR Novel transgenic plants and plant cells capable of synthesizing high
 PT amylose starch, comprising a genetic modification which leads to
 PT reduction of activity of branching enzymes I and II and R1 proteins.
 CC Disclosure; Col 89-93; 47pp; English.
 CC The invention relates to transgenic plants and plant cells capable of
 CC synthesizing high amylose starch, comprising a genetic modification which
 CC leads to reduction of activity of branching enzymes (BE) I and II and R1
 CC proteins. The invention is useful for producing starch, by extracting
 CC starch from transgenic plant and/or from starch-storing parts of such a
 CC plant and/or from a plant cell such as transgenic plant cell. The present
 CC sequence is maize BEII protein
 PS
 XX
 SQ Sequence 814 AA;

Query Match 86.1%; Score 3588.5; DB 6; Length 814;
 Best local similarity 84.7%; Pred. No. 0;
 Matches 662; Conservative 32; Mismatches 49; Indels 39; Gaps 4;

Qy 11 LGVAPPPAAAGPELQIPEDIEBQTAENVNTGTAEKLESSEPTQ----- 55
 Db 38 LSGAEVVDQPELQIPF-----AEI-----TVEK-TSSSPQTSTSAVAEASGVAE 85
 Qy 56 -----GIVETITDGVTKGVAELVYGEKPRVVPKRGDQKYEIDPTLKDFRSH 103

Db 86 ERPDLSEVIGVGCGGTIKIDAGIRAKAPLVLEKERVLPFPDGGRIYEIDPVLBGRGH 145
 Qy 104 LDYRYSEYRRAAIDQHEGGLAPASRGYELGFTRSAGITRYREMAPAHSAALVGDEN 163
 Db 146 LDYRYSEYRRAAIDQHEGGLAPASRGYELGFTRSAGITRYREMAPAHSAALVGDEN 205
 Qy 164 MNMNADMTMTDDYGVWAEIIFLPNNADGSPAIPIHSGRVKIRMDTPSGVKDISAMIKFSVQ 223
 Db 206 MNMNADMTMTDDYGVWAEIIFLPNNADGSPAIPIHSGRVKIRMDTPSGVKDISAMIKFSVQ 265
 Qy 224 APGEIPIFGIYYDDPEEEKYVFQHPQKRPESLRIYESHIGSSPEPKINSYANFDEVL 283
 Db 266 APGEIPIFGIYYDDPEEEKYVFQHPQKRPESLRIYESHIGSSPEPKINSYANFDEVL 325
 Qy 284 PRIRKLGYNVQIMAIQEHSTYASFGYVNTNFAASSRGTBEDLSLIDRAHELGLVL 343
 Db 326 PRIRKLGYNVQIMAIQEHSTYASFGYVNTNFAASSRGTBEDLSLIDRAHELGLVL 385
 Qy 344 MDIVSHSSNNTLDGLNGFDGDTHTYFHGPRGHMMMDRLFNYSWEVLRFILSNARV 403
 Db 386 MDIVSHSSNNTLDGLNGFDGDTHTYFHGPRGHMMMDRLFNYSWEVLRFILSNARV 445
 Qy 404 WLEBYKPDGFRFDGVTSMYTHGLQMTFTNGYGEYFGPATDVAVVYLMVNDLIRGLH 463
 Db 446 WLEBYKPDGFRFDGVTSMYTHGLQMTFTNGYGEYFGPATDVAVVYLMVNDLIRGLH 505
 Qy 464 PDVSGISGDSGMPFCIPVPDGVGFDYRLMAVADKRIELLKQSDDEYKMGDIYHTLT 523
 Db 506 PEAVSIGSDVSGMPFCIPVPDGVGFDYRLMAVADKRIELLKQSDDEYKMGDIYHTLT 565
 Qy 524 NRRWLEKCVTAESHDQALVGDKTIAFMLMDXDMTDFMALDRPSTPRIDRGIALHKMIRL 583
 Db 566 NRRWLEKCVTAESHDQALVGDKTIAFMLMDXDMTDFMALDRPSTPRIDRGIALHKMIRL 625
 Qy 584 VTMGLGEGYLTNFMNGEFGHPEDIDPFRGPQTLPTGKVLPGNNNSYDKCRRRFDLDGADY 643
 Db 626 VTMGLGEGYLTNFMNGEFGHPEDIDPFRGPQTLPTGKVLPGNNNSYDKCRRRFDLDGADY 685
 Qy 644 LRYHGMQEPDOAQHLEKYGEMTSEHQYVSKRHEEDKXIIIFERGLVVFNFHMSNSYF 703
 Db 686 LRYHGMQEPDOAQHLEKYGEMTSEHQYVSKRHEEDKXIIIFERGLVVFNFHMSNSYF 745
 Qy 704 DYRVGCSRPQKYKVALDSDDALFEGGFSRLDDVDVFTTEHPHNDPRPSFSVYTPSRATV 763
 Db 746 DYRVGCSRPQKYKVALDSDDALFEGGFSRLDDVDVFTTEHPHNDPRPSFSVYTPSRATV 805
 Qy 764 YA 765
 Db 806 YA 807

RESULT 4
 ID AAU76219 standard; protein; 855 AA.
 XX AAU76219;
 AC 08-MAY-2002 (first entry)
 DT Wheat starch branching enzyme IIb protein from clone wdk2c_pk009.j17.
 XX Wheat starch branching enzyme IIb protein from clone wdk2c_pk009.j17.
 DE Wheat starch branching enzyme; starch synthesis; transgenic plant;
 KM wdk2c_pk009.j17; antibody; gene mapping; enzyme.
 OS Triticum aestivum.
 FH Key Location/Qualifiers
 FT 161..855
 FT /note="This sequence is shown in sequence ID no. 2 and
 FT is specifically claimed in claim 2 of the specification"
 XX

US2002002713-A1.

XX 03-JAN-2002.
 PD 23-FEB-2001; 2001US-00792127.
 XX 01-MAR-2000; 2000US-0186098P.
 XX (ALLEN/) ALLEN S M.
 PA (BECK/) BECKLES D M.
 PA (BUTL/) BUTLER K H.
 PA (PEAR/) PEARLSTEIN R W.
 PI Allen SM, Beckles DM, Butler KH, Pearlstein RW,
 DR WPI; 2002-178959/23.
 XX N-PSDB; ABX15494.
 PT Novel isolated polypeptide having starch iib enzyme activity, useful for
 PT preparing antibodies to the proteins which are used to detect the
 PT polypeptides in situ in cells or in vitro in cell extracts.

Claim 2; Fig 1; 27bp; English.

This invention relates to the cDNA and protein sequences of a novel wheat starch branching enzyme iib enzyme. Starch branching enzymes are responsible for the formation of alpha 1-6 linkages in amylopectin in the starch synthesis pathway. The nucleotide sequence of the invention is useful for producing a transgenic plant expressing the starch branching enzyme. The protein sequence is useful for preparing antibodies against starch branching enzyme iib protein, which are useful for detecting the proteins in situ in cells or in vitro in cell extracts. The protein is also useful for selecting an isolated polynucleotide that affects the level of expression of a starch branching enzyme iib protein or enzyme activity in a plant cell. All or substantial portion of the nucleotide sequence can be used as probe for genetic and physical mapping of the genes and can be used as markers for traits linked to those genes. This information is useful in plant breeding in order to develop lines with desired phenotypes. A polynucleotide fragment is useful for isolating cDNAs and genes encoding homologous proteins from the same or other plant species. They are also useful as DNA hybridisation probes or as polymerase chain reaction (PCR) amplification primers. The fragments are also useful for creating transgenic plants and may be useful as restriction fragment length polymorphism markers. Nucleic acid probes derived from the cDNA sequence may also be used for physical mapping or for fluorescence in situ hybridisation (FISH) mapping. The present sequence represents the wheat starch branching enzyme iib protein encoded by the cDNA from clone wdk2c.pk009.j17

XX Sequence 855 AA:

Query Match 80.7%; Score 3363; DB 5; Length 855;
 Best Local Similarity 79.5%; Pred. No. 1.le-306;

Matches 607; Conservative 75; Mismatches 68; Indels 14; Gaps 4;

QY 7 SGATLGAAPPAAGP-----EIQIPEDIEBQTEAVMTGSGTAKLESSEPTQGIIVETI 61
 DB 98 SGGT-----PESIDGPFQVDSDDLKP-FIDET--SLQDGGEDSINSSEFNQVSEED 148
 QY 62 TDGVTGKVELVGEKPRVVPKPGDGQKIYEIDPTLKDFRSHLDYRSEYRIRAAIDQH 121
 DB 149 AEDTSRMDKESSTREKRLILPPENGQOIYEIDPLRPFKYLERYSLYRIRSIDBH 208
 QY 122 EGGLEAFSGRGYKLGFTSAGETTYREWAPGAHSAALYGDENNANPNADYTFRDYGVWE 181
 DB 209 EGGMDVFSRGYKLGFTSAGETTYREWAPGAHSAALYGDENNANPNADYTFRDYGVWE 268
 QY 182 IFLNNNDGSPALIPGSGRVKIRMDTPSGVKSISAMIKSVQAPGIPNGIYYDPPEEE 241
 DB 269 IFLNNNDGSPALIPGSGRVKIRMDTPSGVKSISAMIKSVQAPGIPNGIYYDPPEEE 328
 QY 242 KYVFQHPQPKPESIRIYESHIGMSPEEKINSYANFRDEVLPRIKELGYNAVOIMAOE 301
 DB 329 KYVFQHPQPKPESIRIYESHIGMSPEEKINSYANFRDEVLPRIKELGYNAVOIMAOE 388

QY 302 HSYAASFGYHTNFPAPSSRPGTPEDLKSLIDRAHELGLVLMIDIVSHSSNNITLDGLNG 361
 DB 389 HSYAASFGYHTNFPAPSSRPGTPEDLKSLIDRAHELGLVLMIDIVSHSSNNITLDGLNG 448
 QY 362 FDGTDTHYFHGGPRGHMMWMDSRLENYGSWEYAREFLSNARWMLBEYKEDGERFDGVTSM 421
 DB 449 FDGTDTHYFHGGPRGHMMWMDSRLENYGSWEYAREFLSNARWMLBEYKEDGERFDGVTSM 508
 QY 422 MYTHGLQMTTNGNGEYFGFATDYDAVYVLMVNDLHGLHPDAYSIGEDVSGMPTFC 481
 DB 509 MYTHGLQMTTNGNGEYFGFATDYDAVYVLMVNDLHGLHPDAYSIGEDVSGMPTFC 568
 QY 482 FVPDGGVGFEDYRLHMAVADKMTIELLKQSDSWMKQDIYHTLNNRWLEKCVTYAESHDQ 541
 DB 569 FVPDGGVGFEDYRLHMAVADKMTIELLKQSDSWMKQDIYHTLNNRWLEKCVTYAESHDQ 626
 QY 542 LVGDKTIAFWLMDKMDYDPMALDRPSTPRIDRGIALHKMIRLVTMGLGEBGYLNEVGNF 601
 DB 629 LVGDKTIAFWLMDKMDYDPMALDRPSTPRIDRGIALHKMIRLVTMGLGEBGYLNEVGNF 688
 QY 602 GHPWIDPPRGQDTLPTGKVLPGNNNSYDKCRRRDLGADFLRYHGMQEFQDMQHLLE 661
 DB 689 GHPWIDPPRGQDTLPTGKVLPGNNNSYDKCRRRDLGADFLRYHGMQEFQDMQHLLE 748
 QY 662 KYGFMTSHQYVSRKHEEDKVIIFERGLVVFENFHMNSFFDYRGVSGRPGKYKVALDS 721
 DB 749 KYGFMTSHQYVSRKHEEDKVIIFERGLVVFENFHMNSFFDYRGVSGRPGKYKVALDS 808
 QY 722 DDALFGFGRDLDDYDFTTEHPHNDPRPSFVYTPSRITAVVYA 765
 DB 809 DAGLFGFGRDLDDYDFTTEHPHNDPRPSFVYTPSRITAVVYA 852

RESULT 5

AA060811 ID AA060811 standard; protein; 825 AA.

AA060811; 05-JUL-1995 (first entry)

Rice starch branching enzyme.

Starch branching enzyme; rice; starch content.

Oryza sativa.

Oryza sativa.

Oryza sativa.

Oryza sativa.

Oryza sativa.

Oryza sativa.

Oryza sativa.

Oryza sativa.

Oryza sativa.

Oryza sativa.

Oryza sativa.

Oryza sativa.

Oryza sativa.

Oryza sativa.

Oryza sativa.

Claim 1; Page 9-12; 13pp; Japanese.
 The rice starch branching enzyme (AA060811) and cDNA encoding it have

QY 413 FRPDGVTSMYTHHGLQMTFTNGYGEFGATVDVAVYMLVNDLHGLHPDAVISGD 472
 DB 444 FRPDGVTSMYTHHGLQMTFTNGYGEFGATVDVAVYMLVNDLHGLHPDAVISGD 503
 QY 473 VSGMPTFCIPVPGGVGPDYRLHMAVADKWTLLKQSDGSMKMDIVHTLNNRRLKCV 532
 DB 504 VSGMPTFCIPVPGGVGPDYRLHMAVADKWTLLKQSDGSMKMDIVHTLNNRRLKCV 563
 QY 533 TYAESHDQALVGDXTIAFWLMDKMDYFMAIDRSTPRIDRGIALHKMIRLVTMGLGSEG 592
 DB 564 TYAESHDQALVGDXTIAFWLMDKMDYFMAIDRSTPRIDRGIALHKMIRLVTMGLGSEG 623
 QY 593 YLNFMGNEFGHPMTIDPRPGQTLPTGKVLPGNNNSYDKCRRRPDLGADYLRYHGMQEF 652
 DB 624 YLNFMGNEFGHPMTIDPRPGQTLPTGKVLPGNNNSYDKCRRRPDLGADYLRYHGMQEF 683
 QY 653 DOAMQHLEEKYGFMTSEHQYVSRKHEEDKVIIFERGLVFNFMHMSNPFDPYVGCGRP 712
 DB 684 DOAMQHLEEKYGFMTSEHQYVSRKHEEDKVIIFERGLVFNFMHMSNPFDPYVGCGRP 743
 QY 713 GKXKVALDSDDALFGGFSRLDHDVYFTTEHPHNDPRPSFSVYTPSRVAVYALTE 768
 DB 744 GKXKVALDSDDALFGGFSRLDHDVYFTTEHPHNDPRPSFSVYTPSRVAVYALTE 799

RESULT 7

AAW56489
 ID AAW56489 standard; protein; 799 AA.

AAW56489;

11-SEP-1998 (first entry)

Zea mays starch branching enzyme II.

SEB; starch-encapsulating region; fusion vector;
 starch branching enzyme II; glucosyl transferase.

Zea mays.

MO9814601-A1.

09-APR-1998.

30-SEP-1997; 97WO-US017555.

30-SEP-1996; 96US-0026855P.

(EXSE-) EXSEED GENETICS LLC.

Keeling P, Guan H;

WPI; 1998-240100/21.

N-PSDB; AAV29757.

Hybrid polypeptide comprising starch-encapsulating region and protein -
 useful for, e.g. producing protein(s) resistant to degradation by stomach
 acids.

Example 2; Page 43; 156pp; English.

The sequence is that of starch branching enzyme II. It can be used in the
 production of a hybrid polypeptide comprising a starch-encapsulating
 region (SEB) fused to a payload protein. The hybrid polypeptide can be
 used to make modified starches comprising the payload protein, selected
 from, e.g. hormones, growth factors, antibodies, enzymes, dyes,
 immunoglobulins, etc. The modified starch can also be used to provide
 grain feeds enriched in amino acids. By encapsulating the payload protein
 in starch, it is more resistant to degradation by stomach acids

Sequence 799 AA;

Query Match

80.2%; Score 3342; DB 2; Length 799;

Best Local Similarity 78.4%; Pred. No. 9e-305;
 Matches 608; Conservative 67; Mismatches 79; Indels 22; Gaps 4;

QY 4 FAVSGATLGV-----ARPPAAQPEELQIPEDIEBQTAENVMTGTAELKESSE----- 52
 DB 35 FLTRGARVCGSGTHGMAAAARAKAVMVEGEND-----GLASRADSAQFQSD 85
 QY 53 PFGIVETITDGVTKVKEVLVNGEKRVYKPKSDGQKIYEDTLQDPRHLDVRYSEYR 112
 DB 86 EVDPISEETGCA--GVAQAQALNRRVVRPPSDGQKIFQIDPMLOGYKTHLEYRILYR 143
 QY 113 RIRPAIDQHEGGLAEPFRGKELGFTSAEGITYREMAPGASALVGDPRNNPNADTM 172
 DB 144 RIRSDIDEHGGLEAFSRSEYKGFNASAGITYREMAPGAFSALVGVNNMDPNADM 203
 QY 173 TRDDYGVMEIFLPNNADGSPALPHGSRVKIRMDTPSGVKDSISAMIKFSVQAPGEIPNG 232
 DB 204 SKNEFGVMEIFLPNNADGSPALPHGSRVKIRMDTPSGVKDSISAMIKFSVQAPGEIPNG 263
 QY 233 IYDPEEEKYVQHPQPKRPSRLTYESHIGSSPEPKINSYANFRDEVLPRIKRLGYN 292
 DB 264 IYDPEEEKYVQHPQPKRPSRLTYESHIGSSPEPKINSYANFRDEVLPRIKRLGYN 323
 QY 293 AVQIMAIQESHYSYASFGYHVTNFFAPSSRFTEDELKSLIDRAHELGLVLMDIVSHSS 352
 DB 324 AVQIMAIQESHYSYASFGYHVTNFFAPSSRFTEDELKSLIDRAHELGLVLMDIVSHSS 383
 QY 353 NNTLDGLNGFDGDTYFHGSGRHHMMMDSLFNTGSMWELRPLLSNARWMLSEYKDG 412
 DB 384 NNTLDGLNGFDGDTYFHGSGRHHMMMDSLFNTGSMWELRPLLSNARWMLSEYKDG 443
 QY 413 FRPDGVTSMYTHHGLQMTFTNGYGEFGATVDVAVYMLVNDLHGLHPDAVISGD 472
 DB 444 FRPDGVTSMYTHHGLQMTFTNGYGEFGATVDVAVYMLVNDLHGLHPDAVISGD 503
 QY 473 VSGMPTFCIPVPGGVGPDYRLHMAVADKWTLLKQSDGSMKMDIVHTLNNRRLKCV 532
 DB 504 VSGMPTFCIPVPGGVGPDYRLHMAVADKWTLLKQSDGSMKMDIVHTLNNRRLKCV 563
 QY 533 TYAESHDQALVGDXTIAFWLMDKMDYFMAIDRSTPRIDRGIALHKMIRLVTMGLGSEG 592
 DB 564 TYAESHDQALVGDXTIAFWLMDKMDYFMAIDRSTPRIDRGIALHKMIRLVTMGLGSEG 623
 QY 593 YLNFMGNEFGHPMTIDPRPGQTLPTGKVLPGNNNSYDKCRRRPDLGADYLRYHGMQEF 652
 DB 624 YLNFMGNEFGHPMTIDPRPGQTLPTGKVLPGNNNSYDKCRRRPDLGADYLRYHGMQEF 683
 QY 653 DOAMQHLEEKYGFMTSEHQYVSRKHEEDKVIIFERGLVFNFMHMSNPFDPYVGCGRP 712
 DB 684 DOAMQHLEEKYGFMTSEHQYVSRKHEEDKVIIFERGLVFNFMHMSNPFDPYVGCGRP 743
 QY 713 GKXKVALDSDDALFGGFSRLDHDVYFTTEHPHNDPRPSFSVYTPSRVAVYALTE 768
 DB 744 GKXKVALDSDDALFGGFSRLDHDVYFTTEHPHNDPRPSFSVYTPSRVAVYALTE 799

RESULT 8

AAW19212
 ID AAW19212 standard; protein; 799 AA.

AAW19212;

10-SEP-1997 (first entry)

Corn starch branching enzyme IIb.

Starch branching enzyme IIb; SEBIIb; corn; maize; antisense; amylopectin;

transgenic plant; pBE240.

Zea mays.

MO9722703-A2.

Tue Apr 20 10:02:28 2004

us-09-508-377-12.rag

Page 7

26-JUN-1997.
12-DEC-1996; 96WO-US019678.
20-DEC-1995; 95US-0009113P.
(DUPO) DU PONT DE NEMOURS & CO E I.
Hubbard NL, Klein TM, Broglie KE;
WPI, 1997-341694/31.
N-PSDB; AAT69729.
Transgenic corn in which grain derived starch fine structure is
controlled - specifically branch chain distribution of amylopectin,
useful in preparation of thickened foodstuff.
Example 1; Page 50-53; 92pp; English.
Corn starch branching enzyme IIb (SBEIIb) (AAW19212) is an isoform of
starch branching enzyme that shows higher rates of branching with
amylopectin rather than amylose as substrate. A CDNA insert (AAT69729) in
plasmid clone pBR240 that expresses SBEIIb has been used as a starting
point in the assembly of DNA constructs (see also AAT69730, AAT69736-37)
designed to achieve suppression of SBEIIb expression in transgenic corn
plants, and thereby to produce novel starches that have properties
beneficial in food and industrial applications

Sequence 799 AA;

Query Match 80.1%; Score 3341; DB 2; Length 799;
Best Local Similarity 78.4%; Pred. No. 1.1e-304;
Matches 608; Conservative 67; Mismatches 79; Indels 22; Gaps 4;

4 FAVSAGATLGV-----ARPPAAQPEELQIPEDIEEQTAENVMTGTAKESSE----- 52
35 FLTRGARVCGSGTHGAMRAAARAAKAVMVEGEND-----GLASRADSAQFOSDEL 85
53 PROGIYETITDGTGKVKELVGEKPRVVKPGDGQKIYEIDPTLKDFRSHLDYRSEYR 112
86 EWPDISETTCGA--GVADAQALNRVVPVPPSDQKIFQIDPWLQGYKTLERYSYR 143
113 RIRPAIDQHEGGEAFSGRYEKLQFTRSAGGITRYEMAPGAHSAALVGFNNMNPNDTM 172
144 RIRSDIDHEHGGEAFSGRYEKLQFTRSAGGITRYEMAPGAHSAALVGFNNMNPNDTM 203
173 TRDDYGVWEIFLPPNADGSPAIPIHSSRYKIRMDTPSGVKDSISAMIKRSVQAPGPIPN 232
204 SKNEFGWEIFLPPNADGSPAIPIHSSRYKIRMDTPSGVKDSISAMIKRSVQAPGPIPN 263
233 IYDPEEEKRYVQHPKPKPESIRIYESHIGSSPEPKINSYANFREVLPRIRLGYN 292
264 IYDPEEEKRYVQHPKPKPESIRIYESHIGSSPEPKINSYANFREVLPRIRLGYN 323
293 AVOIMAIQHSYVYASFGYHVTNFPAPSGRFGTPEDLKSLIDRAHELGLVIMDIYHSHS 352
324 AVOIMAIQHSYVYASFGYHVTNFPAPSGRFGTPEDLKSLIDRAHELGLVIMDIYHSHS 383
353 NNTLDGNGFDGTDTHYFHGGPRGHMMWDSRLFNYSGWMEVLRFLSNARWLEEKYKPDG 412
384 NNTLDGNGFDGTDTHYFHGGPRGHMMWDSRLFNYSGWMEVLRFLSNARWLEEKYKPDG 443
413 FRPQGVSNMTHHGLQMTFTGNGYGEYGFATPDVAVVYLMVNDLIGLHPDAVIGSD 472
444 FRPQGVSNMTHHGLQMTFTGNGYGEYGFATPDVAVVYLMVNDLIGLHPDAVIGSD 503
473 VSGMPFCIPVDPGVGVDFYRLHNAVADKWIELLKQSDSWKMGDIIVTLINRWLEKCV 532
504 VSGMPFCIPVDPGVGVDFYRLHNAVADKWIELLKQSDSWKMGDIIVTLINRWLEKCV 563
533 TYAASHDQALVGKTIATFWMKDMYDPMALDRPSTPRIDGIALHKKILRLVTMGLGSG 592

593 YLNMENEPFGHPWIDPPRGQTLPTGKVLPGNNNSYKCRRRPDLGADAPLRHGMQEP 652
624 YLNMENEPFGHPWIDPPRGQTLPTGKVLPGNNNSYKCRRRPDLGADAPLRHGMQEP 683
653 DQAMQHLEKXGEMTSEHQYSRKHEEDKXVIFEEGDLVFVFNFMNSFFDYRVGCSRP 712
684 DQAMQHLEKXGEMTSEHQYSRKHEEDKXVIFEEGDLVFVFNFMNSFFDYRVGCSRP 743
713 GKXVALDSDDALFGFSRLDHDVDYFTTEHPHNRPRFSYVTPSRATVAYALTE 768
744 GYKRVLDSDAGLFGFSRHHAAHFTALDCHDRPFYSSSVYTSRITCVVYAPVE 799

RESULT 9

AAW62600 standard; protein; 848 AA.

AAW62600;

21-SEP-1998 (first entry)

Starch branching enzyme II (SBE II).

Starch branching enzyme; SBE; cassava.

Manihot esculenta.

Key Location/Qualifiers

Misc-difference 143.145 /note="proline elbow"

W09820145-A2.

14-MAY-1998.

04-NOV-1997; 97WO-GB003032.

05-NOV-1996; 96GB-00023095.

(NAT) NAT STARCH & CHEM INVESTMENT HOLDING COR.

Jobling SA, Safford R;

WPI, 1998-286958/25.

N-PSDB; AAW62600.

Starch branching gene from cassava - useful for producing altered plants
giving modified starch.

Claim 1; Fig 13; 67pp; English.

The present sequence represents starch branching enzyme (SBE) II. The DNA
sequence was isolated from cassava tubers. The products can be used for
CC producing plants having altered starch quantities and qualities. They can
also be used for producing altered plants such as cassava, banana,
CC potato, pea, tomato, maize, wheat, barley, oat, sweet potato and rice
CC plants

Sequence 848 AA;

Query Match 79.0%; Score 3292; DB 2; Length 848;
Best Local Similarity 77.3%; Pred. No. 5.1e-300;
Matches 595; Conservative 71; Mismatches 72; Indels 32; Gaps 4;

23 BELQIPEP-----IEQTAENMTG-----GIAEKL-----ESSPTQGIIV 58
68 EKVLPVDDQIDGSSSTYQLETTGYLIESQVLGDSLSVMEDDKAVEDEVKESVYVH 127
59 EITTDGVTGKVELVVGKPRVVPKPGDGQKIYEIDPTLKDFRSHLDYRSEYRIRPAI 118
128 EITISIKSF-----SKPRSTPPGSGQRITDIDPSLNGFRGLDYRSQYKRLREI 179

XX AAU80169;
AC 15-JUL-2002 (first entry)
XX Potato starch branching enzyme, SBE II.
XX Potato; starch branching; enzyme; SBE II; glucan branching enzyme; GBE;
XX plant; transgenic; antisense; food industry; paper industry;
XX chemical industry.
XX Solanum tuberosum.
XX GH2360521-A.
XX 26-SEP-2001.
XX 20-MAR-2000; 2000GB-00006733.
XX 20-MAR-2000; 2000GB-00006733.
XX (DANI-) DANISCO AS.
XX Poulsen P, Sorensen IS;
XX WPI; 2001-650142/75.
XX N-PSDE; ABK50301.
XX
XX New transformed plants with reduced endogenous starch branching enzyme
XX PT and heterologous glucan branching enzyme activities, useful for producing
XX PT starch with improved properties, which is in the food, paper and chemical
XX PT industries.
XX
XX Example 1; Page 31-35; 61pp; English.
XX
XX The invention relates to a transformed organism, preferably a transformed
XX CC plant, having a reduced endogenous starch branching enzyme (SBE)
XX CC activity, and having a heterologous glucan branching enzyme (GBE)
XX CC activity. The reduced SBE activity is effected via expression of a
XX CC nucleotide sequence that is antisense to at least part of a SBE exon.
XX CC Also included are a method of producing starch with altered
XX CC characteristics comprising (a) providing a plant having reduced
XX CC endogenous SBE activity, and having heterologous GBE activity (b)
XX CC propagating the plant of (a) and optionally (c) obtaining starch from the
XX CC plant; starch obtainable from the transformed plant; and a nucleic acid
XX CC construct system capable of directing the expression of all or part of
XX CC one or more antisense SBE exons and optionally one or more heterologous
XX CC GBE. The transformed plants are useful for producing starch with modified
XX CC and improved properties, which is an important raw material and used in
XX CC the food, paper and chemical industries. The present sequence represents
XX CC potato SBE II, used to make transgenic plants of the invention
XX
XX Sequence 849 AA;
SQ
Query Match 76.7%; Score 3197; DB 4; Length 849;
Best Local Similarity 72.6%; Pred. No. 4.5e-291;
Matches 586; Conservative 82; Mismatches 91; Indels 46; Gaps 6;
QY 2 ATFAVSGATL--GVAPPPAAQPEELQIPE-----DIEBQTAE----- 37
DB 38 STVAASGKVLVGTGSDSSSSSTDDFEFTSPENSASTDVDSSTMEHSAQIKTENDDV 97
QY 38 ---VAMTGTAE-----KLESSEPTQGVITITGVTVGKEIVVGEKPRVY 81
DB 98 EPSSDLTSVEELDPAASISIQLOEGGKLESKTLNTEFTIIDSDE-IRE-----RGI 149
QY 82 PKPGDQGIYEIDPTLKDFRSHLDYRYSEYRIRAIADIDHGGLEAFSGYKLGFTRSA 141
DB 150 PPPGCGKIVYEIDPLILNVRQLDLYRISQYKTLREALIDYEGGLEAFSGYKMGFTRSA 209
QY 142 EGIYREVAAPGAAHALLVGDPPNNAMPNATMTTRDDYGVWEIPLPNNADSPALPHGSRYK 201
DB 210 TGIYREVAAPGAAHALLVGDPPNNAMPNATMTTRDDYGVWEIPLPNNADSPALPHGSRYK 269

QY 202 IMDTSPGVKDISAMIKFVQAPGEIPNGIYYDPEEERKYYFOHPQPKRPESLRIYES 261
DB 270 IMDTSPGVKDISAMINYSLOLPDEIPNGIYYDPEEERKYYFOHRRPKPKSLRIYES 329
QY 262 HIGMSSPEPKINSYANFDEVLPRIRLGNVAQVIAIQSHSYASGCHYTNFFAPSSR 321
DB 330 HIGMSSPEPKINSYANFDEVLPRIRLGNVAQVIAIQSHSYASGCHYTNFFAPSSR 389
QY 322 FGTPEDLKSLIDRAHGLGLVMDIVSHSSNNLTGLNFPDGDTHYFFGPGGHHMMW 381
DB 390 FGTPEDLKSLIDRAHGLGLVMDIVSHSSNNLTGLNFPDGDTHYFFGPGGHHMMW 449
QY 382 DSRLFNYSQMEVLRFLISNARWMLLEBYKFDGFRPDGVTSMNYTHGLOMTFTNGYGEYFG 441
DB 450 DSRLFNYSQMEVLRFLISNARWMLLEBYKFDGFRPDGVTSMNYTHGLOMTFTNGYGEYFG 509
QY 442 FATVDVAVVYLMVNDLIHGLHPDAVSIGEDVSGMPFCTIPVDDGSGYFDRILMAVADK 501
DB 510 LATVDVAVVYLMVNDLIHGLHPDAVSIGEDVSGMPFCTIPVDDGSGYFDRILMAVADK 569
QY 502 WTELKQSDPSWKGDIYHTITRRRLKCVTAESHDQALVGDKTAFMLMDKMDYDFM 561
DB 570 WTELKQSDPSWKGDIYHTITRRRLKCVTAESHDQALVGDKTAFMLMDKMDYDFM 629
QY 562 ALDRPSTPRIDRIGIALHKMIRLVTMGIGSGEYINFMGNEFGHPMIDFPKPGQTLPTGKV 621
DB 630 ALDRPSTPRIDRIGIALHKMIRLVTMGIGSGEYINFMGNEFGHPMIDFPKPGQTLPTGKV 689
QY 622 LPGNNSYDKCRRRPDLGDALFIRHGMQFPDQAMQTLKRYGTMSEHQVSKKHEBDK 681
DB 690 IPGNQFSYDKCRRRPDLGDALFIRHGMQFPDQAMQTLKRYGTMSEHQVSKKHEBDK 749
QY 682 VIFERGDIVFVNFPMNSFPDPRVGCSPRGKKVALLDSDALFGFSRLHDHVDYFTT 741
DB 750 MIVFEKGNLVFVNFPMNSFPDPRVGCSPRGKKVALLDSDALFGFSRLHDHVDYFTT 809
QY 742 EHPDNRPRSPSYTTPSRITAVYALTE 768
DB 810 EGMVDDRPISIMYVAPSRTAVYVYALVD 836
RESULT 13
AAM19113
ID AAM19113 standard; protein; 878 AA.
AC AAM19113;
XX 26-AUG-1997 (first entry)
DT 26-AUG-1997 (first entry)
XX Potato starch branching enzyme II.
DB Potato starch branching enzyme II.
XX Starch branching enzyme II; bell gene; potato; transgenic plant;
XX amylopectin; amylose; starch.
XX Solanum tuberosum.
OS Solanum tuberosum.
XX Key Location/Qualifiers
FH Peptide 1..48
FT Misc-difference 33 /label= Sig_peptide
FT /note= "residue 33 was not detd. owing to degeneracy of
FT Protein coding sequence (codon NTR)"
FT Misc-difference 406 /label= Mat_protein
FT /note= "residue 406 was not detd. owing to degeneracy of
FT Misc-difference 570 coding sequence (codon TTN)"
FT /note= "residue 570 was not detd. owing to degeneracy of
FT coding sequence (codon TNR)"
XX
XX W09720040-A1.

XX 05-JUN-1997.
 XX 28-NOV-1996; 96WO-SE001558.
 XX 29-NOV-1995; 95SE-00004272.
 XX 19-APR-1996; 96SE-00001506.
 XX (AMYL-) AMYLOGENE HB.
 XX Ek B, Khosnoodi J, Larsson C, Larsson H, Raak L;
 XX MPI, 1997-310596/28.
 XX N-PSDB; AAT69587.
 XX Isolated potato starch branching enzyme II - useful for altering degree
 XX of amylopectin branching and amylopectin/amylose ratio in potato starch.
 XX Claim 1; Page 12-15; 24pp; English.
 CC The amino acid sequence (AAW19113) for potato starch branching enzyme II
 CC (BEII) was deduced from a cDNA clone (AAT69587) isolated from tuber cDNA
 CC using primers (AAT69588-89) based on BEII tryptic peptides. It shows 68%
 CC identity to potato starch branching enzyme I and about 80% identity to
 CC BEII from other plant species. BEII, or functional active parts of the
 CC enzyme, can be expressed in transgenic potatoes. The starch obd. from
 CC such plants will show a changed pattern of amylopectin branching and an
 CC altered amylopectin to amylose ratio
 XX Sequence 878 AA;

Query Match 76.6%; Score 3193; DB 2; Length 878;
 Best Local Similarity 72.6%; Pred. No. 1,1e-290;
 Matches 566; Conservative 82; Mismatches 91; Indels 48; Gaps 6;

QY 2 ATEVAGATL--GVAPPAAPPELQIP-----DIEQQLA----- 37
 DB 60 STVAASGKVLVPQTQSSSSSTQPEFTSPENSPASTDVDSSTWEHASQIKTENDV 119
 QY 38 ---VAMTGTAAE-----KLESEPTQIVETITDVTGKVKELVGEKPRV 81
 DB 120 EPSSDLTGVEELDPASSLQLOEGGKLESEKTLNTSETLITDESDR--IRF-----RGI 171
 QY 82 PKRGDQKQIYEIDPTLKDFRSHLDYRYSEYRIRAPAIIDHGGGLAERSGKELGFTRSA 141
 DB 172 PRPGLGQKIYEIDPLLTNYQHLDYRSQYKRLAIDKVEGGLAERSGKELGFTRSA 231
 QY 142 EGTYYEAMAGAHSAALVGDPNNNPNACTMTTRDDYGVWETFLNNADGSAIIRHGSVYK 201
 DB 232 TGITTYREMAFPAQSAALIGDPNNWDANADITRNEFGWEFLPNNVDGSAIIRHGSVYK 291
 QY 202 IRMDTSGVVDSTISAWTKESVQAGEIPFNGIYDPEEEKYVPOHPKPKESIRIYES 261
 DB 292 IRMDTSGVVDSTISAWTKESVQAGEIPFNGIYDPEEEKYVPOHPKPKESIRIYES 351
 QY 262 HIGMSSEPKINSYANFRDEVLPRIKELGYNAVOIMAIQHSYVAFSGYHVTNFPAPSR 321
 DB 352 HIGMSSEPKINSYANFRDEVLPRIKELGYNAVOIMAIQHSYVAFSGYHVTNFPAPSR 411
 QY 322 FGTPEDELKSLIDRAHEIGLVMDIVSHSGNNTLDGNGDGTDTYHFGGPRHHMMW 381
 DB 412 FGTPEDELKSLIDRAHEIGLVMDIVSHSGNNTLDGNGDGTDTYHFGGPRHHMMW 471
 QY 382 DSRLEFNGSWEVRLFLISNAKMWLEEKPFDFPDGVTSMMYTHHGLQMTFTGNGEYFG 441
 DB 472 DSRLEFNGSWEVRLFLISNAKMWLEEKPFDFPDGVTSMMYTHHGLQMTFTGNGEYFG 531
 QY 442 FATDVDAVVVIMLVNDLIHGLHPDAVSIIGEDVSGMPTFCIPVDPGVGFDYRLMAVADK 501
 DB 532 LATDVDAVVVIMLVNDLIHGLHPDAVSIIGEDVSGMPTFCIPVDPGVGFDYRLMAVADK 591

DB 592 WIELKKRDEDMRVGDIIVHTLTNRMSSEKCVSYAESHQALVGDXTIAFRLMDKMYDFM 651
 QY 562 ALDRPSTPRIDRGIALHRIYLVMTGCGEGYLTNMGNEFGHPENIDFPRGQTLPTQKY 621
 DB 652 ALDRPSTSLIDRGIALHRIYLVMTGCGEGYLTNMGNEFGHPENIDFPRGQTLPTQKY 711
 QY 622 LFGNNNSYDKCRPRPDLDADPLRHYHGOEFPQAOHLEEKYGFMTSEHQVSRKHEBDK 681
 DB 712 IPGNQFSTDKCRPRPDLDADPLRHYHGOEFPQAOHLEEKYGFMTSEHQVSRKHEBDK 771
 QY 682 VIFERGLVFEVFNHWNSEFPDYRVGSGRPGKYKVALDSDDALFGGSRLLDHDVFTT 741
 DB 772 MIVFEKGLVFEVFNHWNSEFPDYRVGSGRPGKYKVALDSDDALFGGSRLLDHDVFTT 831
 QY 742 EHPHDPSPSPSVTPSRATVYALTE 768
 DB 832 EGWYDDRPSPSPSVTPSRATVYALTE 858

RESULT 14
 ID AAW06400 standard; protein; 847 AA.
 XX AAW06400;
 XX 25-FEB-1997 (first entry)
 DE Class A starch branching enzyme (psbe2con.seq - clone psj30).
 XX Starch branching enzyme; SBE; class A; Solanum tuberosum;
 KM amylose; viscosity; potato.
 OS Solanum tuberosum.

Key Location/Qualifiers
 FH Peptide 1..11
 FT /label= sig_peptide
 FT Protein 12..847
 FT /label= mat_protein

MO9634968-A2.
 PD 07-NOV-1996.
 PF 03-MAY-1996; 96WO-GB001075.
 XX 05-MAY-1995; 95GB-00009229.
 PR 10-APR-1996; 96GB-00007409.
 XX (NAT) NAT STARCH & CHEM INVESTMENT HOLDING COR.
 PI Cooke D, Debet M, Gidley MJ, Jobling SA, Safford R;
 PI Sidebottom CM, Westcott RJ;
 DR MPI, 1996-506170/50.
 DR N-PSDB; AAT42631.
 XX New potato plant starch having high amylose content - also class A starch
 XX branching enzyme and corresp. DNA to alter the viscosity of starch; for
 XX use in food, biodegradable products, adhesives, etc.
 PS Disclosure; Fig 12; 142pp; English.
 CC Class A starch branching enzyme (SBE) has been obtained from potatoes. In
 CC class A SBE mols., a flexible N-terminal domain, is found, which is not
 CC found in class B mols
 XX Sequence 847 AA;

Query Match 76.5%; Score 3189; DB 2; Length 847;
 Best Local Similarity 72.5%; Pred. No. 2,5e-290;
 Matches 585; Conservative 80; Mismatches 94; Indels 48; Gaps 6;


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Best Local Similarity 75.2%; Pred. No. 4,1e-287;
Matches 561; Conservative 90; Mismatches 79; Indels 16; Gaps 3;
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Dd 109 BEAQETETL-DQTSALSTSGSISYKEDFAKMSHV-----DQEVQ-Q-RKIP 152
QY 83 KPGDQKTYEIDPTLKDFRSHLDYRSEYRRIAPAIQDHEGGEAFSRGYEKUGFTSAAE 142
Dd 153 PPGDQKRTYIDPMLNSRNMHLDYRQYRKIREIDKMEGGEAFSRGYEIGFTSAT 212
QY 143 GITYREMAPGASALVQDFNNMNPADTTRDDYGVMEIFLENNADGSPAIHGSRVKI 202
Dd 213 GITYREMAPGAKAASLIGDFNNMNAKSDVMAHNDFGVWEIFLENNADGSPAIHGSRVKI 272
QY 203 RMDTPGVKDSISAAIKFSVQAPGEIPFGIYVDPREEKYVQHOPRRESLRIYESH 262
Dd 273 RMDTPSGIKDSIPAIKTSVQPGEPYNGVYIDPEEBKVAKHPKPKPTSLRIYESH 332
QY 263 IGMSSPEPRKINSYANFRDEVLPRIKRLGYNVQIQAIOHSHSYASFGYHVTNFPASSRF 322
Dd 333 VGMSTEKIKNTYANFRDQVLPRIKRLGYNVQIQAIOHSHSYASFGYHVTNFPASSRF 392
QY 323 GTPEDLKSLIDRAHGLGLVLTMDIVSHSSNNTLDGNGDFDGTDTYFFHGGPRGHHMWD 382
Dd 393 GTPEDLKSLIDRAHGLGLVLTMDIVSHSKNTLDELDFDGDGQYFHSGSGYHMMWD 452
QY 383 SRLFNYSWVYLRFLNLSNARWMLSEYKFDGPFDDGTSMMWYTHGLQMTPTNGYGEYEGF 442
Dd 453 SRLFNYSWVYLRFLNLSNARWMLSEYKFDGPFDDGTSMMWYTHGLQMTPTNGYGEYEGF 512
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Tue Apr 20 10:02:28 2004

us-09-508-377-12.rag

Page 14

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Db	513	STVDVAVVYLYLWNLHGLYEPALVGBDVSGMPVPCVPEBGGVGFYRHLHMAVADKM	572
Qy	503	IELLKODSESWMGDVIHVLITNRMLKECVTAESHDAJVDKTTAFYLMDCMDYFMA	562
Db	573	IELLKQREBDQVGGITFTLITNRNGEKVCVYAESHDALVBDKTTAFYLMDCMDYFMA	632
Qy	563	LDRPSTPIRDIQALAHKMLRIVTMGLIGBQZYNFMGNFGHPWEIDFPRGPQTLPTGXYL	622
Db	633	YDRQATPRVDRIALAHKMLRILITMGLIGBQZYNFMGNFGHPWEIDFPRDQHLPGRAYI	692
Qy	623	PGNNNSYDKCRRRFDLGDADFLRYHMGQFDDAQMLLEKYGWMTSEHQVYSKXKHEDKY	682
Db	693	AGNNNSYDKCRRRFDLGDADFLRYHMLQGFDDAQMLLEKYGWMTSEHQVYSKXKHEDRY	752
Qy	683	IFEEGDLVFEVNEFMHNSNFFPYRVGCSPGGKXVALJDSODALFGGFSRLDHDVDFTTE	742
Db	753	IVFEESGNLLEFVNEFMHTNSYSYDRICQSPGKIKYIVLDSDNSLFGGFSRNLDSASAEFTSD	812
Qy	743	HPHDNRPRGFSYVTPSRITAVVYALTE	768
Db	813	GRHDDRPGCSFMYVYAPCRITAVVYAAVD	838

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GenCore version 5.1.6
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Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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SUMMARIES

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4	3342	80.2	799	3	US-08-941-445A-15
5	3175	76.2	878	3	US-09-087-277-2
6	3175	76.2	878	4	US-09-658-499-2
7	2213	53.1	444	3	US-09-087-277-2
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13	1608	38.6	566	4	US-09-609-040-2
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15	541.5	13.0	762	4	US-09-537-120-2
16	538	12.9	768	4	US-09-489-039A-1131
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21	282.5	6.8	559	3	US-08-242-680A-15
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23	282.5	6.8	559	4	US-09-908-855-15
24	279	6.7	1938	4	US-09-514-302-2
25	276.5	6.6	893	4	US-09-514-302-4
26	267.5	6.4	793	4	US-09-463-238-5
27	253.5	6.1	606	3	US-09-187-124-2

28	253.5	6.1	606	4	US-09-850-936-2	Sequence 2, Appl1
29	246	5.9	829	4	US-09-514-559-6	Sequence 6, Appl1
30	246	5.9	862	3	US-09-346-237-1	Sequence 1, Appl1
31	241.5	5.8	740	2	US-08-410-784A-4	Sequence 1, Appl1
32	240	5.8	838	4	US-09-463-238-14	Sequence 14, Appl1
33	237.5	5.7	789	4	US-09-731-166-16	Sequence 16, Appl1
34	236.5	5.7	818	2	US-08-410-784A-2	Sequence 2, Appl1
35	236.5	5.7	818	3	US-09-346-237-11	Sequence 11, Appl1
36	233	5.6	589	1	US-08-399-646-2	Sequence 2, Appl1
37	233	5.6	589	1	US-08-607-321-2	Sequence 2, Appl1
38	233	5.6	589	2	US-08-607-321-2	Sequence 2, Appl1
39	233	5.6	589	2	US-08-605-501-2	Sequence 2, Appl1
40	233	5.6	596	1	US-08-399-646-12	Sequence 12, Appl1
41	233	5.6	596	1	US-08-607-321-12	Sequence 12, Appl1
42	233	5.6	596	2	US-08-961-240-12	Sequence 12, Appl1
43	233	5.6	596	2	US-08-605-501-12	Sequence 12, Appl1
44	230	5.5	597	1	US-08-399-646-4	Sequence 4, Appl1
45	230	5.5	597	1	US-08-607-321-4	Sequence 4, Appl1

ALIGNMENTS

RESULT 1									
US-09-609-040-4									
Sequence 4, Application US/09609040									
Patent No. 6570066									
GENERAL INFORMATION:									
APPLICANT: Wilitizer, et al.									
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES ENCODING ENZYMES THAT ALTER THE CARBOHYDRAT									
FILE REFERENCE: 51413-3515.1									
CURRENT FILING DATE: 2000-06-30									
PRIOR APPLICATION NUMBER: PCT/EP92/00302									
PRIOR FILING DATE: 1992-02-11									
NUMBER OF SEQ ID NOS: 4									
SOFTWARE: Patent version 3.0									
SEQ ID NO 4									
LENGTH: 729									
TYPE: PRT									
ORGANISM: Triticum aestivum									
US-09-609-040-4									
Query Match 93.9%; Score 3915; DB 4; Length 729;									
Best Local Similarity 98.2%; Pred. No. 0;									
Matches 716; Conservative 7; Mismatches 6; Indels 0; Gaps 0;									
QY	40	MTGTAKEKLESEPTQIGVETITTDGTVKVELVGEKPRVVRKPGDGCKIYEIDPLKD	99						
DB	1	MTGTAKEKLESEPTQIGVETITTDGTVKVELVGEKPRVVRKPGDGCKIYEIDPLKD	60						
QY	100	FSHLDYRSEYRRIRAIIDQHEGGLAERSGVEKLGFTSAEGITYREMAFGAHSALV	159						
DB	61	FSHLDYRSEYRRIRAIIDQHEGGLAERSGVEKLGFTSAEGITYREMAFGAHSALV	120						
QY	160	GDENNPNADMTTRDDYGVWEIFLPNADGSPALPHGSRAVKTRMDTPSGVKSISAWIK	219						
DB	121	GDENNPNADMTTRDDYGVWEIFLPNADGSPALPHGSRAVKTRMDTPSGVKSISAWIK	180						
QY	220	FEVQAPGEIPNGIYVDPPEEKYVVOHOPKPEESLRITESHIGMSPEPKINSYANFR	279						
DB	181	FEVQAPGEIPNGIYVDPPEEKYVVOHOPKPEESLRITESHIGMSPEPKINSYANFR	240						
QY	280	DEVLPRIKELGVNAVOINAIQESHYSYASFGYHTNFPAPSSRGTPEDLKLIDRAHELG	339						
DB	241	DEVLPRIKELGVNAVOINAIQESHYSYASFGYHTNFPAPSSRGTPEDLKLIDRAHELG	300						
QY	340	LIVLMDIVSHSSNNTLDGLNGFDGTDTHYFHGGPGRGHMMMSRLFNYSWELRFLLS	399						
DB	301	LIVLMDIVSHSSNNTLDGLNGFDGTDTHYFHGGPGRGHMMMSRLFNYSWELRFLLS	360						
QY	400	NARWMLIEKXKPGFPRDVTSMWYTHGLQMTGTANYGEYFGFATVDVAVYLMVLVNDLI	459						

Tue Apr 20 10:02:28 2004

us-09-508-377-12.ra1

Page 2

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Db 361 NAWMIEBYVFDGPRFGVTSNMYTHHGLQWTFNGYGEYGFATDVAVVYLMVNDLI 420
Qy 460 HGHAPDAVSGEDVSGMPTFCIPVDPGVGFVDRILHNAVADKMTIELLKQSDSEMKMGDIY 519
Db 421 HGIYPDAVSGEDVSGMPTFCIPVDPGVGFVDRILHNAVADKMTIELLKQSDSEMKMGDIY 480
Qy 520 HTLNBRWLEKCVTYAASHQALVGDKTIAFWLMDKMYDFMALDRPSTPRIDGIALHK 579
Db 481 HTLNBRWLEKCVTYAASHQALVGDKTIAFWLMDKMYDFMALDRPSTPRIDGIALHK 540
Qy 580 MRLVTMGLGEGYLNFMGNEFGHPWIDPFRGPQTLPTGKVLPGNNNSYDKCRRRFDLG 639
Db 541 MRLVTMGLGEGYLNFMGNEFGHPWIDPFRGPQTLPTGKVLPGNNNSYDKCRRRFDLG 600
Qy 640 DADFLRHGQEFDOAQHLEKYGFMTSSEHOYYSRKHEEDKVIIFERGDVFNFMHMS 699
Db 601 DAEFLRYRGQEFDOAQHLEKYGFMTSSEHOYYSRKHEEDKVIIFERGDVFNFMHMS 660
Qy 700 NSFEDVVGCSRGPKYKVALDSDDALFGFSRLDHDVDYFTTEHPHNRPRSFSVYTPSR 759
Db 661 NSFEDVVGCSRGPKYKVALDSDDALFGFSRLDHDVDYFTTEHPHNRPRSFSVYTPSR 720
Qy 760 TAVVYALTE 768
Db 721 TAVVYALTE 729
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RESULT 2
US-09-731-166-10
; Sequence 10, Application US/09731166
; Patent No. 6639126
; GENERAL INFORMATION:
; APPLICANT: Sewalt, Vincent J. H.
; APPLICANT: Singletary, George W.
; TITLE OF INVENTION: Production of Modified Polysaccharides
; FILE REFERENCE: 35718/206348
; CURRENT APPLICATION NUMBER: US/09/731,166
; CURRENT FILING DATE: 2000-12-06
; PRIOR FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 814
; TYPE: PRT
; ORGANISM: Zea mays
US-09-731-166-10
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Query Match 86.1%; Score 3588.5; DB 4; Length 814;
Best Local Similarity 84.7%; Pred. No. 0;
Matches 662; Conservative 32; Mismatches 49; Indels 39; Gaps 4;
Qy 11 LGVAPPPAAQPEELQIPEDIEBQTAENVMTGTAKLESSEPTQ----- 55
Db 38 LLSAEPVVDQTPEELQIPE-----AEL-----TYEK-TSSSPTQTTSAVAEASGVAE 85
Qy 56 -----GIYETITDGVTKGKELVGEKPRVVPKPGGQKIYEIDPTLKDPRSH 103
Db 86 ERPELSEVIGVGGTGTAKIDGAKAKADLVSEKPPVLPFGGQKIYEIDPTLKGPRGH 145
Qy 104 LDYRSEYRIRAAIDQHEGGLAEFSRGYKLGFTRSAGCITYREMAPGASHAALVGFEN 163
Db 146 LDYRSEYRIRAAIDQHEGGLAEFSRGYKLGFTRSAGCITYREMAPGASHAALVGFEN 205
Qy 164 NNPNADVTMDQYGVWEIFLNNADGSPALIPHGSVYKTRMDTPSGVKSISAWITFSVQ 223
Db 206 NNPNADVTMDQYGVWEIFLNNADGSPALIPHGSVYKTRMDTPSGVKSISAWITFSVQ 265
Qy 224 APGEIPNGIYVDPPEEKYVFOHPQKRPESLRITYESHIGMSSPPKINSYANFDEVL 283
Db 266 APGEIPNGIYVDPPEEKYVFOHPQKRPESLRITYESHIGMSSPPKINSYANFDEVL 325
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Qy 284 PRKELGVNAVQIAIOEHSYASFGYHTNFFAPSSRFGTPEDLKSLIDRAHELGLVL 343
Db 326 PRKELGVNAVQIAIOEHSYASFGYHTNFFAPSSRFGTPEDLKSLIDRAHELGLVL 385
Qy 344 MDIVHSHSNNTLDGLNGFDGTDTHYFHGPRGHHMMPSRLFNYSWEYLREPLSNARW 403
Db 386 MDIVHSHSNNTLDGLNGFDGTDTHYFHGPRGHHMMPSRLFNYSWEYLREPLSNARW 445
Qy 404 WLEEXKFDGFRDGYTSNMYTHHGLQWTFNGYGEYGFATDVAVVYLMVNDLIHGLH 463
Db 446 WLEEXKFDGFRDGYTSNMYTHHGLQWTFNGYGEYGFATDVAVVYLMVNDLIHGLH 505
Qy 464 PDVAVSGEDVSGMPTFCIPVDPGVGFVDRILHNAVADKMTIELLKQSDSEMKMGDIY 523
Db 506 PDVAVSGEDVSGMPTFCIPVDPGVGFVDRILHNAVADKMTIELLKQSDSEMKMGDIY 565
Qy 524 NNRWLEKCVTYAASHQALVGDKTIAFWLMDKMYDFMALDRPSTPRIDGIALHKMIRL 583
Db 566 NNRWLEKCVTYAASHQALVGDKTIAFWLMDKMYDFMALDRPSTPRIDGIALHKMIRL 625
Qy 584 VTMGLGEGYLNFMGNEFGHPWIDPFRGPQTLPTGKVLPGNNNSYDKCRRRFDLGADP 643
Db 626 VTMGLGEGYLNFMGNEFGHPWIDPFRGPQTLPTGKVLPGNNNSYDKCRRRFDLGADP 685
Qy 644 LRYHGMQEFDOAQHLEKYGFMTSSEHOYYSRKHEEDKVIIFERGDVFNFMHMSFF 703
Db 686 LRYHGMQEFDOAQHLEKYGFMTSSEHOYYSRKHEEDKVIIFERGDVFNFMHMSFF 745
Qy 704 DYRVGCSRGPKYKVALDSDDALFGFSRLDHDVDYFTTEHPHNRPRSFSVYTPSR 763
Db 746 DYRVGCSRGPKYKVALDSDDALFGFSRLDHDVDYFTTEHPHNRPRSFSVYTPSR 805
Qy 764 YA 765
Db 806 YA 807
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RESULT 3
US-09-731-166-12
; Sequence 12, Application US/09731166
; Patent No. 6639126
; GENERAL INFORMATION:
; APPLICANT: Sewalt, Vincent J. H.
; APPLICANT: Singletary, George W.
; TITLE OF INVENTION: Production of Modified Polysaccharides
; FILE REFERENCE: 35718/206348
; CURRENT APPLICATION NUMBER: US/09/731,166
; CURRENT FILING DATE: 2000-12-06
; PRIOR FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 799
; TYPE: PRT
; ORGANISM: Zea mays
US-09-731-166-12
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Query Match 80.4%; Score 3351; DB 4; Length 799;
Best Local Similarity 78.5%; Pred. No. 1,1e-309;
Matches 609; Conservative 68; Mismatches 77; Indels 22; Gaps 4;
Qy 4 FAVSGATLVG-----APPAAQPEELQIPEDIEBQTAENVMTGTAKLESSE----- 52
Db 35 FLTRGARVVGSGTGHGARRAAARAAVVPBGEND-----GLASRAASQAQOSDEL 85
Qy 53 PLOGIVETITDGVTKGKELVGEKPRVVPKPGGQKIYEIDPTLKDPRSHLDYRSEYR 112
Db 86 EVDPISEETTCGA--GAADAQALNRVAVPPPSDQKIQIDPMLQGYKHYHEVYSLYR 143
Qy 113 RIRAAIDQHEGGLAEFSRGYKLGFTRSAGCITYREMAPGASHAALVGFENNNPNADVTM 172
Db 144 RIRSDIDHEGGLAEFSRGYKLGFTRSAGCITYREMAPGASHAALVGFENNNPNADVTM 203
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QY	173	TRDVGWEI LPLNNADSPALPHOSRYKIMDTPGVNDSTSAMIKFSYOAAGELPENG	232
Db	204	SKNPFGEWEI LPLNNADGSP LPHOSRYKIVNRDTPGIDSLAMIKYSVOAGELPYDG	263
QY	233	IYYPREEEKVFCQHPQKRPESLR IYESHIGMSPEPKINSYANRDEYLPRIKELGYN	292
Db	264	IYYPREEKVYFRHAQPRKSL IYEHVGMSSPEKINTYVNRDEYLPRIKELGYN	323
QY	293	AVQIMAIQESHYSYASFGYHVTNFPADSSFGFPBEDIKSLIDRAHEIGLYMDIYNSHSS	352
Db	324	AVQIMAIQESHYSYSGFYHVTNFPADSSFGFPBEELKSLIDRAHEIGLYMDIVNHSAS	383
QY	353	NMTLDGLNGFOSTDPHYHFGSPRGHHMMDSRLFNYSGSEVULRFLSNARWMLBEEKYFDG	412
Db	384	SNITLDGLNGFODTDPHYHFGSPRGHHMMDSRLFNYSGBEVLRLSNARWMLBEEKYFDG	443
QY	413	FRFDGVTSMWYTHHGLQMTFTNGYGEFQFATDVDAVVYMLTNDLIHGLHPDAVSIGED	472
Db	444	FRFGGVISMWYTHHGLQVYTFITGNPNDEYFQFATDVDAVVYMLTNDLIHGLYPAVYIGED	503
QY	473	VSGMPTFCIPLVPDGGVGDYRLHMAVADKMIELKOSDSMKXGDIYVHTLTNRMLEKCY	532
Db	504	VSGMPTFALPVHADGGVGGEYRMHMAVADKMIIDLKOSDEWYXGDIYVHTLTNRMLEKCY	563
QY	533	TYASHDQALVGDKIIAFLMLKDMWDENALBPSRPRIDRGALHKMTLVYMGLOGEG	592
Db	564	TYASHDQALVGDKIIAFLMLKDMWDENALBPSRPTIDRGALHKMTLVYMGLOGEG	623
QY	593	YLNFPGNEFGHPEWIDFPRGPQLTPTKVLPGNNSYDKCRARRFDLGDADFLRYHGMQEF	652
Db	624	YLNFPGNEFGHPEWIDFPRGPQLRPGEKFLPGNNNSYDKCRARRFDLGDADFLRYHGMQEF	683
QY	653	DOAMQHEBEKYGFMISEHOYVSRKHEDKVI IIPERDVLVVFNFHMSNSFQDVRVGCSSRP	712
Db	684	DOAMQHEBEKYGFMISDHQYISRKHEDEKVI IYFEKEDLVVFNFHCONSFEYDRIQGRKP	743
QY	713	GKYKVALSDDALFGGFSRLDSDVVFTEHPRPDNRPRSRYVTPPSRTAVVAYALTE	768
Db	744	GKYKVALSDDALFGGFSRIIRHAAHEFTADCSIDNRPRYSRYVTPPSRTAVVAYALTE	799

RESULT 4
 US-08-941-445A-15
 Sequence 15, Application US/08941445A
 Patent No. 6107060
 GENERAL INFORMATION:
 APPLICANT: Keeling, Peter
 APPLICANT: Guan, Hanning
 TITLE OF INVENTION: Starch Encapsulation
 NUMBER OF SEQUENCES: 37
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
 STREET: 5370 Manhattan Circle
 CITY: Boulder
 STATE: CO
 COUNTRY: US
 ZIP: 80303
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/941,445A
 FILING DATE: 30-SEP-1997
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/026,855
 FILING DATE: 30-SEP-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Winner, Ellen P
 REGISTRATION NUMBER: 28 547

```

: REFERENCE/DOCKET NUMBER: 89-97
:
: TELECOMMUNICATION INFORMATION:
:
: TELEPHONE: (303) 499-8080
:
: TELEFAX: (303) 499-8089
:
: INFORMATION FOR SEQ ID NO: 15:
:
: SEQUENCE CHARACTERISTICS:
:
: LENGTH: 799 amino acids
:
: TYPE: amino acid
:
: TOPOLOGY: linear
:
: MOLECULE TYPE: protein
:
: OS-08-941-445A-15

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Query Match:	80.2%;	Score 3342;	DB 3;	Length 799;
Best Local Similarity	78.4%;	Pred. No. 7.9e-309;		
Matches 608;	Conservative 67;	Mismatches 79;	Indels 22;	Gaps 4;

QY	4	FANSGATLGV-----APPPAAOGEELQIPEDIEEQTAENVNMGTAEKLESSE-----	52
Db	35	FLTRGAVGVGSGTHGARARAAAAAKAWVGEEND-----GLSRADSAQFOSDEL	85
QY	53	PTQIGIVETITDGVTKGVKEIVGGEKPRVVPKPGGQKIYEIDPTLKDFRSHLDVRYSEYR	112
Db	86	EVPIISETTCGA--GVADAQALNRVAVVPPSPGQKIFQIDPMLQGVKHYLEIRYSLYR	143
QY	113	RIRAAIDQHEBGLLEAFSRGYEKLGFTRSAAGITIYREWAPGAHSALVGFENNPNADTM	172
Db	144	RIRSDIDEHGEGJLEAFSRSEYKFFGNASAEGITIYREWAPGAFSAALVGVNMPNDMRM	203
QY	173	TRDQYGVWEITFLPNNAAGSPAIPIGGSVYKIMQIPSGVKSISAMIKFSVQAPQEIPIPNQ	232
Db	204	SKNEFGWEITFLPNNAAGTSIPITPGSSVYKXKMDPSGKOSIPAMIKFSVQAPGSIIPDG	263
QY	233	IYYDPREEKTVFQHPQPKRPESLIRIYESHIGMSSPEBKINSYANFRDEVLPRIKRLGYN	292
Db	264	IYYDPREEKTVFPHAQPKRPKSLIRIETHVGMSSPEBKINTYVNFREVLPRIKXKLYN	323
QY	293	AVQIMAIQESHSYASFQHYVTNFFAPSSRFGTPEDLKSLIDRAHELGLVIMDIVHSSS	352
Db	324	AVQIMAIQESHSYASFQHYVTNFFAPSSRFGTPEDLKSLIDRAHELGLVIMDIVHSHAS	383
QY	353	NTNLDGLNGPCTDTHYEHGSPRCHMMNMSRLFNYSWEYLRELLSNARWMLSEYKDG	412
Db	384	NTNLDGLNGPCTDTHYFHSGSPRCHMMNMSRLFNYSWEYLRELLSNARWMLSEYKDG	443
QY	413	FRPDGVTSMYTHHGLQMTFGTNGCEYFGFATDVAVVYLMVLNLDLHGLHPDAVSIGED	472
Db	444	FRPDGVTSMYTHHGLQVTFGTNGNEVFEGFATDVAVVYLMVLNLDLHGLVPEANTIGED	503
QY	473	VSGMPFPCIPVDPGGVGDFYRLMAVADKMTLLKQSDSKMGDIYHTLTNRKMLECV	532
Db	504	VSGMPFPAFLPVHDGCVGFYRMENAVADKMTLLKQSDETKMGDIYHTLTNRKMLECV	563
QY	533	TYASHOALVGDGDTIAFWLMDKMYOPMALDRSTPIIDGIALHKRIKRLVTMGLGEG	592
Db	564	TYASHOALVGDGDTIAFWLMDKMYOPMALDRSTPIIDGIALHKRIKRLITMGLGEG	623
QY	593	YLNFMGNFEGHPEWIDPRGPQRLPTQKVLFGNNNSYDKCRRRPDLGADFLRYHGOEF	652
Db	624	YLNFMGNFEGHPEWIDPRGPQRLPSGKFIPIGNNSYDKCRRRPDLGADYLYRYHGOEF	683
QY	653	DOAMQHLLEKKGPNTSSEHQYVSRKGBEBKXVLIIFRGDLVFYFNTHMGSFPDYRNGSRP	712
Db	684	DOAMQHLLEKKEFMTSDHQYVSRKGBEBKXVLFERGDVVFYFNTHMGSFPDYRNGSRP	743
QY	713	GKYKVALDSDALRGFSRLDHDVYFTEBPHONRPRFSFVYVPSRTAVVYALTE	768
Db	744	GKYKVALDSDALRGFSRIRHAAEHFTADCSHNRPRFSFVYVPSRCVVYALPE	799

RESULT 5
US-09-087-277-2
; Sequence 2, Application US/09087277B
; Patent No 6169226

```

GENERAL INFORMATION:
APPLICANT: EK, Bo
APPLICANT: KHOSNOODI, Jamshid
APPLICANT: LARSSON, Clas-Tomas
APPLICANT: LARSSON, Hakan
APPLICANT: RASK, Lars
TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
FILE REFERENCE: 003300-486
CURRENT APPLICATION NUMBER: US/09/087, 277B
CURRENT FILING DATE: 1998-05-29
EARLIER APPLICATION NUMBER: PCT/SE96/01558
EARLIER FILING DATE: 1996-11-28
EARLIER APPLICATION NUMBER: SE 9504272-7
EARLIER FILING DATE: 1995-11-29
EARLIER APPLICATION NUMBER: SE 9601506-0
EARLIER FILING DATE: 1996-04-19
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 878
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Description of Unknown Organism:be11 gene (branching enzyme II)
US-09-087-277-2

Query Match 76.2%; Score 3175; DB 3; Length 878;
Best Local Similarity 72.2%; Pred. No. 7.3e-293;
Matches 583; Conservative 83; Mismatches 93; Indels 48; Gaps 6;

2 ATFAVSGATL--GVARPPAAQPELOIPE-----DIEQTAE----- 37
60 STVAASGKVLVPTQSDSSSSSTQDFETSPENSPASTVDVSTHMAQIKTENDV 119
38 ---VNMTGTAE-----KLESSEPTQGIIVETITDGYTKGKELVGEKPRVY 81
120 EPSDDLGSVEELDFASLQLOEGGKLEESKLTNSETIITDESDR--IRE-----RGI 171
82 PKPGDGQKIYEIDPTLKDFRSHLDYRSEYRRIATAIDQHEGGLAFBSRGYKLGFTSA 141
172 PPGGLGQKIYEIDPLTNRYQHLDRYQYKKEALDKYEGGLAFBSRGYKMGFTSA 231
142 EGIITYREAPAGSAALVGGDFNNMNPADMTTRDYGWEIFLPPNADGSPAIPIGSRVY 201
232 TGIITYREAPAGSAALVGGDFNNMNPADMTTRDYGWEIFLPPNADGSPAIPIGSRVY 291
202 IRMDTPSGVXDSISAMIKFSVQAPGEIPFNGIYYDPPEEEKYVFOHPQKRESLRIVES 261
292 IRMDTPSGVXDSISAMIKFSVQAPGEIPFNGIYYDPPEEEKYVFOHPQKRESLRIVES 351
262 HIGMSSEPKINSYANFRDEVLPRIKLGYNAAVOIMAOESHYASFGYHVTNFXAPSSR 321
352 HIGMSSEPKINSYANFRDEVLPRIKLGYNAAVOIMAOESHYASFGYHVTNFXAPSSR 411
322 FGTPEEDLKSLIDRAHEGLVLMIVSHSSNNTLDGLNGFDGTDHYHFGSPRGHMMW 381
412 FGXPDDLKSLIDRAHEGLVLMIVSHSSNNTLDGLNGFDGTDHYHFGSPRGHMMW 471
382 DSRLEFNYGSEWEYLRFLSNARWMLSEYKDFGRFDGVTSMYTHHGLQMTFTGNVGEYFG 441
472 DSRLEFNYGSEWEYLRFLSNARWMLSEYKDFGRFDGVTSMYTHHGLQMTFTGNVGEYFG 531
442 FATVDVAVYVLMVNDLHGLHPDAVSTEDVSGMPTFCIPVPDGSVGDYRLHMAVAAR 501
532 LATVDVAVYVLMVNDLHGLHPDAVSTEDVSGMPTFCIPVPDGSVGDYRLHMAVAAR 591
502 MIELLKQSDSKWMDIVHTLTNRRLSEKVTYAESHDQALVGDKTIATWMDKMDYDPM 561
592 WIELKKKDEDEKRVGDIVHTLTNRRLSEKVTYAESHDQALVGDKTIATWMDKMDYDPM 651
562 ALDRSTPRIDGIALHXRIRLVTVNGLGEGYLNFGNFGHEWTDPPGPGTLEFGKY 621
652 ALDRSTPRIDGIALHXRIRLVTVNGLGEGYLNFGNFGHEWTDPPGPGTLEFGKY 711

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622 LFGNNNSYDKCRRRFDLGDADFLRYHGMQFQAOHMLEEKYGFMTSEHQYVSRKHEEDK 681
712 IPGNQFSYDKCRRRFDLGDADFLRYHGMQFQAOHMLEEKYGFMTSEHQYVSRKHEEDK 771
682 VIFERGLVFEVFNHMSNFPDYGCSRPFGKYKVALDSDDALFGGFSRLHDVDVFTT 741
772 MIVFEGKLVFEVFNHMSNFPDYGCSRPFGKYKVALDSDDALFGGFSRLHDVDVFTT 831
742 EHPHNRPSSESVYTPSRATVYALTE 768
832 EGMWDRPRASIMVYAPSRATVYALVD 858

RESULT 6
US-09-658-499-2
Sequence 2, Application US/09658499
Patent No. 6469231
GENERAL INFORMATION:
APPLICANT: EK, Bo
APPLICANT: KHOSNOODI, Jamshid
APPLICANT: LARSSON, Clas-Tomas
APPLICANT: LARSSON, Hakan
APPLICANT: RASK, Lars
TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
FILE REFERENCE: 003300-486
CURRENT APPLICATION NUMBER: US/09/658, 439
CURRENT FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 09/087, 277
PRIOR FILING DATE: 1998-05-29
PRIOR APPLICATION NUMBER: PCT/SE96/01558
PRIOR FILING DATE: 1996-11-28
PRIOR APPLICATION NUMBER: SE 9504272-7
PRIOR FILING DATE: 1995-11-29
PRIOR APPLICATION NUMBER: SE 9601506-0
PRIOR FILING DATE: 1996-04-19
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 878
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Description of Unknown Organism:be11 gene (branching enzyme II)
US-09-658-499-2

Query Match 76.2%; Score 3175; DB 4; Length 878;
Best Local Similarity 72.2%; Pred. No. 7.3e-293;
Matches 583; Conservative 83; Mismatches 93; Indels 48; Gaps 6;

2 ATFAVSGATL--GVARPPAAQPELOIPE-----DIEQTAE----- 37
60 STVAASGKVLVPTQSDSSSSSTQDFETSPENSPASTVDVSTHMAQIKTENDV 119
38 ---VNMTGTAE-----KLESSEPTQGIIVETITDGYTKGKELVGEKPRVY 81
120 EPSDDLGSVEELDFASLQLOEGGKLEESKLTNSETIITDESDR--IRE-----RGI 171
82 PKPGDGQKIYEIDPTLKDFRSHLDYRSEYRRIATAIDQHEGGLAFBSRGYKLGFTSA 141
172 PPGGLGQKIYEIDPLTNRYQHLDRYQYKKEALDKYEGGLAFBSRGYKMGFTSA 231
142 EGIITYREAPAGSAALVGGDFNNMNPADMTTRDYGWEIFLPPNADGSPAIPIGSRVY 201
232 TGIITYREAPAGSAALVGGDFNNMNPADMTTRDYGWEIFLPPNADGSPAIPIGSRVY 291
202 IRMDTPSGVXDSISAMIKFSVQAPGEIPFNGIYYDPPEEEKYVFOHPQKRESLRIVES 261
292 IRMDTPSGVXDSISAMIKFSVQAPGEIPFNGIYYDPPEEEKYVFOHPQKRESLRIVES 351
262 HIGMSSEPKINSYANFRDEVLPRIKLGYNAAVOIMAOESHYASFGYHVTNFXAPSSR 321
352 HIGMSSEPKINSYANFRDEVLPRIKLGYNAAVOIMAOESHYASFGYHVTNFXAPSSR 411
322 FGTPEEDLKSLIDRAHEGLVLMIVSHSSNNTLDGLNGFDGTDHYHFGSPRGHMMW 381
412 FGXPDDLKSLIDRAHEGLVLMIVSHSSNNTLDGLNGFDGTDHYHFGSPRGHMMW 471
382 DSRLEFNYGSEWEYLRFLSNARWMLSEYKDFGRFDGVTSMYTHHGLQMTFTGNVGEYFG 441
472 DSRLEFNYGSEWEYLRFLSNARWMLSEYKDFGRFDGVTSMYTHHGLQMTFTGNVGEYFG 531
442 FATVDVAVYVLMVNDLHGLHPDAVSTEDVSGMPTFCIPVPDGSVGDYRLHMAVAAR 501
532 LATVDVAVYVLMVNDLHGLHPDAVSTEDVSGMPTFCIPVPDGSVGDYRLHMAVAAR 591
502 MIELLKQSDSKWMDIVHTLTNRRLSEKVTYAESHDQALVGDKTIATWMDKMDYDPM 561
592 WIELKKKDEDEKRVGDIVHTLTNRRLSEKVTYAESHDQALVGDKTIATWMDKMDYDPM 651
562 ALDRSTPRIDGIALHXRIRLVTVNGLGEGYLNFGNFGHEWTDPPGPGTLEFGKY 621
652 ALDRSTPRIDGIALHXRIRLVTVNGLGEGYLNFGNFGHEWTDPPGPGTLEFGKY 711

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Db 352 HIGMSPEPKINSYVNFDEVLPRIKLGYNVQIMAIQESHSTYASFGYHTNFXAPBSR 411
QY 322 FGTPEDLKSLIDRAHELGILVLMDIVSHSSNNLTDLGNGFDGTDTHYFHGGPRGHMMW 381
Db 412 FGAPDLKSLIDKAHELGIYVLMDIVSHSSNNLTDLGNGFDGTDTHYFHGGPRGHMMW 471
QY 382 DSRLEFVNGWEVIRFLISNARWMLBEEKFPGDGTSMYTHHGLQMTTGNYGEYFG 441
Db 472 DSRLEFVNGWEVIRFLISNARWMLBEEKFPGDGTSMYTHHGLQMTTGNYGEYFG 531
QY 442 FARDVAVVYMLVNDLHGLHPDAVSIAGEDVSGMPTFCIPVGGVGFDPYRLHNAVADK 501
Db 532 LATDVDAVYMLVNDLHGLHPDAVSIAGEDVSGMPTFCIPVGGVGFDPYRLHNAVADK 591
QY 502 WIELLKQSDSWKMGDIVHTLTNRWLEKCYTVAESHDAVGDXTIAFWLMDKMDYDFM 561
Db 592 WIELLKQSDSWKMGDIVHTLTNRWLEKCYTVAESHDAVGDXTIAFWLMDKMDYDFM 651
QY 562 ALDRPSTPRIDRGIALHKMIRLVTMGLGEGYLTFMNGEFGHPHVIDPRGPQTLPTGKV 621
Db 652 ALDRPSTPRIDRGIALHKMIRLVTMGLGEGYLTFMNGEFGHPHVIDPRGPQTLPTGKV 711
QY 622 LFGNNNSYDCRRRFDGADFLRYHGMQEPDQAMOHLEEKYGFMTSEHOYVSRKHEEDK 681
Db 712 LFGNNNSYDCRRRFDGADFLRYHGMQEPDQAMOHLEEKYGFMTSEHOYVSRKHEEDK 771
QY 682 VIFERGDVLFVENFHMNSGFYDVCSPRGKYKVALSDDALFGFGRDLHDVYFTT 741
Db 772 MIVFEGNULVFVFNFMHTKSYSDYRIGCLKRGKYKVALSDDALFGFGRDLHDVYFTT 831
QY 742 EHPHNDPRSGFSYTTBRTAVYVLTLE 768
Db 832 EGYWDRPFRSINMYAPSRITAVYVLTLE 858

RESULT 7
US/09/087
/ Sequence 4, Application US/09087277B
/ Patent No. 6169226
/ GENERAL INFORMATION:
/ APPLICANT: EK, Bo
/ APPLICANT: KHOSNODI, Jamehid
/ APPLICANT: LARSSON, Clas-Tomas
/ APPLICANT: RASK, Lars
/ TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
/ FILE REFERENCE: 003300-486
/ CURRENT APPLICATION NUMBER: US/09/087, 277B
/ PRIOR FILING DATE: 1998-05-29
/ EARLIER APPLICATION NUMBER: PCT/SE96/01558
/ EARLIER FILING DATE: 1996-11-28
/ EARLIER APPLICATION NUMBER: SE 9504272-7
/ EARLIER FILING DATE: 1995-11-29
/ EARLIER APPLICATION NUMBER: SE 9601506-0
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 4
/ LENGTH: 464
/ TYPE: PRT
/ ORGANISM: Unknown
/ FEATURE:
/ OTHER INFORMATION: Description of Unknown Organism:bell gene fragment (branching enz
US/09/087,277-4

Query Match 53.1%; Score 2213; DB 3; Length 464;
Best Local Similarity 86.0%; Pred. No. 9.3e-202;
Matches 398; Conservative 31; Mismatches 34; Indels 0; Gaps 0;

QY 184 LFNNDGSPALPHGSRVYKRMIDTPSGVSDSISAMIKFSVQAPGELPFNGIYYDPPEEKY 243
Db 1 LFNNDGSPALPHGSRVYKRMIDTPSGVSDSISAMIKFSVQAPGELPFNGIYYDPPEEKY 60

QY 244 VQHPQPKPESLRITYESHIGMSSPEPKINSYVNFDEVLPRIKLGYNVQIMAIQESH 303
Db 61 IFQHPRPKPKSLIRITYESHIGMSSPEPKINSYVNFDEVLPRIKLGYNVQIMAIQESH 120
QY 304 YVASFGYHTNFXAPBSRFGTPEDLKSLIDRAHELGILVLMDIVSHSSNNLTDLGNGFD 363
Db 121 YVASFGYHTNFXAPBSRFGTPEDLKSLIDRAHELGILVLMDIVSHSSNNLTDLGNGFD 180
QY 364 GTDTHYFHGGPRGHMMWMDSRLFNYSWEVIRFLISNARWMLBEEKFPGDGTSMY 423
Db 181 GDSICYFHSGANGYHMMWMDSRLFNYSWEVIRFLISNARWMLBEEKFPGDGTSMY 240
QY 424 THHGLQMTTGNYGEYFGATVDVAVYMLVNDLHGLHPDAVSIAGEDVSGMPTFCIPV 483
Db 241 THHGLQMTTGNYGEYFGATVDVAVYMLVNDLHGLHPDAVSIAGEDVSGMPTFCIPV 300
QY 484 PGGVGFDPYRLHNAVADKIELLKQSDSWKMGDIVHTLTNRWLEKCYTVAESHDAV 543
Db 301 QGGVGFDPYRLHNAVADKIELLKQSDSWKMGDIVHTLTNRWLEKCYTVAESHDAV 360
QY 544 GDKTIAFWLMDKMDYDFMALARPSTPRIDRGIALHKMIRLVTMGLGEGYLTFMNGEFGH 603
Db 361 GDKTIAFWLMDKMDYDFMALARPSTPRIDRGIALHKMIRLVTMGLGEGYLTFMNGEFGH 420
QY 604 PEMIDPRGPQTLPTGKVLPFGNNNSYDCRRRFDGADFLRY 646
Db 421 PEMIDPRGPQTLPTGKVLPFGNNNSYDCRRRFDGADFLRY 463

RESULT 8
US-09-658-499-4
/ Sequence 4, Application US/09658499
/ Patent No. 6469231
/ GENERAL INFORMATION:
/ APPLICANT: EK, Bo
/ APPLICANT: KHOSNODI, Jamehid
/ APPLICANT: LARSSON, Clas-Tomas
/ APPLICANT: RASK, Lars
/ TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
/ FILE REFERENCE: 003300-486
/ CURRENT APPLICATION NUMBER: US/09/658, 499
/ PRIOR FILING DATE: 2000-09-08
/ PRIOR APPLICATION NUMBER: 09/087, 277
/ PRIOR FILING DATE: 1998-05-29
/ PRIOR APPLICATION NUMBER: PCT/SE96/01558
/ PRIOR FILING DATE: 1996-11-28
/ PRIOR APPLICATION NUMBER: SE 9504272-7
/ PRIOR FILING DATE: 1995-11-29
/ PRIOR APPLICATION NUMBER: SE 9601506-0
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 4
/ LENGTH: 464
/ TYPE: PRT
/ ORGANISM: Unknown
/ FEATURE:
/ OTHER INFORMATION: Description of Unknown Organism:bell gene fragment (branching en
US-09-658-499-4

Query Match 53.1%; Score 2213; DB 4; Length 464;
Best Local Similarity 86.0%; Pred. No. 9.3e-202;
Matches 398; Conservative 31; Mismatches 34; Indels 0; Gaps 0;

QY 184 LFNNDGSPALPHGSRVYKRMIDTPSGVSDSISAMIKFSVQAPGELPFNGIYYDPPEEKY 243
Db 1 LFNNDGSPALPHGSRVYKRMIDTPSGVSDSISAMIKFSVQAPGELPFNGIYYDPPEEKY 60
QY 244 VQHPQPKPESLRITYESHIGMSSPEPKINSYVNFDEVLPRIKLGYNVQIMAIQESH 303
Db 61 IFQHPRPKPKSLIRITYESHIGMSSPEPKINSYVNFDEVLPRIKLGYNVQIMAIQESH 120

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QY 304 YVAFYGVHTNFAPSSRFCTPEDLKSILDRABHEGLVLMNDIVHSHSSNNTLDGLNGFD
Db 121 YVAFYGVHTNFAPSSRFCTPEDLKSILDRABHEGLVLMNDIVHSHSSNNTLDGLNGFD 180
QY 364 GTDTHYHGGGRHHMMWDSRLFNYSGVSWVTRFLISNARWMLLEEKYKFGFDDGVTSMXY 423
Db 181 GTDSCYHSGARGYHMMWDSRLFNYSGVSWVTRFLISNARWMLLEEKYKFGFDDGVTSMXY 240
QY 424 THHLOMTFTGNGVGEYGFATDVAVVYLMVNDLHGLHPAVSIGEDVSGMPTFCIPV 483
Db 241 THHLSVSGFTNGYEEYGFATDVAVVYLMVNDLHGLHPAVSIGEDVSGMPTFCIPV 300
QY 484 PDGSGVGFYRLHMAVADKMIELKQSDSWKMGDIHVTLTNRWLEKCVTYAESHDQALV 543
Db 301 QDGGVGFYRLHMAVADKMIELKQSDSWKMGDIHVTLTNRWLEKCVTYAESHDQALV 360
QY 544 GDKTIAFWLMKMDKMDYDFMALDPSFTPRIDRGIALHKTIRLVMTGIGSGYINFMGNEFGH 603
Db 361 GDKTIAFWLMKMDKMDYDFMALDPSFTPRIDRGIALHKTIRLVMTGIGSGYINFMGNEFGH 420
QY 604 PEWIDFPRGPGOTLPTGKVLPGNNNSYDKCRRRFEDLGDADFLRY 646
Db 421 PEWIDFPRGPGOTLPTGKVLPGNNNSYDKCRRRFEDLGDADFLRY 463

RESULT 9
US-09-367-895-41
/ Sequence 41, Application US/09367895
/ Patent No. 6483009
/ GENERAL INFORMATION:
/ APPLICANT: POLISEN, PETER
/ TITLE OF INVENTION: ANTISENSE INTRON INHIBITION OF STARCH BRANCHING ENZYME
/ FILE REFERENCE: 078883/0112
/ CURRENT APPLICATION NUMBER: US/09/367, 895
/ PRIOR FILING DATE: 1999-12-08
/ PRIOR APPLICATION NUMBER: PCT/IB98/00270
/ PRIOR FILING DATE: 1998-02-23
/ PRIOR APPLICATION NUMBER: GB/9703663.6
/ PRIOR FILING DATE: 1997-02-21
/ PRIOR APPLICATION NUMBER: GB/9706060.2
/ PRIOR FILING DATE: 1997-03-24
/ NUMBER OF SEQ ID NOS: 43
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 41
/ LENGTH: 906
/ TYPE: PRT
/ ORGANISM: Solanum tuberosum
US-09-367-895-41

Query Match 51.7%; Score 2156.5; DB 4; Length 906;
Best Local Similarity 58.0%; Pred. No. 6.9e-196;
Matches 400; Conservative 94; Mismatches 169; Indels 27; Gaps 7;

QY 90 IYEIDPTLKDFRSHLDYRYSEYRIRRAALDQHEGGLAEFSRGYKLGFTSAGIYREW 149
Db 99 LINDPTLEPYLDHFRHRMRKRYVDQKMLEKYEGLPEEPAQGLKRGFNEDDCIYREW 158
QY 150 APGASALVDCPRNNWNPADTMTBDYGVWEFLFNMDGSAIHHGSRVYKIRMTDPSG 209
Db 159 APAAGEAEVYIGFNGNGSNHMEKQDFGVMSIRIP-DVDSKVIPIHNSVKRFRYHGNG 217
QY 210 V-KDSISAMIKFSVQAPGEI--PFGIYVDPPEEKVYQHPQKPSERIRIYESHIGMS 266
Db 218 VAVDILPAWIKATATADATFAAFYDGVYMDPPESEKHYHFKYPPRPAPRARIYEAHYGMS 277
QY 267 SPEPKINSYANFRDEVLPRIKLGYNVAVOIMAIQESHYSYASFGYHVTNFPAPSSRGFTPE 326
Db 278 SSEPRVNSYREPADVDLPRIKANNYTVQIMAEHSYSGSGYHVTNFPAPVSSRYGNPE 337
QY 327 DKSILDRABHEGLVLMNDIVHSHSSNNTLDGLNGFD---GDTTHYHGGGRHHMMWDS 383

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Db 338 DLKYLIDKASHISLGQVLDVVVHSHASNNTVDGLNGFDIGGQSGQSESYFHAGERHYKXLMDS 397
QY 384 RLFNYSGVSWVTRFLISNARWMLLEEKYKFGFDDGVTSMTHHGLQMTFTGNYGEYGF 443
Db 398 RLFNYSGVSWVTRFLISNARWMLLEEKYKFGFDDGVTSMTHHGLQMTFTGNYGEYGF 457
QY 444 TVDVAVYVLMVNDLHGLHPDAVSGIEDVSGMPTFCIPPDGSGVGFYRLHMAVADKMI 503
Db 458 TVDVAVYVLMVNDLHGLHPDAVSGIEDVSGMPTFCIPPDGSGVGFYRLHMAVADKMI 517
QY 504 ELK--QSDSWKMGDIHVTLTNRWLEKCVTYAESHDQALVGDKTIAFWLMKMDKMDYDFMA 562
Db 518 DYIKKNDSDMSKKEVTSSTNRRYREKCAVAFETHQSLVGDKTIAFWLMKMDKMDYDFMA 577
QY 563 LDRPSTPRIDRGIALHKTIRLVMTGIGSGYINFMGNEFGHPEWIDFPRGPGOTLPTGKVL 622
Db 578 CLTDASPVYDRGIALHKTIRLVMTGIGSGYINFMGNEFGHPEWIDFPRGPGOTLPTGKVL 626
QY 623 PGNNNSYDKCRRRFEDLGDADFLRYHGMQEBDQAMQHEEKYKFGFDDGVTSMTHHGLQMT 682
Db 627 EGNNSYDKCRRRFEDLGDADFLRYHGMQEBDQAMQHEEKYKFGFDDGVTSMTHHGLQMT 686
QY 683 IIPERGDVFPFPHNSNPFYRGVSGRPDKYKVALDSDDALFGFSRLDHDVYFTT- 741
Db 687 VYPERGDVFPFPHNSNPFYRGVSGRPDKYKVALDSDDALFGFSRLDHDVYFTT- 746

QY 742 -----EHPHNRPRSPSYTTPSRITAVVY 764
Db 747 EGIPGVETNFGRPNSFKVLSPARITCAVY 776

RESULT 10
US-08-941-445A-17
/ Sequence 17, Application US/08941445A
/ Patent No. 6107060
/ GENERAL INFORMATION:
/ APPLICANT: Keeling, Peter
/ TITLE OF INVENTION: Starch Encapsulation
/ NUMBER OF SEQUENCES: 37
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Greenlee, Winner and Sullivan, P.C.
/ STREET: 5370 Manhattan Circle
/ CITY: Boulder
/ STATE: CO
/ COUNTRY: US
/ ZIP: 80303
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/941,445A
/ FILING DATE: 30-SEP-1997
/ CLASSIFICATION: 800
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 60/026,855
/ FILING DATE: 30-SEP-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Winner, Ellen P
/ REGISTRATION NUMBER: 28,547
/ REFERENCE/DOCKET NUMBER: 89-97
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (303) 499-8080
/ TELEFAX: (303) 499-8089
/ INFORMATION FOR SEQ ID NO: 17:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 822 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-941-445A-17

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Tue Apr 20 10:02:28 2004

us-09-508-377-12.ra1

Page 7

Query Match 51.5%; Score 2146; DB 3; Length 822;
Best Local Similarity 57.0%; Pred. No. 5,8e-195;
Matches 395; Conservative 101; Mismatches 171; Indels 26; Gaps 6;

QY DGOKIYEIDPLTKDRSHLDYRSEYRIRRAIDQHEGGLAERSCYKLGFTSAEGIT 145
DB DHPITVDLPKLEIFKDHFRYRMKRFLEOKSIEENEGSLESFSGYKLGINTNEDGTV 139
QY 146 YREWAPGAHSAALVGDENNPNADTMRDYGWEIFLNNADSPALPHGSRVYIRMD 205
DB 140 YREWAPGAOEAELIDFNDMNGANHMEKDKFGVWSIKI-DHYKGRPALPHNSKVXFRFL 198
QY 206 TPGSVKDSISAMIKFSVQAPGEI--PENGIIYDPEBEKRYVQHPQKAPESLRITYESHI 263
DB 199 HGVWVWDRIPALIRYATVDASKFGAPYDGVHMDPSPASERTYFKHPRPSKPAAPRIYEAHV 258
QY 264 GMSSEPKINSYANFRDEVLPRIKLGYNVQVMAIOEHSYASFGYHTNFPAPSRFG 323
DB 259 GMSGEKPAVSTYREFADNVLPRIRANNNTVOQMAVMEHSYASFGYHTNFFAVSSRG 318
QY 324 TPEDLKSLIDRAHEGLLVMDIVSHSSNNITLDGNGPD--GTDTHYHGGPRGHMM 380
DB 319 TPEDLKSLIDRAHSLGLRVLMVDVSHASNNVTDGLNGYDVGOSTQESYFHAGDRGYHKL 378
QY 381 WDSRLFNYSMEVLRFLLSNARMWLEEKYKDFGFRDGVTSMMYTHGLQMTFTGNGEYF 440
DB 379 WDSRLFNANMEVLRFLLSNARMWLEEKYKDFGFRDGVTSMMYTHGLQMTFTGNGEYF 438
QY 441 GPATVDAAVYVYMLVNDLHGLHPDAVSGEDVSGMPTFCIPVDDGVGFDYRLHMAVAD 500
DB 439 SLDTAVDAVYVYMLANHLMEKLLPEATVVAEDVSGMPTFCIPVDDGVGFDYRLHMAVAD 498
QY 501 KMIELLKQSDS-WKMGDIIVHTLTNRWLEKCVTYAESHDQALVGDKTIAFWLMDKMYD 559
DB 499 RMIDYLNKDDSEWNGEIAHTLTNRWLEKCVTYAESHDQALVGDKTIAFWLMDKMYD 558
QY 560 FMAIDRPSPTIRIDRIGIALHMKIRLVMTGLGEGYINFMNGEFGHPMIDPRPQTLPTG 619
DB 559 GMSDLOPASPITDRIGIALQKMIHFTMLGCGGYLNFNGEFGHPMIDPRPQTLPTG 610
QY 620 KVLPGNNNSYDKCRRRFDIGADFLRYHGMQEFDOAMQHLBEKYGFTSEHQVYSRKHEE 679
DB 611 ---EGNWSYDKCRQMSLVDTDLRYKYMNAFDQAMNALLDERFSFLSSKOIVSDNDE 667
QY 680 DKVITFERGDLVFNFNHNSNFPDVRGCSRGKTKVALLSDDALFGGSRSLDHDVDF 739
DB 668 EKIVIFERGDVFNFNHNSNFPDVRGCSRGKTKVALLSDDALFGGSRVGHADVDF 727
QY 740 TT-----EHPHNRPSFSYVTPSRVAVY 764
DB 728 TSPEGVPGVPEFTNPNRPNFSFKVLSPPRTCVAY 760

RESULT 11
US-09-731-166-14
Sequence 14, Application US/09731166
Patent No. 6639126
GENERAL INFORMATION:
APPLICANT: Sewalt, Vincent J. H.
APPLICANT: Singletary, George W.
TITLE OF INVENTION: Production of Modified Polysaccharides
FILE REFERENCES: 35718/206348
CURRENT APPLICATION NUMBER: US/09/731,166
PRIOR FILING DATE: 2000-12-06
PRIOR APPLICATION NUMBER: 60/169,993
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14
LENGTH: 822
TYPE: PRT
ORIG: NT
ORIG: NT

US-09-731-166-14

Query Match 51.5%; Score 2146; DB 4; Length 822;
Best Local Similarity 57.0%; Pred. No. 5,8e-195;
Matches 395; Conservative 101; Mismatches 171; Indels 26; Gaps 6;

QY DGOKIYEIDPLTKDRSHLDYRSEYRIRRAIDQHEGGLAERSCYKLGFTSAEGIT 145
DB DHPITVDLPKLEIFKDHFRYRMKRFLEOKSIEENEGSLESFSGYKLGINTNEDGTV 139
QY 146 YREWAPGAHSAALVGDENNPNADTMRDYGWEIFLNNADSPALPHGSRVYIRMD 205
DB 140 YREWAPGAOEAELIDFNDMNGANHMEKDKFGVWSIKI-DHYKGRPALPHNSKVXFRFL 198
QY 206 TPGSVKDSISAMIKFSVQAPGEI--PENGIIYDPEBEKRYVQHPQKAPESLRITYESHI 263
DB 199 HGVWVWDRIPALIRYATVDASKFGAPYDGVHMDPSPASERTYFKHPRPSKPAAPRIYEAHV 258
QY 264 GMSSEPKINSYANFRDEVLPRIKLGYNVQVMAIOEHSYASFGYHTNFPAPSRFG 323
DB 259 GMSGEKPAVSTYREFADNVLPRIRANNNTVOQMAVMEHSYASFGYHTNFFAVSSRG 318
QY 324 TPEDLKSLIDRAHEGLLVMDIVSHSSNNITLDGNGPD--GTDTHYHGGPRGHMM 380
DB 319 TPEDLKSLIDRAHSLGLRVLMVDVSHASNNVTDGLNGYDVGOSTQESYFHAGDRGYHKL 378
QY 381 WDSRLFNYSMEVLRFLLSNARMWLEEKYKDFGFRDGVTSMMYTHGLQMTFTGNGEYF 440
DB 379 WDSRLFNANMEVLRFLLSNARMWLEEKYKDFGFRDGVTSMMYTHGLQMTFTGNGEYF 438
QY 441 GPATVDAAVYVYMLVNDLHGLHPDAVSGEDVSGMPTFCIPVDDGVGFDYRLHMAVAD 500
DB 439 SLDTAVDAVYVYMLANHLMEKLLPEATVVAEDVSGMPTFCIPVDDGVGFDYRLHMAVAD 498
QY 501 KMIELLKQSDS-WKMGDIIVHTLTNRWLEKCVTYAESHDQALVGDKTIAFWLMDKMYD 559
DB 499 RMIDYLNKDDSEWNGEIAHTLTNRWLEKCVTYAESHDQALVGDKTIAFWLMDKMYD 558
QY 560 FMAIDRPSPTIRIDRIGIALHMKIRLVMTGLGEGYINFMNGEFGHPMIDPRPQTLPTG 619
DB 559 GMSDLOPASPITDRIGIALQKMIHFTMLGCGGYLNFNGEFGHPMIDPRPQTLPTG 610
QY 620 KVLPGNNNSYDKCRRRFDIGADFLRYHGMQEFDOAMQHLBEKYGFTSEHQVYSRKHEE 679
DB 611 ---EGNWSYDKCRQMSLVDTDLRYKYMNAFDQAMNALLDERFSFLSSKOIVSDNDE 667
QY 680 DKVITFERGDLVFNFNHNSNFPDVRGCSRGKTKVALLSDDALFGGSRSLDHDVDF 739
DB 668 EKIVIFERGDVFNFNHNSNFPDVRGCSRGKTKVALLSDDALFGGSRVGHADVDF 727
QY 740 TT-----EHPHNRPSFSYVTPSRVAVY 764
DB 728 TSPEGVPGVPEFTNPNRPNFSFKVLSPPRTCVAY 760

RESULT 12
US-08-104-158-2
Sequence 2, Application US/08104158
Patent No. 6215042
GENERAL INFORMATION:
APPLICANT: Wallmiller, Lothar
APPLICANT: Sonnwald, Uwe
APPLICANT: Kossmann, Jens
APPLICANT: Mueller-Roeber, Bernd
APPLICANT: Visser, Richard Gerardus Franciscus
TITLE OF INVENTION: PLASMIDS CONTAINING DNA-SEQUENCES THAT
CAUSE CHANGES IN THE CARBOHYDRATE CONCENTRATION AND THE
CARBOHYDRATE COMPOSITION IN PLANTS, AS WELL AS PLANT CELLS
TITLE OF INVENTION: AND PLANTS CONTAINING THESE PLASMIDS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ostrolenk, Faber, Gebt & Soffen

Tue Apr 20 10:02:28 2004

us-09-508-377-12.ra1

Page 8

STREET: 1180 Avenue of the Americas
City: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-8403
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/104,158
FILING DATE: 13-AUG-1993
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP PCT/EP92/00302
FILING DATE: 11-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 41 04 782.6
FILING DATE: 13-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meliman, Edward A.
REGISTRATION NUMBER: 24,735
REFERENCE/DOCKET NUMBER: FA-1996 PCT (951-91)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-382-0700
TELEFAX: 212-382-0888
TELEX: 236925
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 566 amino acids
Type: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
JS-08-104-158-2

Query Match	38.6%	Score 1608	DB 3	Length 566
Best Local Similarity	57.8%	Pred. No. 5,1e-144		
Matches 298	Conservative	72	Mismatches 133	Indels 8
				Gaps 5
QY	90	LYEIDPTLKDPSHLDYRYSERYRIRPAIDQEGGLEAFSRGEXKLTGRTSAGETTYREW	149	
Db	52	LLNDPTLEPLDHPHRMKRYVDQKMLIEKXEGGLEFAQCYLTFGNREDCGVREW	111	
QY	150	APGASHALVGDENNMMNNADMTMDDDGWMEIFLPNNADSPAIPIGSRVYKIRMDTPSG	209	
Db	112	APAAQEAVIDDPENRNGNSNNHMEKDGQGVMSIRIP-DVDSAPVYFPHNSRYKFRFKHNG	170	
QY	210	V-KDSISMIKFSYQAPGEI--FNGIYYDDPEEBEKYVFOHQDPRESLRITYESHIGNS	266	
Db	171	VWVRIRPAMIKATADACKPAAPYDGVWDPPEPSRRYHPKYRPRPKPRAPRIYEAHVQMS	230	
QY	267	SPEPKINSYANFRDEVIRIKRLGYNAOIMIOHSYXASGCVTVNFEASRSRGPTE	326	
Db	231	SSEPVSNSYREPADVLPRIKANNNTYQVLAIMEHSYIGSGIHYTNFANSNYKQPE	290	
QY	327	DLKSLIDBAHEGLVLVMDIVHSHSSNNVLLDGLNGFD--GTDTHYFHGQPRGHHMMDS	383	
Db	231	DLKYLIDKXHSGLQVLYDVVASHASNNVTDGLNGFDIQGQSGESYFAHGEYGHKLMDS	350	
QY	364	RLEFNYSWVLFRLFLLSNMAWMLLEKYKFDGFRRDQVLSMMYTHHGLOMFTGNYGEYFPA	443	
Db	351	RLEFNANNEVLFLLSNRMLLEEYNFDGFRDGLTISMLYHSHGIMGTGNNIEYFSA	410	
QY	444	TVDAVVYVLMVNDLILGHLPDAVSIGEDVSGMPTFCIEPVDGQVGFEDRLMAVAQXVI	503	
Db	411	TDVDAVVYVLMANNLIHKIFPDATVIAEDVSGMPSRSEVSGGIGFYDLALALPDKMI	470	
QY	504	ELLK-QSDSEWKKGGDIIVHTLTNRKMLEKYVTAESDQALVDGKTATAPFLMKDXYDFMA	562	
Db	471	DYLNKKNDEMDMKVEYTSGLTRRRYREKCIATAESDQSIIVGDKTATAPFLMKXEMTSGMS	530	
QY	563	LDPSTPRIDRGIALHKMIRLYTMGLGGEQYNTFMG	598	

Db 531 CTTDASEPVWDAGIALDKMIHFPHNGJGRRGVPGPHG 566

RESULT 13

US-09-609-040-2

Sequence 2, Application US/09609040

Patent No. 6570066

GENERAL INFORMATION:

APPLICANT: Wilmutizer, et al.

TITLE OF INVENTION: NUCLEOTIDE SEQUENCES ENCODING ENZYMES THAT ALTER THE CARBOHYDRATE

TITLE OF INVENTION: CONCENTRATION AND COMPOSITION IN PLANTS

FILE REFERENCE: 51413-3515.1

CURRENT APPLICATION NUMBER: US/09/609,040

CURRENT FILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: PCT/EP92/00302

PRIOR FILING DATE: 1992-02-11

NUMBER OF SEQ ID NOS: 4

SOFTWARE: PatentIn version 3.0

SEQ ID NO 2

LENGTH: 566

TYPE: prt

ORGANISM: Solanum tuberosum

US-09-609-040-2

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Query Match      38.6%, Score 1608 : DB 4: Length 566;
Best Local Similarity 57.8%, Pred. No.5,1e-144,
Matches 298; Conservative 72; Mismatches 138; Indels 8; Gaps 5;

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QY 150 APGAASALVDEFNMMFNADMTMTDDYGAWEIFLPNNAAGSPALPHGSRVXIRMDTPBG 209
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QY 210 V-KDSISAMIKPSVQAPGEI--PFNGIYDPEEEKYVQFQHPQKRPEESLRITYESHIGMS 266
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 171 VAVDRIIPMIKATATADATKFAAPYDGYWDPSPSRHYHKYRPRKRAPRIYEAHVGS 230

QY 267 SEEPKINSYANFERDEVLEPRIKLGYNAVOIMAIQESHYYASFGYHYTNFPAPSPRGTEP 326
DB 231 SEEPKINSYREPADVLEPRIKANNYNTVQIMAIMESHSYGSFGYHYTNFPAPSVNRXGNPE 250

QY 327 DLKSLIDRAHEIGLLVMDIVHSHSNNTLDLGNPD---GPDTHYFHGGPRCHMMWDS 383
DB 291 DLKYIIDKSHSIGLQVLVDVHSHASNNTDGLNGFDLQGSSESTFHAGGERGYHLMD5 350

QY 384 RLFNYSGEWEVLEFLLSNARWMLSEYKFDGFRFEDGVTSNMYTHHGLQMTFTGNYGEYFGFA 443
DB 351 RLFNANMEVLEFLLSNLFWMLEYNFDGFRFDGILSMLYVHHGIMNGFGTGNNEYFSEA 410

QY 444 TDVDVAVYIMLVNDLILHGLHPDAVSIGEYVSGMPTTCIYVPOGCVGPDVRLHAAVADKWI 503
DB 411 TDVDVAVYIMLVNANNLIHKIFPDATYLAEVSGMPLSRPVSSEGIGFIDRLAAVAPDKWI 470

QY 504 ELTK-QSDSEWMOGDI VHTLTNRMRLEKCVTAESHDQALVGSKTAFWIMDXMDYDENA 562
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 471 DYLNKNNDDSDMSKEYTSSLTNRRITYEKTIAAESHDDGSLVBDKTIATFLMNMENWISGMS 530

QY 563 LDRSPSTRIDRGIALHKMILRYTMGIJGEGYINFWG 538
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DB 531 CLTDASPVVDAGIALDKMIHFPHNGJGRGAVDQFHG 566

RESULT 14
US-09-579-365-2
; Sequence 2, Application US/09579365
; Patent No. 6566585
; GENERAL INFORMATION:
; APPLICANT: MARTIN QUANZ
; TITLE OF INVENTION: GENETICALLY MODIFIED PLANT CELLS AND PLANTS WITH AN

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;; TITLE OF INVENTION: INCREASED ACTIVITY OF AN ANYLOSUCRASE PROTEIN AND A
;; FILE OF INVENTION: BRANCHING ENZYME
;; FILE REFERENCE: 0147-0200P
;; CURRENT APPLICATION NUMBER: US/09/579,365
;; CURRENT FILING DATE: 2000-05-25
;; NUMBER OF SEQ ID NOS: 15
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 2
;; LENGTH: 762
;; TYPE: PRT
;; ORGANISM: Neisseria denitrificans
US-09-579-365-2

Query Match 13.8%; Score 576; DB 4; Length 762;
Best Local Similarity 24.9%; Pred. No. 1,4e-45;
Matches 187; Conservative 126; Mismatches 227; Indels 210; Gaps 37;

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DB 106 REEDDYRFG---SALQHTDAMLGEGTHLRPEYTLGAHFAMDGVSQVFAVMAVNA 159
QY 154 HSAALVGFENNNPNADTM--TRDDYGVWEIFLFPN-----NADGS---PAIPHG 197
DB 160 RAVSVIGENGMSRRAHMRPHGTGMDIFIPVGLNALYKFSVDANGIRKADPYA 219
QY 198 SRVXRMDTPSGVKDISAMIKFSVQAPGEIPENGIIYDPEPEEKYVFQHPQRPBSLR 257
DB 220 FGAELRPTASVVR-----GL---PAKAAAPFRRRANSVEAPIS 256
QY 258 IYESHIGMSPEEKIN---SYANPRDSEVLRIRKLGNAVQVMAIQHSYASFGYHTN 314
DB 257 IYEVHLGSRARNENNYWLTYYTQLABLVVYVXDMGTHIELPLSEPPGSGWGYQATG 316
QY 315 FPAFSRFGTPEDLKSLIDRAHELGILVMDIYHSHSSNNTLDGLNGFDGDTYFPGP 374
DB 317 LVAFTRFSGPDLKALIDAAHAAAGISVILDDVAGHFPSTD--KGLNTPDGI--ALYEHADP 374
QY 375 R-GHHMMWDSRLFNYSWEVLAFLLSNARWLDEYKDFGDFGVTSMMYTHHGLQMTFT 433
DB 375 RGYHODMNTLLIYNFGSEVKNFLQGNALYIERFDFGDIRVDVASMITYN-----YS 428
QY 434 GNYGEI---FGATVDVAVVYMLVNDLHGHPDVAISGEDVSGMPTFCIPYPDGVG 489
DB 429 RKDGEWIPRKYGSSENLIAFLRQTNVAVLKSETPGGSFAEST---SFADVTREAGLN 485
QY 490 FVRLIMAVADKMI--ELLKQSDSWKMGDIVHTLTNRMLEKCVT-----YAE----- 536
DB 486 FDFKMMNG---WMNDTLRYMGE---DVBH---RKYHNGKMTFGMMYYSSENFVLP 532
QY 537 SHDQALVGDXTIA---FWLMDKDM---YDFMALDRPSTPRIDGIALHKMLRYVTMG 587
DB 533 SHDEVVHGKRSLLGKMPGDCWQOFANRAYYGFV-----YG 568
QY 588 LGGEGVLNMGNEFGH--PEWIDFPRGPQTLPTGKVLFGNNNSYDKCRRRPLGADFLRY 646
DB 569 FPGKLL--FMGNSFAQREM--NYOEG-----LDW 595
QY 647 H-----GMQEPDQAMQHL-----EKKYGFMTSEHQYVSRKHEEDKYLIF 685
DB 596 HLLDEAGMKHGYQDYVRLNHTYTAAPRYQDQCEGF-----EWLVADDSNSVFFV 650
QY 686 EREGD---LVFVNF-----HMSNSFFDYRVGCSRPKGYKVALDSDDALFGFSRLDH 734
DB 651 ERDRAGNIIIVISNFTPVVREH-----YRFGVNAFGRYTEILNDRDTQYG--SGIAN 702
QY 735 DVDFYFTEHHDNRPRSFSVYTPSRATVY 764
DB 703 GADITAEVNPSSHGKQSLSLTLP--LATVY 731

;; Patent No. 6608018
;; GENERAL INFORMATION:
;; APPLICANT: No. 6608018cyzmes A/S
;; APPLICANT: Shinohara, Mari U.
;; TITLE OF INVENTION: Polypeptides having branching enzyme activity and nucleic acids
;; FILE REFERENCE: 5860.200-US
;; CURRENT APPLICATION NUMBER: US/09/537,120
;; CURRENT FILING DATE: 2001-08-17
;; NUMBER OF SEQ ID NOS: 2
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 2
;; LENGTH: 621
;; TYPE: PRT
;; ORGANISM: Rhodothermus obamensis
US-09-537-120-2

Query Match 13.0%; Score 541.5; DB 4; Length 621;
Best Local Similarity 26.2%; Pred. No. 2e-42;
Matches 175; Conservative 114; Mismatches 243; Indels 135; Gaps 28;

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QY 178 GWEIIFLNNADGSPALPHGSRVKIRMDTPSGVKDISAMIKFSVQAPGEIPENG 233
DB 67 GLMAGYVPGARPG---HTYKXIRIRHGFYQADKTPYA---FAMEPPTGSPTEGLASII 118
QY 224 ---YDPEPEEKYVFGHPQ--KRPESLRIYESHIG---SSPEKINSYANFRPEVL 283
DB 119 TRLDYTHMD---DMMRRRKQPAISLYEPVSIYEVHLGSRHKKRPGESF--SYREIAPLA 173
QY 284 PRKLGNAVQVMAIQHSYASFGYHTNFPAPSRFGTPEDLKSLIDRAHELGILV 343
DB 174 DYQMGSGFTHBELLVMEHPYIGSWCYGVYAPFRFGSPDMLYLDLHQRGIGVI 233
QY 344 MDIYHSHSSNNTLDGLNGFDGDTYFHGGRPGHMMWDSRLFNYSWEVLAFLLSNARW 403
DB 224 LDWVSHPAADP--QGLVFEFDGTTLPEDYDPRKMYHDPDWGTYVDPYDKPGVRNPLISNALF 292
QY 404 WLEEKYKPGFRFDGVTSMYTHHGLQMTFTGNYGEYFGATVDVAVVYMLVNDLHGLH 463
DB 293 WLEKTHVGLRVDVAASMLYRYS--RKEWTPN---IFGRENLEALDIFIKKEETVYLHF 348
QY 464 PDAVIGEDVSGMPTFCIPVDPGVGFYRLHMAVADKMIELLKQSDSWKMGDIVHTLT 523
DB 349 PEAMTIAESTMPPVSAAPTYNNGIGFLYK-----NNMGMMHTLTD 389
QY 524 NRMWLEKCVTAESHDQALVGDXTIAFWLMDKDMYDFMALDRPSTPRIDGIALHKM 580
DB 390 ---YIQRDPIYKXAHDEL---TSLMYAFSEHY--VLPLSHDEVH--GKGSJMGKMPGD 440
QY 581 ---IRLVYMGIGGE--GYLNFMGNEFG--HPEWIDFPRGPQTLPTGKVLFGNNNSYD 630
DB 441 DMQKAAVRLRLFGHMGHPGDKLLFPNGSFGQHHEH-----NHTT-- 480
QY 631 KCRARFDGADDFLRYHGMQEPDQAMQHL-----EKKYGFMTSEHQYVSRKHEEDK 681
DB 481 ---QLEMHLLDQPY--HRGQLWVCIDLNIYKRNPAALMHGPREF-----EMIDFSRBDQS 531
QY 682 VIFERGD---LVFVNF-----HMSNSFFDYRVGCSRPKGYKVALDSDDALFGFSRLDH 728
DB 532 VICYRKAKAGRWLLFLVNFPTPVREH-----YRVGVPIGFGWHEVLNSDAVAYGSSGM 584
QY 729 --FSRLD 733
DB 585 GNFGKVE 591

Tue Apr 20 10:02:28 2004

us-09-508-377-12.rapb

Page 1

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 15, 2004, 08:38:16 ; Search time 48 Seconds
(without alignments)
4410.770 Million cell updates/sec

Title: US-09-508-377-12

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Gapop 10.0 , Gapext 0.5

Searched: 1124875 seqs, 275673149 residues

Total number of hits satisfying chosen parameters: 1124875

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	3363	80.7	855	9	US-09-792-127-4
3	3348.5	80.3	829	9	US-09-792-127-5
4	3342.5	80.2	798	12	US-10-336-753-70
5	3342.5	80.2	870	12	US-10-336-753-54
6	3329	79.9	895	9	US-09-792-127-2
7	3325.5	79.8	870	12	US-10-424-599-273691
8	3175	76.2	878	14	US-10-254-534-2
9	3135	75.2	882	14	US-10-056-454-15
10	2213	53.1	464	14	US-10-254-534-4
11	2146	51.5	776	12	US-10-336-753-56
12	2146	51.5	822	12	US-10-171-008-9
13	1978	47.4	674	12	US-10-425-114-53683
14	1917.5	46.0	874	15	US-10-369-493-3969
15	1915	45.9	421	12	US-10-425-114-45676

15	1896	45.5	681	15	US-10-369-493-5706	Sequence 5706, Ap
16	1795.5	43.1	704	15	US-10-369-493-1720	Sequence 1720, Ap
17	1656	39.7	647	15	US-10-369-493-10283	Sequence 10283, A
18	1642	39.4	546	14	US-10-171-008-8	Sequence 8, Appl1
19	1284	30.8	309	14	US-10-171-008-4	Sequence 4, Appl1
20	851	20.4	337	12	US-10-262-511-108	Sequence 108, App
21	745.5	17.9	375	12	US-10-424-599-283934	Sequence 283934,
22	579	13.9	726	15	US-10-369-493-19590	Sequence 19590, A
23	575.5	13.8	750	15	US-10-369-493-19848	Sequence 19848, A
24	574	13.8	737	15	US-10-369-493-12299	Sequence 12299, A
25	573	13.7	710	9	US-09-738-626-4854	Sequence 2780, Ap
26	564.5	13.5	721	9	US-09-738-626-4854	Sequence 4854, Ap
27	560.5	13.4	159	12	US-10-369-493-20849	Sequence 20849, Ap
28	559	13.4	120	12	US-10-424-599-230110	Sequence 230110, A
29	558	13.4	730	12	US-10-282-1228-58499	Sequence 58499, A
30	556.5	13.3	756	15	US-10-369-493-20951	Sequence 20951, A
31	554	13.3	735	15	US-10-369-493-19307	Sequence 19307, A
32	553.5	13.3	728	15	US-10-369-493-23588	Sequence 23588, A
33	553.5	13.3	785	12	US-10-336-753-36	Sequence 36, Appl
34	553	13.3	617	15	US-10-369-493-9891	Sequence 9891, Ap
35	550.5	13.2	705	15	US-10-369-493-632	Sequence 632, App
36	549.5	13.2	630	15	US-10-369-493-50	Sequence 50, Appl
37	543	13.0	719	15	US-10-369-493-10019	Sequence 10019, A
38	537	12.9	732	12	US-10-389-647-471	Sequence 471, App
39	532	12.8	628	15	US-10-369-493-9028	Sequence 9028, Ap
40	532	12.8	677	15	US-10-200-055-63	Sequence 63, Appl
41	526	12.6	717	15	US-10-369-493-7769	Sequence 7769, Ap
42	520.5	12.5	718	15	US-10-369-493-15576	Sequence 15576, A
43	520.5	12.5	720	15	US-10-369-493-15952	Sequence 15952, A
44	520.5	12.5	720	15	US-10-369-493-16316	Sequence 16316, A
45	520.5	12.5	720	15	US-10-369-493-16316	Sequence 16316, A

ALIGNMENTS

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44	US-10-171-008-10	Sequence 10, Appl1	US/10171008
45	US-10-171-008-10	Sequence 10, Appl1	US/10171008

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QY 164 NNNPNADTMTDDYGVWEI FLPNNA DGS PAI PHGSRVKIRMDTPSGVKS ISAMIKESVQ 223
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DB 266 APGEIPYNGIYDPPPEEKVYFQHPQRPBESLR IYSHIGMSSPEPKINSYANFRDEVL 325
QY 284 PRKRGYNVAVOIMAOEHSYVAFGYHVNFFAPSSRFGTPEDLKSLIDRAHEGLLV 343
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DB 386 MDIVSHSSNNTLDGLNGFDGTDHYFGHGRGHMMWDSRLFNYSWEVLRLISNARW 445
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DB 446 WLEEYKDFRFGDVTSMYTHHGLQMTFTGNIGEYGFATDVAVYVLMVNDLIRGLY 505
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DB 686 LRHGMQEPFOAMHLEKXGFMTESEHQYSRKHEEDKVIIFERGDVLFVNFHMSNSFF 745
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DB 746 DYRVCSPRGKYKVALDSDDALFGGFSRLDHDVDVFTTEHPHNDPRSFVYTPSRITAV 805
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DB 806 YA 807

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RESULT 2

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US-09-792-127-4
; Sequence 4, Application US/09792127
; Patent No. US20020002713A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Beckles, Diane M.
; APPLICANT: Butler, Karla
; APPLICANT: Pearlstein, Rich
; TITLE OF INVENTION: Starch Branching Enzyme IIB
; FILE REFERENCE: B81439 US NA
; CURRENT APPLICATION NUMBER: US/09/792,127
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/186098
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 4
; LENGTH: 855
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-09-792-127-4

```

Query Match 80.7%; Score 363; DB 9; Length 855;
 Best Local Similarity 79.5%; Pred. No. 1,3e-306;
 Matches 607; Conservative 75; Mismatches 68; Indels 14; Gaps 4;

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QY 7 SGATIGVAPPAAP-----BELOIPEDIEEQTAENVMTGTGAETLESSEPTQIVETI 61
DB 98 SGGT-----PSIDPVPVDFSDDLKVP-FIDET---SLQDGEDSIWSEINQVSEID 148
QY 62 TDGVTKGVKELVYVSEKPRVPRKPGDGOKIYEIDPTLKDRSHLDYVSEYRRIRAAIDQH 121
DB 149 AEDTSRMKESSTREKRLILPPPGNGQCIYEIDPTLRDKHLEXYLSLRRIRSDIDEH 208
QY 122 EGGLEAFSGRYEKLGFTEGSAEGITYREMAFGHSAALVQDFNNMNNADTMTDDYGVWE 181
DB 209 EGMQDVFERGYEKFPMRSASAGITYREMAFGHSAALVQDFNNMNNADTMTDDYGVWE 268
QY 182 IFLPNNA DGS PAI PHGSRVKIRMDTPSGVKS ISAMIKESVQAPGEIPFNGIYDPEEE 241
DB 269 IFLPNNA DGS PAI PHGSRVKIRMDTPSGVKS ISAMIKESVQAPGEIPFNGIYDPEEE 328
QY 242 KYVFOHPQRPBESLR IYSHIGMSSPEPKINSYANFRDEVLPRIRLGYNAVQIMAOE 301
DB 329 KYVFOHPQRPBESLR IYSHIGMSSPEPKINSYANFRDEVLPRIRLGYNAVQIMAOE 388
QY 302 HSYVAFGYHVNFFAPSSRFGTPEDLKSLIDRAHEGLLVMDIYHSSNNTLDGLNG 361
DB 369 HSYVAFGYHVNFFAPSSRFGTPEDLKSLIDRAHEGLLVMDIYHSSNNTLDGLNG 448
QY 362 PEGTDTYHFGHGRGHMMWDSRLFNYSWEVLRLISNARWLEEKDFRFGDVTSM 421
DB 449 PEGTDTYHFGHGRGHMMWDSRLFNYSWEVLRLISNARWLEEKDFRFGDVTSM 508
QY 422 MYTHHGLQMTFTGNIGEYGFATDVAVYVLMVNDLIRGLHAPDAVSGEDVSGMPTFCI 481
DB 509 MYTHHGLQMTFTGNIGEYGFATDVAVYVLMVNDLIRGLHAPDAVSGEDVSGMPTFCI 568
QY 482 PVPDGVGFDRFLHMAVADKWIILLKQSDSWKMGDI VHTLTNRNMLEKCVTYAESHDQ 541
DB 569 PVPDGVGFDRFLHMAVADKWIILLKQSDSWKMGDI VHTLTNRNMLEKCVTYAESHDQ 628
QY 542 LVGDXTIAFWLMDKMYDFMALDRPSTPRIDRGIALHQMIRLVTMGLGEGYLINFMGNEF 601
DB 629 LVGDXTIAFWLMDKMYDFMALDRPSTPRIDRGIALHQMIRLVTMGLGEGYLINFMGNEF 688
QY 602 GHPEWIDPRGPOTLPFGKVLPGNNNSYDKCRRRFDGADDFLRHGMQEPFOAMHLE 661
DB 689 GHPEWIDPRGPOTLPFGKVLPGNNNSYDKCRRRFDGADDFLRHGMQEPFOAMHLE 748
QY 662 KYGFMTESEHQYSRKHEEDKVIIFERGDVLFVNFHMSNSFFDYRVCSPRGKYKVALDS 721
DB 749 KYGFMTESEHQYSRKHEEDKVIIFERGDVLFVNFHMSNSFFDYRVCSPRGKYKVALDS 808
QY 722 DDALFGGFSRLDHDVDVFTTEHPHNDPRSFVYTPSRITAVYA 765
DB 809 DDALFGGFSRLDHDVDVFTTEHPHNDPRSFVYTPSRITAVYA 852

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RESULT 3

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US-09-792-127-5
; Sequence 5, Application US/09792127
; Patent No. US20020002713A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Beckles, Diane M.
; APPLICANT: Butler, Karla
; APPLICANT: Pearlstein, Rich
; TITLE OF INVENTION: Starch Branching Enzyme IIB
; FILE REFERENCE: B81439 US NA
; CURRENT APPLICATION NUMBER: US/09/792,127
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/186098
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 5
; LENGTH: 829
; TYPE: PRT

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Tue Apr 20 10:02:28 2004

us-09-508-377-12.rapb

Page 3

ORGANISM: Hordeum vulgare
US-09-792-127-5

Query Match 80.3%; Score 3348.5; DB 9; Length 829;
Best Local Similarity 79.1%; Pred. No. 2.8e-305;
Matches 605; Conservative 72; Mismatches 75; Indels 13; Gaps 3;

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QY      8 GATLGAARPPAAA-----OPEELQIP--EDIEBQTAENVNTGGTAELSESSEPTQIVET 60
DB      68 GGGGGGGTTPSISGVSQFESDDLEVPID-----BPSLHDGGEPTIRSEETQIVTEEI 121
QY      61 ITDVTGKVELVGEKPRVVPKPGDQKTYEIDPTLKDRSHLDYRYSEYRRAIDQ 120
DB      122 DAGVGRMKESSTVKKIRIVPQFGNGQIYDIDPMLRDKYHLEYRSLYRRIRSDIDE 181
QY      121 HEGGLEAFSRGYEKLGFTRSAEGITTYEMAPGAHSALVGFNNMNPADTMTREDYGVW 180
DB      182 YDGGMVVFSRGYKFGFVRSABEGITTYEMAPGADSAALVGFNNMNPADTMTREDYGVW 241
QY      181 EIFLNNADGSPAIPIHGSRYKIRMDTPSGVDSISAMIKESVQAPGEIPENGIIYDPEE 240
DB      242 EIFLNNADGSPAIPIHGSRYKIRMDTPSGVDSISAMIKESVQAPGEIPENGIIYDPEE 301
QY      241 EKYVFOHPQKRPESLRIYSHIGMSPEPKINSYANFRDEVLPRIKLGYNVQVMAIQ 300
DB      302 EKYVFOHPQKRPESLRIYSHIGMSPEPKINSYANFRDEVLPRIKLGYNVQVMAIQ 361
QY      301 EHSYVAFGHVYNFPASRFGTPEDLKSLIDRAHELGILLVMDIVSHSSNNTLDELIN 360
DB      362 EHSYVAFGHVYNFPASRFGTPEDLKSLIDRAHELGILLVMDIVSHSSNNTLDELIN 421
QY      361 GPDGDTIHYFGHGRGHMMWDSRLFNYSGWELRFLSNARWMLBEEKYDFGFRDGYTS 420
DB      422 GPDGDTIHYFGHGRGHMMWDSRLFNYSGWELRFLSNARWMLBEEKYDFGFRDGYTS 481
QY      421 KMYTHGLQMTFTNGYGEYGFATDVAVYTLMLVNDLHGLHPDAYSIGDVGMPFFC 480
DB      482 KMYTHGLQMTFTNGYGEYGFATDVAVYTLMLVNDLHGLHPDAYSIGDVGMPFFC 541
QY      481 IPRPDGCVGDYLLHMAVADKTEILLKQSDSWKMGDVTTLTRRMLEKCTVAESHDQ 540
DB      542 LPAQVGVGVGYRHHMAVADKTEILLKQSDSWKMGDVTTLTRRMLEKCTVAESHDQ 601
QY      541 ALVGDXTIAFLMDKMDYDFMALDRPSTPRIDRGIALHKMIRLVTMGLGEGYINPMGNE 600
DB      602 ALVGDXTIAFLMDKMDYDFMALDRPSTPRIDRGIALHKMIRLVTMGLGEGYINPMGNE 661
QY      601 FGHPEWIDPRPGQPTLTPTGKYLPGNNNSYDKCRRRFDLGDADFLRYHMOEFDQMOHLE 660
DB      662 FGHPEWIDPRPGQPTLTPTGKYLPGNNNSYDKCRRRFDLGDADFLRYHMOEFDQMOHLE 721
QY      661 EKYGEMTSEHCYRKKEBEDKVIIFERGLVFEVFNHNSNFFDYRGCSRPGRKXVALD 720
DB      722 EKYGEMTSDHCYRKKEBEDKVIIFERGLVFEVFNHNSNFFDYRGCSRPGRKXVALD 781
QY      721 SDDALFGGSRLLDHDVDYFTTEHHPDNRPRSFSVYTPSRITAVVYA 765
DB      782 SDDALFGGSRLLDHDVDYFTTEHHPDNRPRSFSVYTPSRITAVVYA 826
```

RESULT 4
US-10-336-753-70
; Sequence 70; Application US/10336753
; Publication No. US20030226176A1

GENERAL INFORMATION:
; APPLICANT: Guan, Hanping
; APPLICANT: Keeling, Peter L.
; TITLE OF INVENTION: PLANT LIKE STARCHES AND THE METHOD OF MAKING THEM IN
; FILE REFERENCE: 2461-52
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US/09/402.254

PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US98/06660
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/042,939
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-04-04
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 70
; LENGTH: 798
; TYPE: PRT
; ORGANISM: Zea mays
US-10-336-753-70

Query Match 80.2%; Score 3342.5; DB 12; Length 798;
Best Local Similarity 76.0%; Pred. No. 3.8e-305;
Matches 613; Conservative 65; Mismatches 76; Indels 53; Gaps 5;

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QY      4 FAVSGATIGVA-RPP-----AAAQPEELQI 27
DB      3 FRVSGAVLGAARAPRLTGGGEGSLVFRHTGLELTRGARVGCSTGAMAAAAAARAAV 62
QY      28 PEDIEBQTAENVNTGGTAELSESSE-----PTQIVETITDVTGKVELVGEKPRV 81
DB      63 PEGEND-----GLASRADSAQFQSDLEVPDISEETTCGA--GVADAQALNRVAV 111
QY      82 PEPGQKTYEIDPTLKDRSHLDYRYSEYRRAIDQHEGGLAERSGYKLGTRSA 141
DB      112 PEPGQKTYEIDPTLKDRSHLDYRYSEYRRAIDQHEGGLAERSGYKLGTRSA 171
QY      112 PEPGQKTYEIDPTLKDRSHLDYRYSEYRRAIDQHEGGLAERSGYKLGTRSA 201
DB      142 EBITREMAFGAHSALVGFNNMNPADTMTREDYGVWEIFLNNADGSPAIPIHGSRYK 231
QY      172 EBITREMAFGAHSALVGFNNMNPADTMTREDYGVWEIFLNNADGSPAIPIHGSRYK 261
DB      202 IPRPDGCVGDYLLHMAVADKTEILLKQSDSWKMGDVTTLTRRMLEKCTVAESHDQ 291
QY      232 VAMDTPSGIKDSIPAVIKYSVQAPGEIPYDGIYDPEEYKVFRRHAQPRKSLRIYET 321
DB      262 HIGMSPEPKINSYANFRDEVLPRIKLGYNVQVMAIOGHSYASFGYVYNFPASR 351
QY      292 HIGMSPEPKINSYANFRDEVLPRIKLGYNVQVMAIOGHSYASFGYVYNFPASR 381
DB      322 FGTPEDLKSLIDRAHELGILLVMDIVSHSSNNTLDELINFGDGTIHYFSGRGHMMW 411
QY      352 FGTPEDLKSLIDRAHELGILLVMDIVSHSSNNTLDELINFGDGTIHYFSGRGHMMW 441
DB      412 DSRLEFNGSWEYLRFLLSNARWMLBEEKYDFGFRDGYTSKMYTHGLQMTFTNGYGEY 471
QY      442 FATDVAVYTLMLVNDLHGLHPDAYSIGDVGMPFFC.PVPRDGGVGFYRLHMAVADK 501
DB      472 FATDVAVYTLMLVNDLHGLHPDAYSIGDVGMPFFC.PVPRDGGVGFYRLHMAVADK 531
QY      502 WTEILLKQSDSWKMGDVIHITLITNRMLLEKCTVAESHDQALVGBKTIAPFLMDKMDYDF 561
DB      532 WTEILLKQSDSWKMGDVIHITLITNRMLLEKCTVAESHDQALVGBKTIAPFLMDKMDYDF 591
QY      562 ALDRPSTPRIDRGIALHKMIRLVTMGLGEGYINPMGNEFGHPWIDPRPGQPTLTPTGK 621
DB      592 ALDRPSTPRIDRGIALHKMIRLVTMGLGEGYINPMGNEFGHPWIDPRPGQPTLTPTGK 651
QY      622 LRGNNNSYDKCRRRFDLGDADFLRYHMOEFDQMOHLEKYGEMTSEHCYRKKEBEDK 681
DB      652 LRGNNNSYDKCRRRFDLGDADFLRYHMOEFDQMOHLEKYGEMTSEHCYRKKEBEDK 711
QY      682 VIIFERGLVFEVFNHNSNFFDYRGCSRPGRKXVALDSDDALFGGSRLLDHDVDYFTT 741
DB      712 VIIFERGLVFEVFNHNSNFFDYRGCSRPGRKXVALDSDDALFGGSRLLDHDVDYFTT 771
QY      742 EHPDNRPRSFSVYTPSRITAVTALTE 768
DB      772 DCSHDNRPRSFSVYTPSRITAVTALTE 798
```

RESULT 5

US-10-336-753-54
 / Sequence 54, Application US/10336753
 / Publication No. US20030226176A1
 / GENERAL INFORMATION:
 / APPLICANT: Guan, Hanning
 / APPLICANT: Keeling, Peter L.
 / TITLE OF INVENTION: PLANT LIKE STARCHES AND THE METHOD OF MAKING THEM IN
 / TITLE OF INVENTION: HOSTS
 / FILE REFERENCE: 2461-52
 / CURRENT APPLICATION NUMBER: US/10/336,753
 / CURRENT FILING DATE: 2003-01-06
 / PRIOR APPLICATION NUMBER: US/09/402,254
 / PRIOR FILING DATE: 1999-10-01
 / PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US98/06660
 / PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-03
 / PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/042,939
 / PRIOR FILING DATE: EARLIER FILING DATE: 1997-04-04
 / NUMBER OF SEQ ID NOS: 77
 / SOFTWARE: PatentIn Ver. 2.1
 / SEQ ID NO 54
 / LENGTH: 870
 / TYPE: PRT
 / ORGANISM: Zea mays
 US-10-336-753-54

Query Match 80.2%; Score 3342.5; DB 12; Length 870;
 Best Local Similarity 76.0%; Pred. No. 1.1e-304;

Matches 613; Conservative 65; Mismatches 76; Indels 53; Gaps 5;

4 FAVSGATGTGA-RPP-----AAQPELQI 27
 3 FRVSGAVTGVAVRPRLLTGGGSLVFRHTGLFRGARVCGSGTGMARAAAANKAV 62
 28 PEDIEQTAEVMTGTGAEKLESE-----PTGIVETITDGTGKVELVGEPRVY 81
 63 PEGEND-----GLASRADSAQFQSDLEVPDISEETCGA--GVADAQALNVRVY 111
 82 PKPGDQKIYEIDPLKDFRSLDRYSYRIRAIADHDEGLEAFSGYEGLGFTRSA 141
 112 PPPSGQKIFQIDPLMGKYLERYSLYRIRISDIDHEGGLXFSRYEFGNASH 171
 142 EGITREAVAPGASHAALVGFNNMNPADTMRDYGWEIFLNNADSPALPHSGRYK 201
 172 EGITREAVAPGASHAALVGDVNNMNPADMRKNGEWEIFLNNADGTSPPHSGRYK 211
 202 IRMDTPSGVKDSISAMIKFSVQAPGEIPNGIYYDPPEEEKYVFGHPQKRPESLR 261
 232 VRMDTPSGIKDSIPAMIKFSVQAPGEIPYDGIYYDPPEEEKYVFRHAQKRPESLR 291
 262 HIGMSPPPKINSYANFRDEVLPRIKLGYNVQVMAIOEHSYVAFGYVTFNPPSSR 311
 292 HVGMSPPPKINTYVNFDEVLPRIKLGYNVQVMAIOEHSYVAFGYVTFNPPSSR 351
 322 FGTPEDLSLIDRAHELGLVLMIDIVHSHSNNTLDGLNGFGDGTDTTHYFHGGR 381
 352 FGTPEDLSLIDRAHELGLVLMIDIVHSHSNNTLDGLNGFGDGTDTTHYFHGGR 411
 382 DSRLFNYSWEVLRFLLSNARWMLBEYKFDGFRPDGVTSMTYTHGLQVTFNFEYFG 441
 412 DSRLFNYSWEVLRFLLSNARWMLBEYKFDGFRPDGVTSMTYTHGLQVTFNFEYFG 471
 442 PATDVAVYVYMLVNDLHGLHPDVAISGIDVSGMPTFCIPVDDGVGFGPYRLAHMAVADK 501
 472 PATDVAVYVYMLVNDLHGLHPDVAISGIDVSGMPTFCIPVDDGVGFGPYRLAHMAVADK 531
 502 WIELLKQSDSEWKMGIIVHTLTNRWLEKCVTYAESHDQALVGDKTIAFWLMDKMDYDEM 561
 532 WIDLKQSDSEWKMGIIVHTLTNRWLEKCVTYAESHDQALVGDKTIAFWLMDKMDYDEM 591
 562 ALDRSTPRIDRGIALHKIRLVTYVIGGGYINPMKNGEHPWIDFPFGPQTLIPRGY 621

RESULT 6

US-09-792-127-2
 / Sequence 2, Application US/09792127
 / Patent No. US2002002713A1
 / GENERAL INFORMATION:
 / APPLICANT: Allen, Steve
 / APPLICANT: Beckles, Diane M.
 / APPLICANT: Butler, Karla
 / APPLICANT: Pearlstein, Rich
 / TITLE OF INVENTION: Starch Branching Enzyme IIB
 / FILE REFERENCE: BB1439 US NA
 / CURRENT APPLICATION NUMBER: US/09/792,127
 / CURRENT FILING DATE: 2001-02-23
 / PRIOR APPLICATION NUMBER: 60/186098
 / PRIOR FILING DATE: 2000-03-01
 / NUMBER OF SEQ ID NOS: 5
 / SOFTWARE: Microsoft Office 97
 / SEQ ID NO 2
 / LENGTH: 695
 / TYPE: PRT
 / ORGANISM: Triticum aestivum
 US-09-792-127-2

Query Match 79.9%; Score 3329; DB 9; Length 695;
 Best Local Similarity 85.4%; Pred. No. 1.5e-303;

Matches 589; Conservative 60; Mismatches 41; Indels 0; Gaps 0;

76 EKRRVVPKPGDQKIYEIDPLKDFRSLDRYSYRIRAIADHDEGLEAFSGYEGL 135
 3 EKRIILPPNGQKIYEIDPLKDFRSLDRYSYRIRAIADHDEGLEAFSGYEGL 62
 136 GFTRSAEGITYREAVAPGASHAALVGFNNMNPADTMRDYGWEIFLNNADSPALP 195
 63 GFTRSAEGITYREAVAPGASHAALVGFNNMNPADTMRDYGWEIFLNNADSPALP 122
 196 HGSRVKIRMDTPSGVKDSISAMIKFSVQAPGEIPNGIYYDPPEEEKYVFGHPQKRPES 255
 123 HGSRVKIRMDTPSGIKDSIPAMIKFSVQAPGEIPYDGIYYDPPEEEKYVFRHAQKRPES 182
 183 LRIYETIVGMSPPPKINTYVNFDEVLPRIKLGYNVQVMAIOEHSYVAFGYVTFNPPSSR 315
 256 LRIYETIVGMSPPPKINSYANFRDEVLPRIKLGYNVQVMAIOEHSYVAFGYVTFNPPSSR 351
 316 FAPSRFGTPEDLSLIDRAHELGLVLMIDIVHSHSNNTLDGLNGFGDGTDTTHYFHGGR 375
 243 FAPSRFGTPEDLSLIDRAHELGLVLMIDIVHSHSNNTLDGLNGFGDGTDTTHYFHGGR 302
 303 GHMMMDSRFLFNYSWEVLRFLLSNARWMLBEYKFDGFRPDGVTSMTYTHGLQVTFNFEYFG 435
 376 GHMMMDSRFLFNYSWEVLRFLLSNARWMLBEYKFDGFRPDGVTSMTYTHGLQVTFNFEYFG 465
 436 YGEYFGATDVAVYVYMLVNDLHGLHPDVAISGIDVSGMPTFCIPVDDGVGFGPYRLAHMAVADK 495
 363 YGEYFGATDVAVYVYMLVNDLHGLHPDVAISGIDVSGMPTFCIPVDDGVGFGPYRLAHMAVADK 422
 496 MAYVADKTIELLKQSDSEWKMGIIVHTLTNRWLEKCVTYAESHDQALVGDKTIAFWLMDK 555
 423 MAYVADKTIELLKQSDSEWKMGIIVHTLTNRWLEKCVTYAESHDQALVGDKTIAFWLMDK 482

QY 556 DMYDPMALDRPSTPRIDRGIALHMKIRLVMTMGLGEGYLNFMGNEFGHPMIDFPRGPOT 615
DB 483 DMYDPMALDRPSTPRIDRGIALHMKIRLVMTMGLGEGYLNFMGNEFGHPMIDFPRGPOT 542
QY 616 IPTGKYLPGNNNSYDKCRRRFDIGADFLNTHGMOEFDQAMOHLEEKYGMNTHSHQYVSR 675
DB 543 IPSGKFIPEGNNNSYDKCRRRFDIGADFLNTHGMOEFDQAMOHLEEKYGMNTHSHQYVSR 602
QY 676 KHEEKVILFEEDGDIYFVFNHNSFEDYVCGSRGKTKVALLDSDALFGGFSRLDHD 735
DB 603 KHEEDVIAFEKGDIVFVFNHNSFEDYVCGSRGKTKVALLDSDALFGGFSRLDHD 662
QY 736 VDYFTEHPHDNRPSFSVYTPSRTAVVYA 765
DB 663 AEHTVSDCGHNRPHSFVYTPSRTAVVYA 692

RESULT 7
US-10-424-599-273691
; Sequence 273691, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 273691
; LENGTH: 870
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(870)
; OTHER INFORMATION: unsure at all Xaa locations
; OTHER INFORMATION: Clone ID: PAT_MRT3847_89164C.1.pep
US-10-424-599-273691

Query Match 79.8%; Score 3325.5; DB 12; Length 870;
Best Local Similarity 77.7%; Pred. No. 4.5e-303;
Matches 600; Conservative 76; Mismatches 75; Indels 21; Gaps 5;

QY 18 AAAQPEELIPIEDIEQTAEV--NMTGTAELKESSEPT-----OG-IYETITD--- 63
DB 74 SASLTGQLEPDTSEDTQNLDEDTLMEDEKYNISEAASRYHIEDGGGSVSSLVNVI 133
QY 64 -----GYTKGVKEIVGB--KRVVVKPGGQCKTYEIDPTLKDFPSHLDYSEFRARA 116
DB 134 PAKKASVVRKSKIVSDEVKPKXIPEPTQCKIYEIDPSILAHMDHDLFRGQYKRLCY 193
QY 117 AIOHHEGLAFAFGYKLGITRABEGITTYEMAPGAHSALVGFNNMNPADMTD 176
DB 194 EIDHHEGLLTFSGYKFGITRSATGITTYEMAPGAHSALVGFNNMNPADMTD 253
QY 177 YGVWEILPNNADSPAIPIHGSRYKIRMDTPSGVDSISAMIKESVQAGSIFPFGIYD 236
DB 254 FGWEIILPNNVDSPIPIHGSRYKIRMDTPSGIDKISIPAMIKESVQAGSIFPFGIYD 313
QY 237 PPEEEKVYFQHPQKRPBSGLIYSHIGMSPEPINSYANFRDVLVRIKLGYNVQI 296
DB 314 PPEEEKVYFQHPQKRPBSGLIYSHIGMSPEPINSYANFRDVLVRIKLGYNVQI 373
QY 297 MAIOEHSYVASFGVHVNFPAPSSRFQPEDLKSLIDRAHELGILVLDIVASHSSNNTL 356
DB 374 MAIOEHSYVASFGVHVNFPAPSSRFQPEDLKSLIDRAHELGILVLDIVASHSSNNTL 433

QY 357 DGLNGFDGTDTHYHFGGRGHHMMDSRLFNYSWEVLFLLSNANWLEBEYKFDGRFD 416
DB 434 DGLNMFDTGEGYFHPGSGRYHMMDSRLFNYSWEVLFLLSNANWLEBEYKFDGRFD 493
QY 417 GVTSMYTHHGLQMTFTGNYGYPGPATDVDAVVYVLMVNDLHGLHAPDASIGEDVSGM 476
DB 494 GVTSMYTHHGLQMTFTGNYGYPGPATDVDAVVYVLMVNDLHGLHAPDASIGEDVSGM 553
QY 477 PFCIPVDGAGVGFYRLMAVADKMBILKOSDSWKGDIYHTLTNRWLEKCVTYAE 536
DB 554 PFCIPVDGAGVGFYRLMAVADKMBILKOSDSWKGDIYHTLTNRWLEKCVTYAE 613
QY 537 SHDQALVGDKTIAPMLMDKMDYDFALDRPSFPRIDRGIALHMKIRLVMTMGLGEGYLNF 596
DB 614 SHDQALVGDKTIAPMLMDKMDYDFALDRPSFPRIDRGIALHMKIRLVMTMGLGEGYLNF 673
QY 597 MGNRFGHEMIDFPRGPOTLPTGKYLPGNNNSYDKCRRRFDIGADFLNTHGMOEFDQAM 656
DB 674 MGNRFGHEMIDFPRGPOTLPTGKYLPGNNNSYDKCRRRFDIGADFLNTHGMOEFDQAM 733
QY 657 QHLEEKYGMNTHSHQYVSRKHEEDKVIIPERDLYFVFNHNSFEDYVCGSRGKTKYK 716
DB 734 QHLEEKYGMNTHSHQYVSRKHEEDKVIIPERDLYFVFNHNSFEDYVCGSRGKTKYK 793
QY 717 VALDSDALFGGFSRLDHDVYFTTEHPHDNRPSFSVYTPSRTAVVYALTE 768
DB 794 IYLDSDALFGGFSRLDHDVYFTTEHPHDNRPSFSVYTPSRTAVVYALTE 845

RESULT 8
US-10-254-534-2
; Sequence 2, Application US/10254534
; Publication No. US20030046730A1
; GENERAL INFORMATION:
; APPLICANT: EK. Bo
; APPLICANT: KHOSNODI, Jamsheed
; APPLICANT: LARSSON, Clas-tomas
; APPLICANT: LARSSON, Hakan
; APPLICANT: RASK, Lars
; TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
; FILE REFERENCE: 003300-486
; CURRENT APPLICATION NUMBER: US/10/254,534
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US/09/087,277
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: PCT/SE96/01558
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: SE 9504272-7
; PRIOR FILING DATE: 1995-11-29
; PRIOR APPLICATION NUMBER: SE 9601506-0
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 878
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: bet1 gene (branching enzyme II)
US-10-254-534-2

Query Match 76.2%; Score 3175; DB 14; Length 878;
Best Local Similarity 72.2%; Pred. No. 6.5e-289;
Matches 583; Conservative 83; Mismatches 93; Indels 48; Gaps 6;

QY 2 AIFAVSGALV--GVAPPAAGPEELIIP-----DIEQTA----- 37
DB 60 STVAAGKVLVPTQSDSSSTQDFEFTTSPENSPASIDVDSIEHARQITENDV 119
QY 38 ---VMTGCTAE-----XLESSEPTQGIYEITTDGVTGKVELVVGKPRV 81
DB 120 EPSDILTSVVELDFASSIQLOGKLEKSKTLNTESETIITDESDR-IRE-----RGI 171


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QY      82 PKPGDQKIYEIDPTLKDFRSHLDYRYSERYRIRAIIDQHEGGLAERSGYEKLGFTRSA 141
;      172 PPGGLGQKIYEIDPLTNRYQHLDYRYSQYKRLAIDKYEGLLEAFSGYKMGFTRSA 231
;      142 EGIYREMAFGAHSALVGDENNANADMTTRDDYGVWEIFLNNAGSPAIPIHGSRYK 201
;      232 TGIYREMAFGAHSALVGDENNANADMTTRDDYGVWEIFLNNAGSPAIPIHGSRYK 291
;      202 IRMDTSYGVDSISAMIKESVQAGEIPFNGIYDPPRESEKVFQHPQPKRESRIYES 261
;      292 IRMDTSYGVDSISAMIKESVQAGEIPFNGIYDPPRESEKVFQHPQPKRESRIYES 351
;      262 HIGMSSEPKINSYANFRDEVLPRIKLGYNAVOIMAIQEHSYASFGYHVTNFPAPSSR 321
;      352 HIGMSSEPKINSYANFRDEVLPRIKLGYNAVOIMAIQEHSYASFGYHVTNFPAPSSR 411
;      322 FGTPEDLKSLIDRAHEGLVLMIDYVSHSSNNTLDGNGPDGDTTHYFHGGPRGHMMW 381
;      412 FGXPDLDKSLIDRAHEGLVLMIDYVSHSSNNTLDGNGPDGDTTHYFHGGPRGHMMW 471
;      382 DSRLEFNGSMEVLRFLISNARWMLBEEKFDPGFRDGYTSMMYTHHGLQMTFTGNYGEYFG 441
;      472 DSRLEFNGSMEVLRFLISNARWMLBEEKFDPGFRDGYTSMMYTHHGLQMTFTGNYGEYFG 531
;      442 FATVDVAVVYLMVNDLHGLHPDAVSIQEDVSGMPTFCIPVDDGVGFYRLHNAVADK 501
;      532 LATVDVAVVYLMVNDLHGLHPDAVSIQEDVSGMPTFCIPVDDGVGFYRLHNAVADK 591
;      502 WIELLKQSDSWKMGDIYVHTLTNRRLKCYTYAASHOALVGDXTIAFWLMDKMYDM 561
;      592 WIELLKQSDSWKMGDIYVHTLTNRRLKCYTYAASHOALVGDXTIAFWLMDKMYDM 651
;      562 ALDRPSTPRIDRGIALHMKIRLVTMGEGGYLNFMGNEFGHPENIDPRAGQHSLSGVS 621
;      652 ALDRPSTPRIDRGIALHMKIRLVTMGEGGYLNFMGNEFGHPENIDPRAGQHSLSGVS 711
;      622 LFGNNNSYDKCRRRFDLGDADFLRYHGMQEPDQAMQHLBEEKYGMTSEHQYVSRKHEBDK 681
;      712 IPGNQSYDKCRRRFDLGDADFLRYHGMQEPDQAMQHLBEEKYGMTSEHQYVSRKHEBDK 771
;      682 VIFERGDVLFVNFHMSNSFPDYRVGCSRPGRKRYKALDSDALFGGSRDLHDVDYFTT 741
;      772 MIVEKGNLVFVNFHMSNSFPDYRVGCSRPGRKRYKALDSDALFGGSRDLHDVDYFTT 831
;      742 EHPHNRPRRSFYVTPSRATVAVYALTE 768
;      832 EGWYDRPRRSIMYAPCKTAVVYALVD 858

```

RESULT 9
US-10-056-454A-15

; Sequence 15, Application US/10056454A
; Publication No. US2003016919A1

; GENERAL INFORMATION:

; APPLICANT: National Starch and Chemical Investment Holding Corporation
; TITLE OF INVENTION: Improvements in or Relating to Plant Starch Composition
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:

; ADDRESS: National Starch and Chemical Investment Holding Corporation
; STREET: 1000 Unigema Blvd.
; CITY: Newcasle
; STATE: Delaware
; COUNTRY: United States of America
; ZIP: 19720

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; APPLICATION NUMBER: US/10/056,454A
; FILING DATE: 25-Jun-2002
; INFORMATION FOR SEQ ID NO: 15:

```

;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 882 amino acids
;      TYPE: amino acid
;      TOPOLOGY: linear
;      MOLECULE TYPE: protein
;      SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-056-454A-15

```

Query Match 75.2%; Score 3135; DB 14; Length 882;
Best Local Similarity 71.4%; Pred. No. 3.8e-285;
Matches 576; Conservative 86; Mismatches 97; Indels 48; Gaps 6;

```

;      2 ATPVSGATL--GVAPPPAAQPEELQIP-----DIEQTAE----- 37
;      60 STVAASGKVLVPTQSDSSSTDOPEFTSPENSPASTDVDSSTHEASQIKTENDV 119
;      38 ---VMTGTGTAE-----KLESEPTQGIYETITDGVTKVKELVGKEPRV 81
;      120 EBSDDLTSVEEDFPASSLQLEGKLBESKTIANTSETIIDSER-IRE-----RGI 171
;      82 PKPGDQKIYEIDPTLKDFRSHLDYRYSERYRIRAIIDQHEGGLAERSGYEKLGFTRSA 141
;      172 PPGGLGQKIYEIDPLTNRYQHLDYRYSQYKRLAIDKYEGLLEAFSGYKMGFTRSA 231
;      142 EGIYREMAFGAHSALVGDENNANADMTTRDDYGVWEIFLNNAGSPAIPIHGSRYK 201
;      232 TGIYREMAFGAHSALVGDENNANADMTTRDDYGVWEIFLNNAGSPAIPIHGSRYK 291
;      202 IRMDTSYGVDSISAMIKESVQAGEIPFNGIYDPPRESEKVFQHPQPKRESRIYES 261
;      292 IRMDTSYGVDSISAMIKESVQAGEIPFNGIYDPPRESEKVFQHPQPKRESRIYES 351
;      262 HIGMSSEPKINSYANFRDEVLPRIKLGYNAVOIMAIQEHSYASFGYHVTNFPAPSSR 321
;      352 HIGMSSEPKINSYANFRDEVLPRIKLGYNAVOIMAIQEHSYASFGYHVTNFPAPSSR 411
;      322 FGTPEDLKSLIDRAHEGLVLMIDYVSHSSNNTLDGNGPDGDTTHYFHGGPRGHMMW 381
;      412 FGTPEDLKSLIDRAHEGLVLMIDYVSHSSNNTLDGNGPDGDTTHYFHGGPRGHMMW 471
;      382 DSRLEFNGSMEVLRFLISNARWMLBEEKFDPGFRDGYTSMMYTHHGLQMTFTGNYGEYFG 441
;      472 DSRLEFNGSMEVLRFLISNARWMLBEEKFDPGFRDGYTSMMYTHHGLQMTFTGNYGEYFG 531
;      442 FATVDVAVVYLMVNDLHGLHPDAVSIQEDVSGMPTFCIPVDDGVGFYRLHNAVADK 501
;      532 LATVDVAVVYLMVNDLHGLHPDAVSIQEDVSGMPTFCIPVDDGVGFYRLHNAVADK 591
;      502 WIELLKQSDSWKMGDIYVHTLTNRRLKCYTYAASHOALVGDXTIAFWLMDKMYDM 561
;      592 WIELLKQSDSWKMGDIYVHTLTNRRLKCYTYAASHOALVGDXTIAFWLMDKMYDM 651
;      562 ALDRPSTPRIDRGIALHMKIRLVTMGEGGYLNFMGNEFGHPENIDPRAGQHSLSGVS 621
;      652 ALDRPSTPRIDRGIALHMKIRLVTMGEGGYLNFMGNEFGHPENIDPRAGQHSLSGVS 711
;      622 LFGNNNSYDKCRRRFDLGDADFLRYHGMQEPDQAMQHLBEEKYGMTSEHQYVSRKHEBDK 681
;      712 IPGNQSYDKCRRRFDLGDADFLRYHGMQEPDQAMQHLBEEKYGMTSEHQYVSRKHEBDK 771
;      682 VIFERGDVLFVNFHMSNSFPDYRVGCSRPGRKRYKALDSDALFGGSRDLHDVDYFTT 741
;      772 MIVEKGNLVFVNFHMSNSFPDYRVGCSRPGRKRYKALDSDALFGGSRDLHDVDYFTT 831
;      742 EHPHNRPRRSFYVTPSRATVAVYALTE 768
;      832 EGWYDRPRRSIMYAPCKTAVVYALVD 858

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RESULT 10
US-10-254-534-4

; Sequence 4, Application US/10254534
; Publication No. US20030046730A1

Page 7

APPLICANT: Guan, Hanpin;

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; Sequence 56, Application US/10336753
; Publication No. US20030226176A1
; GENERAL INFORMATION:
; APPLICANT: Guan, Hanning

```

QY 740 TT-----EHPDNRPSFSVYTPERTAVVY 764
| : ||||| : |||
Db 665 TSPGCVGPETNNNNPNSFKVLSPTICVAY 697

D5
665 TSPEGVGVETNFNNRPNSEFKLSPRTCAAY 697

Db 590 ETRFNRRNSFKVLSPRTCVAY 612

RESULT 14

US-10-369-493-3969
Sequence 3969, Application US/10369493
Publication No. US2003023675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
PRIOR FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 3969
LENGTH: 874
TYPE: PRT
ORGANISM: Neurospora crassa
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(874)
OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-3969

Query Match 46.0%; Score 1917.5; DB 15; Length 874;

Best Local Similarity 46.8%; Pred. No. 1.2e-170;

Matches 378; Conservative 109; Mismatches 185; Indels 135; Gaps 11;

Db 81 VPKRPGGQKLY-----EIDPTLKDRSHLDVSEYRRIAD 119

Db 23 IPKDGMSLYIRFSLPIQCQKLIQKAGVLSIDPMLRPPKDLKSKAQSHIDITIN 82

Db 120 OHEGGLAERF-----GYEKLGTSAG-ITREMAFGASHAL 158

Db 83 KTEGGLEKFSRVQXALMTLPKLLTHVQLGTEIFGVNDKONTITREMAFNAKQSL 142

Qy 159 VEDFN-----NPNADLTTRDDYGYWEFLPNADGSPAIPIQS 198

Db 143 IGFSTYHDTTPRYCELAGITLTLRQWRRAHKKIEFGVEITIPETAGOPAIPIQS 202

Qy 199 RVK-----IRMDTPSGV-KDSISAMIKSFVQAPGEIP-FNG 232

Db 203 KIKVCECFNSACTPIPIRANVLMFISXOITTELPDQWVDRIPAMIKYTQDLSVPAVEA 262

Qy 233 IYDPEEEXKVFQHPQKRPESLRIYESHIGSSPEPKINSYANFRDEVLPRIKLGYN 292

Db 263 RPNPQSEKTYFKHKRPSKPESLRIYEAHVIGSSPEKVAITYEFKTMPIKILGYN 322

Qy 293 AVQIMAIQESHYASFGHYNTNFPAPSSRGTEPDLKSLIRARLGLVLMDIVSHSS 352

Db 323 AIOQIMAEHAYYASFGYQVNSFPAPSSRGTEPDLKSLIRARLGLVLMDIVSHSS 382

Qy 353 NNTLDGNGPDGDTTHFEHGGPRGHHMMWDBRLFNYSWEVLRFLLSARWMLSEYKPDG 412

Db 383 KAVLDGNEEDGDHOFHGGGRGKDLMDRLPNYGHHEMRLLSLTRMMEBAYDGS 442

Qy 413 FRDGVTSMTYTHGLQMT-----FTGNGEYFGATDVDAVYIMLV 455

Db 443 FRDGVTSMTYTHGLQMT-----FTGNGEYFGATDVDAVYIMLV 502

Qy 456 NDLIHGHPAVSTGEVNSGMPFCIPVDGCGVDFRLHMAVADKMTLLKQ-SDESK 514

Db 503 NENLHOLYEPVITVAEDVSGKPALCLPLSGVGFDYRLAMVITKILKEKDESD 562

Qy 515 MGDIVATLTRRMLEKCVTAESHDAQ-----LVGDKTIAFWLMDXD 556

Db 563 MANITWTLNRRHGKTIACGESHDAQVLYPATGSDGXRNRLLVGDXTLMMHLCDAE 622

Qy 557 MYDFMALDPSSTPIRDRGIALHKMIRLVTMGLGEGEYLPFMGNEFHPEDIPRGQTL 616

Db 623 LYTNMSILPLPLPVIDRGVALHKMIRLTHSLGEGYLPFMGNEFHPEDIPRGQTL 677

Qy 617 PTKVLPGNNSYDRCRRPFDIGDADFLRYHGMQEFDOAMQHLEKYGFTSEHQYRSK 676

Db 678 -----EGQNSFWARQNLTEGDLRYQYLNPNDRSNLTEDKGMILHAPQATSLK 731

Qy 677 HEDRVIIIFERDGLVFNFMHNSPFDYRVGCSRPKVALDSDALFGFSRLDHV 736

Db 732 HEGDKVIFERAGLVFNFMHNSPFDYRVGCSRPKVALDSDALFGFSRLDHV 791

Qy 737 DFTTEHPHNRPRPSVYTPSGRTAVY 763

Db 792 RFTSDLPNNRKNSTHYIIPARTAFV 818

RESULT 15

US-10-425-114-45676
Sequence 45676, Application US/10425114
Publication No. US2004003488A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E.
APPLICANT: Tabaska, Jack E.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 45676
LENGTH: 421
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: 700747645_FLI.pep
US-10-425-114-45676

Query Match 45.9%; Score 1915; DB 12; Length 421;

Best Local Similarity 84.1%; Pred. No. 6.7e-171;

Matches 333; Conservative 38; Mismatches 25; Indels 0; Gaps 0;

Qy 373 GPRGHMMWDBRLFNYSWEVLRFLLSARWMLSEYKPDGFRDGVTSMTYTHGLQMTF 432

Db 1 GSRGTHMMWDBRLFNYSWEVLRFLLSARWMLSEYKPDGFRDGVTSMTYTHGLQMTF 60

Qy 433 TGNVGEYFGATDVDAVYIMLVNDLIHGLHAPDAVIGEDVSGMPFCIPVDGCGVDFY 492

Db 61 TGNVGEYFGATDVDAVYIMLVNDLIHGLHAPDAVIGEDVSGMPFCIPVDGCGVDFY 120

Qy 493 RLHMAVADKMTLLKQSDSCKKGDVHTLITRRMLEKCTYAEASHDAQLVGDKTIAFWL 552

Db 121 RLHMAVADKMTLLKQSDSCKKGDVHTLITRRMLEKCTYAEASHDAQLVGDKTIAFWL 180

Qy 553 MDKXVDFMALDRPSTPIRDRGIALHKMIRLVTMGLGEGEYLPFMGNEFHPEDIPRG 612

Db 181 MDKXVDFMALDRPSTPIRDRGIALHKMIRLVTMGLGEGEYLPFMGNEFHPEDIPRG 240

Qy 613 PQLPLTGKVLPGNNNSYDRCRRPFDIGDADFLRYHGMQEFDOAMQHLEKYGFTSEHQY 672

Db 241 DQHLPLTGKVLPGNNNSYDRCRRPFDIGDADFLRYHGMQEFDOAMQHLEKYGFTSEHQY 300

Qy 673 VSRKNEEDKVIIFERDGLVFNFMHNSPFDYRVGCSRPKVALDSDALFGFSRL 732

Db 301 ISRKNEDKVIIFERDGLVFNFMHNSPFDYRVGCSRPKVALDSDALFGFSRL 360

Qy 733 DHDVDYFTTEHPHNRPRPSVYTPSGRTAVYALTE 766

Tue Apr 20 10:02:28 2004

us-09-508-377-12.rapb

Page 10

```
Db      361 NHTAEYFTSEGWYDDRRPSFLIYAPSRTAVVYALAD 396
```

Search completed: April 15, 2004, 08:44:07
Job time : 50 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 15, 2004, 08:35:16 ; Search time 21 Seconds
(without alignments)

3517.862 Million cell updates/sec

Title: US-09-508-377-12

Perfect score: 4169
Sequence: 1 MATFAVSGATLGVARPPAAA.....PRPSVTTPSRATVAVALTE 768

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 segs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR 78: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being pinned, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4113.5	98.7	823	2	T06574
2	3915	93.9	729	2	T06797
3	3588.5	86.1	814	2	T02041
4	3362	80.6	825	2	A48537
5	3351	80.4	799	2	T01653
6	3346	80.3	922	2	T06453
7	3342	80.2	799	2	T02981
8	3258	78.1	800	2	S65046
9	3258	78.1	805	2	T48392
10	3207	76.9	830	2	T07743
11	3155	75.7	858	2	B84780
12	3135	75.2	854	2	S65045
13	2193.5	52.6	830	2	T06578
14	2168.5	52.0	830	2	T07824
15	2166.5	52.0	820	1	UJ0243
16	2146	51.5	822	2	UJ0968
17	2140	51.3	702	2	A46075
18	2122.5	50.9	861	1	G34730
19	2099.5	48.6	826	2	T06494
20	2027.5	45.5	681	2	T49626
21	1896	45.5	681	2	T49426
22	1795.5	43.1	704	1	S60448
23	1494	35.8	686	2	T06334
24	1048	25.1	383	2	S28422
25	624	15.0	774	1	UQ0550
26	592.5	14.2	666	2	D82511
27	573	13.7	770	2	S76095
28	562	13.5	764	2	AG1895
29	558	13.4	730	1	I64118

30	554	13.3	727	2	AH0479	1,4-alpha-glucan b
31	553.5	13.3	728	1	NO8CA	1,4-alpha-glucan b
32	550.5	13.2	705	2	D75345	probable 1,4-alpha
33	550.5	13.2	728	2	E91163	1,4-alpha-glucan b
34	550.5	13.2	728	2	F86009	1,4-alpha-glucan b
35	549.5	13.2	630	2	D70363	1,4-alpha-glucan b
36	548.5	13.2	728	2	AF0995	1,4-alpha-glucan b
37	548	13.1	735	2	AH3057	glycogen branching
38	548	13.1	735	2	F98228	1,4-alpha-glucan b
39	540.5	13.0	666	2	B56639	1,4-alpha-glucan b
40	540	13.0	638	2	S18599	1,4-alpha-glucan b
41	537	12.9	732	2	H83376	1,4-alpha-glucan b
42	529	12.7	731	2	UC7919	1,4-alpha-glucan b
43	525.5	12.6	731	2	B70770	probable 91GB prot
44	521	12.5	639	1	B41328	1,4-alpha-glucan b
45	517.5	12.4	737	2	C81724	1,4-alpha-glucan b

ALIGNMENTS

```
RESULT 1
T06574
probable 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) II precursor - wheat
C:Species: Triticum aestivum (common wheat)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 20-Jun-2000
C:Accession: T06574
R:Chidbat, R.N.
submitted to the EMBL Data Library, August 1997
A:Reference number: Z15769
A:Accession: T06574
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-823 <CH1>
A:Cross-references: EMBL:Y1282; PIDN:CAA72154.1
A:Experimental source: cv. Fielder; kernels 12 days post anthesis
C:Genetics:
A:Gene: sbe2
C:Function:
A:Description: catalyzes the transglycosylation of a terminal segment of a 1,4-alpha-D-
A:Pathway: glycogen/starch biosynthesis
C:Superfamily: 1,4-alpha-glucan branching enzyme
C:Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase
F:1-56/Domain: transit peptide (amyloplast) #status predicted <TNP>
F:55-823/Product: 1,4-alpha-glucan branching enzyme II #status predicted <MAT>

Query Match          98.7%; Score 4113.5; DB 2; Length 823;
Best Local Similarity 93.0%; Pred. No. 2.5e-301;
Matches 765; Conservative 0; Mismatches 3; Indels 55; Gaps 1;

QY      1 MATFAVSGATLGVARPPAA-----
DB      1 MATFAVSGATLGVARPPAGAGGLPRSGSERRGGVDIPSLLRKXSSRAVLSAASGK 60
QY      20 -----AQPETQIPEDIEBQTAAYVMGTGTAEKLESSEPTQGIIVETIDGV 65
DB      61 VLVPPGESDDLASPAPEPQIIPEDIEBQTAAYVMGTGTAEKLESSEPTQGIIVETIDGV 120
QY      66 TNGVKELVVGKERVVFKPDGGKIYEDPTLQDFRSHLDYRSEYRIRAIQHEGGL 125
DB      121 TNGVKELVVGKERVVFKPDGGKIYEDPTLQDFRSHLDYRSEYRIRAIQHEGGL 180
QY      126 EAFSRGKYELGFRSAEGITFRWAPGASHAALVGDNNMNPADMTTRDDYGVWEITLP 185
DB      181 EAFSRGKYELGFRSAEGITFRWAPGASHAALVGDNNMNPADMTTRDDYGVWEITLP 240
QY      186 NNADGSPALPHGSRVRIKMDTPSGVKDSISAMIKFSVQADGEIPFNGIYYDPPEBEKYVF 245
DB      241 NNADGSPALPHGSRVRIKMDTPSGVKDSISAMIKFSVQADGEIPFNGIYYDPPEBEKYVF 300
QY      246 QHPQPRPSRLRIYESHIGMSPEPKINSYANRDEVLPTIKLGVNAVQIMAIQESHY 305
DB      301 QHPQPRPSRLRIYESHIGMSPEPKINSYANRDEVLPTIKLGVNAVQIMAIQESHY 360
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QY 306 ASFGYHTNFPAPSSRFGTPEDLKSLIDRAHELGLVLMIDIVSHSSNNTLDGLNGFDGT 365
 DB 361 ASFGYHTNFPAPSSRFGTPEDLKSLIDRAHELGLVLMIDIVSHSSNNTLDGLNGFDGT 420
 QY 366 DTHYFHGGPRGHMMWMSRLFNYSWEVLRFLLSNARWMLBEYKDFGDFGVTSMYTH 425
 DB 421 DTHYFHGGPRGHMMWMSRLFNYSWEVLRFLLSNARWMLBEYKDFGDFGVTSMYTH 480
 QY 426 HGLQMTTNGYGEFGATDVAVYYLMLVNDLHGLHPDASIGEDVSGMTFCIPVD 485
 DB 481 HGLQMTTNGYGEFGATDVAVYYLMLVNDLHGLHPDASIGEDVSGMTFCIPVD 540
 QY 486 GGVPFDRILHMAVADKWIELKQSDSWMGDIYHTLTNRRLKCVTAESHDOALVGD 545
 DB 541 GGVPFDRILHMAVADKWIELKQSDSWMGDIYHTLTNRRLKCVTAESHDOALVGD 600
 QY 546 KTIAPWIMDKMYDFMALDRPSTPRIDRGIALHKVIRLVTMGLGEGYLNFMNGEFGHE 605
 DB 601 KTIAPWIMDKMYDFMALDRPSTPRIDRGIALHKVIRLVTMGLGEGYLNFMNGEFGHE 660
 QY 606 WIDPRGQTLPTGKVLFGNNNSYDKCRRRPDLGDADFLRYHGMQEFDDAMHLEBKXGF 665
 DB 661 WIDPRGQTLPTGKVLFGNNNSYDKCRRRPDLGDADFLRYHGMQEFDDAMHLEBKXGF 720
 QY 666 MTSEHOVYSRKHEEDKVIIFERGDVFNFMNSFFDYRGCSRPGRKYVALDSDAL 725
 DB 721 MTSEHOVYSRKHEEDKVIIFERGDVFNFMNSFFDYRGCSRPGRKYVALDSDAL 780
 QY 726 FGGSRLDHDVDYFTTEHPDNRPRSFSVYTPSRVAVYALTE 768
 DB 781 FGGSRLDHDVDYFTTEHPDNRPRSFSVYTPSRVAVYALTE 823

RESULT 2

T06797
 probable 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) - wheat
 N:Alternate names: 1,4-alpha-D-glucan 6-alpha-D-(1,4)-alpha-D-glucanotransferase
 C:Species: Triticum aestivum (common wheat)
 C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 18-Jun-1999
 C:Accession: T06797
 R:Koegeer, C./ Loerz, H./ Inetticke, S.
 submitted to the EMBL Data Library, August 1996
 A:Reference number: Z15822
 A:Accession: T06797
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-729 <KRC>
 A:Cross-references: EMBL:U66376; NID:g1620661; PIRN:AA017086.1; PID:g1620662
 A:Experimental source: cv. Florida; kernels 21 DAP
 C:Function:
 A:Description: converts amylose into amylopectin; catalyzes the formation of 1,6-glucose
 A:Pathway: starch and sucrose metabolism
 C:Superfamily: 1,4-alpha-glucan branching enzyme
 C:Keywords: glycosyltransferase; hexosyltransferase

Query Match 93.9%; Score 3915; DB 2; Length 729;
 Best Local Similarity 98.2%; Pred. No. 1.8e-286;
 Matches 716; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 40 MTGTAELKESSEPTQGIYETITDGTGKVELVGEKPRVVPKPGDGKIVEIDPTLKD 99
 DB 1 MTGTAELKESSEPTQGIYETITDGTGKVELVGEKPRVVPKPGDGKIVEIDPTLKD 60
 QY 100 FRSHLDYRSEYRRIAPADIDHGGLEAFSRGTEKGFTRSAEGITRYEWAAPGAHAAV 159
 DB 61 FRSHLDYRSEYRRIAPADIDHGGLEAFSRGTEKGFTRSAEGITRYEWAAPGAHAAV 120
 QY 160 GFNNMNPADMTPTDYGWEIFLPNNADGSPAIRHSGSVKTRMPTSPGVKDSISAMIK 219
 DB 121 GFNNMNPADMTPTDYGWEIFLPNNADGSPAIRHSGSVKTRMPTSPGVKDSISAMIK 180
 QY 220 FSVQAPGEIPFNGIYDPEEKEKVFQHPQKRPESLRIYESHIGMSPEPKINSYANFR 279

DB 181 FSVQAPGEIPFNGIYDPEEKEKVFQHPQKRPESLRIYESHIGMSPEPKINSYANFR 240
 QY 280 DEVLPRIKLGVNAVOIMIQEHSYYASFGYHTNFPAPSSRFGTPEDLKSLIDRAHBLG 339
 DB 241 DEVLPRIKLGVNAVOIMIQEHSYYASFGYHTNFPAPSSRFGTPEDLKSLIDRAHBLG 300
 QY 340 LVLMDIVSHSSNNTLDGLNGFDGIDTTHYFHGGPRGHMMWMSRLFNYSWEVLRFLLS 399
 DB 301 LVLMDIVSHSSNNTLDGLNGFDGIDTTHYFHGGPRGHMMWMSRLFNYSWEVLRFLLS 360
 QY 400 NARWMLBEYKDFGDFGVTSMYTHHGLQMTTNGYGEFGATDVAVYYLMLVNDLI 459
 DB 361 NARWMLBEYKDFGDFGVTSMYTHHGLQMTTNGYGEFGATDVAVYYLMLVNDLI 420
 QY 460 HGLHPDASIGEDVSGMTFCIPVDGVPDRILHMAVADKWIELKQSDSWMGDIY 519
 DB 421 HGLHPDASIGEDVSGMTFCIPVDGVPDRILHMAVADKWIELKQSDSWMGDIY 480
 QY 520 HTLTNRRLKCVTAESHDOALVGDKTIAPWIMDKMYDFMALDRPSTPRIDRGIALHK 579
 DB 481 HTLTNRRLKCVTAESHDOALVGDKTIAPWIMDKMYDFMALDRPSTPRIDRGIALHK 540
 QY 580 MIRLVTMGLGEGYLNFMNGEFGHEWIDPRGQTLPTGKVLFGNNNSYDKCRRRPDLG 639
 DB 541 MIRLVTMGLGEGYLNFMNGEFGHEWIDPRGQTLPTGKVLFGNNNSYDKCRRRPDLG 600
 QY 640 DADFLRYHGMQEFDDAMHLEBKXGFMTSEHOVYSRKHEEDKVIIFERGDVFNFMNS 699
 DB 601 DADFLRYHGMQEFDDAMHLEBKXGFMTSEHOVYSRKHEEDKVIIFERGDVFNFMNS 660
 QY 700 NSFEDYVSGSRPKKYVALDSDALFGGSRLDHDVDYFTTEHPDNRPRSFSVYTPSR 759
 DB 661 NSFEDYVSGSRPKKYVALDSDALFGGSRLDHDVDYFTTEHPDNRPRSFSVYTPSR 720
 QY 760 TAVVYALTE 768
 DB 721 TAVVYALTE 729

RESULT 3

T02041
 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) Iia - maize (fragment)
 N:Alternate names: starch branching enzyme Iia
 C:Species: Zea mays (maize)
 C:Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 18-Jun-1999
 C:Accession: T02041
 R:Go, M./ Fisher, D.K./ Kim, K.N./ Shannon, J.C./ Gultinan, M.J.
 Plant Physiol. 114, 69-78, 1997
 A:Title: Independent genetic control of maize starch-branching enzymes Iia and Iib. Is
 A:Reference number: Z14509; MUID:97303618; PMID:9159942
 A:Accession: T02041
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-814 <GAO>
 A:Cross-references: EMBL:U65948; NID:G2340107; PIDN:AA067316.1; PID:G2340108
 A:Experimental source: strain B73
 C:Genetics:
 A:Gene: Sbe2a
 C:Function:
 A:Description: catalyzes the transglycosylation of a terminal segment of a 1,4-alpha-D
 A:Pathway: glycogen/starch biosynthesis
 C:Superfamily: 1,4-alpha-glucan branching enzyme
 C:Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

Query Match 86.1%; Score 3588.5; DB 2; Length 814;
 Best Local Similarity 84.7%; Pred. No. 8.4e-262;
 Matches 662; Conservative 32; Mismatches 49; Indels 39; Gaps 4;

QY 11 LGVAPPAAGPEELQIPEDIEBQTAEVNMGTAELKESSEPTQ----- 55
 DB 38 LSSAEPVVDTPPELQIPE-----AEI-----TYEK-TSSSPITQTSVAEASSGVEAE 85

QY 56 -----GIVETITDVTGKVKELVGEKPRVVRPGDGQKIYEIDPTLKDFRSH 103
 DB ERPELSEVIGVGGTGTGKIDGAGIKAKAPLVEEKPRVIPPBGDGRQIYEIDPTLEGRGH 145
 QY 104 LDYRSEVRRIAPADQHEGGLEAFSRGVEKIGFTTSAGGITRMAAPGHSALVGDEN 133
 DB 146 LDYRSEVRRIAPADQHEGGLEAFSRGVEKIGFTTSAGGITRMAAPGHSALVGDEN 205
 QY 164 NNNPAPADMTDPDYGYWEIPLPNNADGSPALPHSGSVKIRMDTPSGKDSISAMIKFSVQ 223
 DB 206 NNNPAPADMTDPDYGYWEIPLPNNADGSPALPHSGSVKIRMDTPSGKDSISAMIKFSVQ 265
 QY 224 APGEIIPNGIYVDPPEEEKYVFQHPQKRPESIRIYESHIGMSPEPKINSYANFDEVL 283
 DB 266 APGEIIPNGIYVDPPEEEKYVFQHPQKRPESIRIYESHIGMSPEPKINSYANFDEVL 325
 QY 284 PRKRLGYNAVOIMAIQESHYASFGYHTNFPABSSRRTPTPDLKSLIRAHGLGLVL 343
 DB 326 PRKRLGYNAVOIMAIQESHYASFGYHTNFPABSSRRTPTPDLKSLIRAHGLGLVL 385
 QY 344 MDIVSHSSNNTLDGLNGFDGTDTHYFHGGPRGHHMMMDSRLFNYSQWEVLRFLLSNARV 403
 DB 386 MDIVSHSSNNTLDGLNGFDGTDTHYFHGGPRGHHMMMDSRLFNYSQWEVLRFLLSNARV 445
 QY 404 WLEBYKFDGFRFDGVTSMYTHHGLQMTFTGNNGEYFGEATDVAVVYLMVNDLIHGLH 463
 DB 446 WLEBYKFDGFRFDGVTSMYTHHGLQMTFTGNNGEYFGEATDVAVVYLMVNDLIHGLH 505
 QY 464 PDVAVSIGEVSGMPFTCIIPVPGGVGPDYRLHMAVADKMTIELLKQSBESKMGDIHTLT 523
 DB 506 PDVAVSIGEVSGMPFTCIIPVPGGVGPDYRLHMAVADKMTIELLKQSBESKMGDIHTLT 565
 QY 524 NRRMLEKCTVYAESHDQALVGDKTIAFWLMDKMDYFMAIDRSTPRIDRIGIALHMKIRL 583
 DB 566 NRRMLEKCTVYAESHDQALVGDKTIAFWLMDKMDYFMAIDRSTPRIDRIGIALHMKIRL 625
 QY 584 VTMGLGSGCYLPMNGNEFGHPENIDPPRGQPLPTGKVLPGNNNSYDKCRRRFDLGDAD 643
 DB 626 VTMGLGSGCYLPMNGNEFGHPENIDPPRGQPLPTGKVLPGNNNSYDKCRRRFDLGDAD 685
 QY 644 LRYHMOEVDQAMQHEEKYGFMTSEHOYYSRCHGEBKXIIIFERGDVFPENFHMNSFF 703
 DB 686 LRYHMOEVDQAMQHEEKYGFMTSEHOYYSRCHGEBKXIIIFERGDVFPENFHMNSFF 745
 QY 704 DYRVGSGRGKTKYVALDSDDALFGGFSRLDHDVYFTEHPHNDRPPSPVYTPSRATV 763
 DB 746 DYRVGSGRGKTKYVALDSDDALFGGFSRLDHDVYFTEHPHNDRPPSPVYTPSRATV 805
 QY 764 YV 765
 DB 806 YV 807
 RESULT 4
 A48537
 starch branching enzyme isoform RBE3 - rice
 C1Species: Oryza sativa (rice)
 C1Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
 C1Accession: A48537
 R.Mizuno, K.; Kawasaki, T.; Shimada, H.; Sato, H.; Kobayashi, E.; Okumura, S.; Arai, Y.
 J. Biol. Chem. 268, 19084-19091, 1993
 A1Title: Alteration of the structural properties of starch components by the lack of an
 A1Reference number: A48537; PMID:9336833; PMID:8360192
 A1Accession: A48537
 A1Status: preliminary
 A1Molecule type: mRNA, protein
 A1Residues: 1-825 <M12>
 A1Cross-references: GB:D16201; NID:G336051; PIDN:BA03738.1; PID:G436052
 A1Experimental source: cv. Kilmaze
 A1Note: sequence extracted from NCBI backbone (NCBIN:136747, NCBI:P.136748)
 C1Superfamily: 1,4-alpha-glucan branching enzyme
 Query Match 80.6%; Score 3362; DB 2; Length 825;

Best Local Similarity 80.1%; Pred. No. 9.7e-245;
 Matches 602; Conservative 68; Mismatches 72; Indels 10; Gaps 2;
 QY 17 PAAAPPELQIPEDIEBQTAENMTGTAEKLESEPPQGIETITDVTGKVKELVGE 76
 DB 84 PVAAGSDDLQPLADDELSTEV-----GAVEIIESSGAD-----VEGKRVVEELAAQ 133
 QY 77 KPRVVPKPGDQKIYEIDPTLKDFRSHLDYYSBRIRIAPADQHEGGLEAFSRGVEKIG 136
 DB 134 KPRVVPKPGDQKIYFQDMSMLNGKYYHLEYRSLYLRRLRSIDIDQYEGGLETSRGEKIG 193
 QY 137 PTRABEGITTEMAFGHSALVGDENNMMNADMTDDVGMVFLPNNADGSPALPH 196
 DB 194 FNSHAGVTRKEMAPGASALVGDENNMMNADMTDDVGMVFLPNNADGSPALPH 253
 QY 197 GSRVYKIRMDTPSGYKDSISAMIKFSVQAPGEIIPNGIYVDPPEEEKYVFQHPQKPEST 256
 DB 254 GSRVYKIRMDTPSGYKDSISAMIKFSVQAPGEIIPNGIYVDPPEEEKYVFQHPQKPEST 313
 QY 257 RYESHIGMSPEPKINSYANFDEVLPRKRLGYNAVOIMAIQESHYASFGYHTNFP 316
 DB 314 RYETHVGMSTPEPKINTYANFDEVLPRKRLGYNAVOIMAIQESHYASFGYHTNFP 373
 QY 317 APSSRFGTPEDLKSLIDRAHELGLVMDIVSHSSNNTLDGLNGFDGTDTHYFHGGPRG 376
 DB 374 APSSRFGTPEDLKSLIDRAHELGLVMDIVSHSSNNTLDGLNGFDGTDTHYFHGGPRG 433
 QY 377 HHMMMDSLFNYGSEVLRFLLSNARMWLEBYKFDGFRFDGVTSMYTHHGLQMTFTGN 436
 DB 434 HHMMMDSLFNYGSEVLRFLLSNARMWLEBYKFDGFRFDGVTSMYTHHGLQMTFTGN 493
 QY 437 GEYGFATDVAVVYLMVNDLIHGLHPDAVSGISGDSMPFTCIIPVPGGVGPDYRLHM 496
 DB 494 SEYGFATDVAVVYLMVNDLIHGLHPDAVSGISGDSMPFTCIIPVPGGVGPDYRLHM 553
 QY 497 AVADKMTIELLKQSBESKMGDIHTLTNRRMLEKCTVYAESHDQALVGDKTIAFWLMDK 556
 DB 554 AVADKMTIELLKQSBESKMGDIHTLTNRRMLEKCTVYAESHDQALVGDKTIAFWLMDK 613
 QY 557 MYDFMALDRPSTPRIDRIGIALHMKIRLVTMGAGSGCYLPMNGNEFGHPENIDPPRGQPL 616
 DB 614 MYDFMALDRPSTPRIDRIGIALHMKIRLVTMGAGSGCYLPMNGNEFGHPENIDPPRGQPL 673
 QY 617 PTGKVLPGNNNSYDKCRRRFDLGDADFLRYHMOEVDQAMQHEEKYGFMTSEHOYYSRK 676
 DB 674 PNGKFIPENNNSYDKCRRRFDLGDADFLRYHMOEVDQAMQHEEKYGFMTSEHOYYSRK 733
 QY 677 HEEDKVIIFERGDVFPENFHMNSGFPDYRVGCSRGKTKYVALDSDDALFGGFSRLDHDV 736
 DB 734 HEEDKVIIFERGDVFPENFHMNSGFPDYRVGCSRGKTKYVALDSDDALFGGFSRLDHDV 793
 QY 737 DYFTEHPHNDRPPSPVYTPSRATVYALTE 768
 DB 794 EFTADCSHDNRPPSPVYTPSRATVYALTE 825
 RESULT 5
 T01663
 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) IIB - maize
 N1Alternate names: starch branching enzyme IIB
 C1Species: Zea mays (maize)
 C1Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 18-Jun-1999
 C1Accession: T01663
 R.Kim, K.N.; Fisher, D.K.; Gao, M.; Guiltinan, M.J.
 submitted to the EMBL Data Library, June 1998
 A1Description: Molecular cloning and characterization of the amylose-extender gene enco
 A1Reference number: Z14387
 A1Accession: T01663
 A1Status: preliminary; translated from GB/EMBL/DBJ
 A1Molecule type: DNA
 A1Residues: 1-799 <KIM>
 A1Cross-references: EMBL:AF072725; NID:G3511235; PIDN:ACC3764.1; PID:G3511236
 A1Experimental source: strain B73

C:Genetics:
 A:Gene: ae
 A:Accession: 38/1, 86/3, 138/2, 171/2, 185/3, 205/3, 232/3, 271/3, 299/3, 340/2, 380/2, 42
 A:Function:
 A:Description: catalyzes the transglycosylation of a terminal segment of a 1,4-alpha-D-g
 A:Pathway: glycogen/starch biosynthesis
 C:Superfamily: 1,4-alpha-glucan branching enzyme
 C:Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

Query Match 80.4%; Score 3351; DB 2; Length 799;
 Best Local Similarity 78.5%; Pred. No. 6.2e-244;
 Matches 609; Conservative 68; Mismatches 77; Indels 22; Gaps 4;

4 FAVSGLTGV-----ARPPAAQPELQIPEDIEQTEVNMVGTGTAELSSR----- 52
 35 FLTRGAVGSGTHGNRAAALAKAVVPPGEND-----GLARADSAQGSDEL 85
 53 PTOGIVETITDGVTKGYKELVVGKKPRVVPKPGDQKIYEIDPTLKDFRSHLDYRSEYR 112
 86 EVRPISEETTCGA--GYADAQALNRVVRVPPSDGQKIFQIDPMLQGYKYLEYRSLXR 143
 113 RIRAIQDHGGLDAFSEGEKLGFTRSABGITTREAFGAHSAALVGDENNANMATM 172
 144 RIRSDIDHEGGLBAFSRSEKFGFNRSABGITYREMAFGAFSAALVGDENNANMATM 203
 173 TRDQYVWEIFLPPNADGSPALPHGSRKIMDPSPGVKDSISAWIKFSVQAPGEIPNG 232
 204 SKNEFGVWEIFLPPNADGSPALPHGSRKIMDPSPGVKDSISAWIKFSVQAPGEIPNG 263
 233 IYVDPPEEKVYFQHPQKPEESLRIYESHIGMSSPEPKINSYANFRDEVLPRIKLGYN 292
 264 IYVDPPEEKVYFQHPQKPEESLRIYESHIGMSSPEPKINSYANFRDEVLPRIKLGYN 323
 293 AVQJMAIOEHSYASFGYHVTNFFAPSSRFGTPELKSILIDRAHELGLLVMDIYHSHS 352
 324 AVQJMAIOEHSYASFGYHVTNFFAPSSRFGTPELKSILIDRAHELGLLVMDIYHSHS 383
 353 NNTLDGLNGPFGDTTHYHGGPRGHMMWDSLFNYGSEVLRFLLSNARWMLSEYKPDG 412
 384 SNLIDGLNGPFGDTTHYHGGPRGHMMWDSLFNYGSEVLRFLLSNARWMLSEYKPDG 443
 413 FRFDGVTSMYTHHGLQMTFTGNVGEYFGFATDVDAVYVLMVNDLIHGLHAPDAVSIGED 472
 444 FRFDGVTSMYTHHGLQMTFTGNVGEYFGFATDVDAVYVLMVNDLIHGLHAPDAVSIGED 503
 473 VSGMPFTFIPVDDGVGVDFYRLHMAVADKWIILKQSDSWMKMGDIIVHTLTNRMLEKV 532
 504 VSGMPFTFIPVDDGVGVDFYRLHMAVADKWIILKQSDSWMKMGDIIVHTLTNRMLEKV 563
 533 TYASHDQALVGDKTIAFWLMDKMDYDFPALDRPSTPRIDRGIALHKMRLVTMGAGGEG 592
 564 TYASHDQALVGDKTIAFWLMDKMDYDFPALDRPSTPRIDRGIALHKMRLVTMGAGGEG 623
 593 YLTFMGNEFGHPWIDPRGPQRLPSGKTFPGNNNSYDKCRFRFDLGDADFLRYHMQEF 652
 624 YLTFMGNEFGHPWIDPRGPQRLPSGKTFPGNNNSYDKCRFRFDLGDADFLRYHMQEF 683
 653 DQAMQHLEBKGFMTSEHQYVSRKHEDEKVIIFERGDLYFVFNFMHNSNFFDFRVCSSP 712
 684 DQAMQHLEBKGFMTSEHQYVSRKHEDEKVIIFERGDLYFVFNFMHNSNFFDFRVCSSP 743
 713 GKVKALDSDDLFGGFSRLDHDVDFTEHHPDNRPSFSVYTPRTAVVYALTE 768
 744 GKVKALDSDDLFGGFSRLDHDVDFTEHHPDNRPSFSVYTPRTAVVYALTE 799

R:Burton, R.A.; Bewley, J.D.; Smith, A.M.; Bhattacharyya, M.K.; Tarce, H.; Ring, S.; B
 Plant J. 7, 3-15, 1995
 A:Title: Starch branching enzymes belonging to distinct enzyme families are different
 A:Reference number: Z15717; MUID:95201826; PMID:7894509
 A:Accession: T06493
 A:Status: preliminary; translated from GB/EMBL/DDDBJ
 A:Molecule type: mRNA
 A:Residues: 1-922 <BUR>
 A:Cross-references: EMBL:X80009; NID:gs10545; PIDN:CA56319.1; PID:gl345570
 C:Genetics:
 A:Gene: SBEI
 C:Superfamily: 1,4-alpha-glucan branching enzyme
 C:Keywords: chloroplast; glycogen/starch biosynthesis; glycosyltransferase; hexosyltra

Query Match 80.3%; Score 3346; DB 2; Length 922;
 Best Local Similarity 77.2%; Pred. No. 1.8e-243;
 Matches 606; Conservative 70; Mismatches 73; Indels 36; Gaps 3;

20 AQPBEIQIED-----TEQTAENVMTGTAELP----- 49
 62 AASDKVLIPEDDNSVSLADQLENPDITSEDAQNLBDLTWKDGKNXIDSTSSRYEVD 121
 50 --SSEPTQIVETITDGVTKGYK---ELVVGKKPRVVPKPGDQKIYEIDPTLKDFRSH 103
 122 EKGSVTSGLVDVNTDQAKTSVHSDKVKVDPKLIPEPPTGQKIYEIDPLQARQH 181
 104 LDYRSEYRIRIRAIQDHGGLDAFSEGEKLGFTRSABGITYREMAFGAHSAAALVGDEN 163
 182 LDFRQGYRIRIBEIDIKYSGGLDAFSEGEKLGFTRSABGITYREMAFGAHSAAALVGDEN 241
 164 NNPENADVTTRDDYVWEIFLPPNADGSPALPHGSRKIMDPSPGVKDSISAWIKFSVQ 223
 242 NNPENADVTTRDDYVWEIFLPPNADGSPALPHGSRKIMDPSPGVKDSISAWIKFSVQ 301
 224 APEIIFNGIYVDPPEEKVYFQHPQKPEESLRIYESHIGMSSPEPKINSYANFRDEVLP 283
 302 APEIIFNGIYVDPPEEKVYFQHPQKPEESLRIYESHIGMSSPEPKINSYANFRDEVLP 361
 284 PRIKLGYNVAVQJMAIOEHSYASFGYHVTNFFAPSSRFGTPELKSILIDRAHELGLLV 343
 362 PRIKLGYNVAVQJMAIOEHSYASFGYHVTNFFAPSSRFGTPELKSILIDRAHELGLLV 421
 344 MDIVSHSSNNTLDGLNGPFGDTTHYHGGPRGHMMWDSLFNYGSEVLRFLLSNARW 403
 422 MDIVSHSSNNTLDGLNGPFGDTTHYHGGPRGHMMWDSLFNYGSEVLRFLLSNARW 481
 404 WLEEVKFDGPRPGVTSMTYTHHGLQMTFTGNVGEYFGFATDVDAVYVLMVNDLIHGLH 463
 482 WLEEVKFDGPRPGVTSMTYTHHGLQMTFTGNVGEYFGFATDVDAVYVLMVNDLIHGLH 541
 464 PDVASHGEDVSGMPFTFIPVDDGVGVDFYRLHMAVADKWIILKQSDSWMKMGDIIVHTLT 523
 542 PDVASHGEDVSGMPFTFIPVDDGVGVDFYRLHMAVADKWIILKQSDSWMKMGDIIVHTLT 601
 524 NRMWLEKCVTYASHDQALVGDKTIAFWLMDKMDYDFPALDRPSTPRIDRGIALHKMRL 583
 602 NRMWLEKCVTYASHDQALVGDKTIAFWLMDKMDYDFPALDRPSTPRIDRGIALHKMRL 661
 584 VTMGLGEGGLTFMGNEFGHPWIDPRGPQRLPSGKTFPGNNNSYDKCRFRFDLGDADFL 643
 662 VTMGLGEGGLTFMGNEFGHPWIDPRGPQRLPSGKTFPGNNNSYDKCRFRFDLGDADFL 721
 644 LRYHMQEFDQAMQHLEBKGFMTSEHQYVSRKHEDEKVIIFERGDLYFVFNFMHNSNFF 703
 722 LRYHMQEFDQAMQHLEBKGFMTSEHQYVSRKHEDEKVIIFERGDLYFVFNFMHNSNFF 781
 704 DYKVGCSRPGKVKALDSDDLFGGFSRLDHDVDFTEHHPDNRPSFSVYTPRTAVV 763
 782 DYKVGCSRPGKVKALDSDDLFGGFSRLDHDVDFTEHHPDNRPSFSVYTPRTAVV 841
 764 YALTE 768
 842 YALAD 846

RESULT 7

1,4-alpha-glucan branching enzyme (EC 2.4.1.18) II - maize
N:Alternate names: starch branching enzyme II
C:Species: Zea mays (maize)
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 18-Jun-1999

C:Accession: T02981

R:Fishier, D.K.; Boyer, C.D.; Hannah, L.C.

Plant Physiol. 102, 1045-1046, 1993

A:Title: Starch branching enzyme II from maize endosperm.

A:Reference number: 214808; MUID:94105320; PMID:8278524

C:Accession: T02981

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-799 <FIS>

A:Cross-references: EMBL:L08065; NID:g168482; PID:AAA18571.1; PID:g168483

A:Experimental source: cultivar W64Ax182E

C:Function:

A:Description: catalyzes the transglycosylation of a terminal segment of a 1,4-alpha-D-

A:Pathway: glycogen/starch biosynthesis

C:Superfamily: 1,4-alpha-glucan branching enzyme

C:Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

C:Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

C:Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

C:Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

C:Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

C:Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

C:Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

C:Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

C:Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

C:Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

C:Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

C:Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

C:Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

C:Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

C:Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

C:Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

C:Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

C:Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

C:Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

RESULT 8

1,4-alpha-glucan branching enzyme (EC 2.4.1.18) isoform SB2.2 precursor - Arabidopsis
N:Alternate names: starch branching enzyme 2.2
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 22-Nov-1996 #sequence_revision 22-Nov-1996 #text_change 18-Jun-1999

C:Accession: S65046

R:Fishier, D.K.; Gao, M.; Kim, K.N.; Boyer, C.D.; Gultinan, M.J.

Plant Mol. Biol. 30, 97-108, 1996

A:Title: Two closely related cDNAs encoding starch branching enzyme from Arabidopsis thaliana

A:Reference number: S65045; MUID:96197401; PMID:8616246

C:Accession: S65046

A:Molecule type: mRNA

A:Residues: 1-800 <FIS>

A:Cross-references: EMBL:U22428; NID:g726489; PID:AA03100.1; PID:g726490

A:Note: only a part of the coding sequence is given

A:Genome: nuclear

C:Genetics:

A:Function:

A:Description: catalyzes the transglycosylation of a terminal segment of a 1,4-alpha-D-

A:Pathway: glycogen/starch biosynthesis

C:Superfamily: 1,4-alpha-glucan branching enzyme

C:Keywords: chloroplast; glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

C:Keywords: chloroplast; glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

C:Keywords: chloroplast; glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

C:Keywords: chloroplast; glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

C:Keywords: chloroplast; glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

C:Keywords: chloroplast; glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

C:Keywords: chloroplast; glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

C:Keywords: chloroplast; glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

C:Keywords: chloroplast; glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

C:Keywords: chloroplast; glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

C:Keywords: chloroplast; glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

C:Keywords: chloroplast; glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

C:Keywords: chloroplast; glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

C:Keywords: chloroplast; glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

C:Keywords: chloroplast; glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

C:Keywords: chloroplast; glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

C:Keywords: chloroplast; glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

C:Keywords: chloroplast; glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

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Db      515 DGVGVFDYRLHMAADKWMLEMLKKRDEDMQGDIIYTLNRRWSEKISYAESHDQALVG 574
QY      545 DKTIAFWLMDKMYDPMALDRPSTPRIDRGIALHKKMRLVTMGLGEGYLPMGNBGRHP 604
Db      575 DKTIAFWLMDKMYDPMALDRPSTPRIDRGIALHKKMRLVTMGLGEGYLPMGNBGRHP 634
QY      605 EWIDPFRGPOTLPTGKVLPGNNNSYDKCRFRFDLGADFLRYHGMQEPDQAMHLEEKY 664
Db      635 EWIDPFRGEBRLDGSVTPGNNSYDKCRFRFDLGADFLRYHGMQEPDQAMHLEEKY 694
QY      665 FMTSEHQVSRKHEEDKVIIFERGDVLFVFNFWMSNPFYRVGCSPPGKYKVALDSDDA 724
Db      695 FMTSEHQVSRKHEEDKVIIFERGDVLFVFNFWMSNPFYRVGCSPPGKYKVALDSDDA 754
QY      725 LFGGFSRLDHDVDYFTTEHPHNDPRSPFSVYTPSRATVYVAL 766
Db      755 LFGGFSRLDHDVDYFTTEHPHNDPRSPFSVYTPSRATVYVAL 796

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RESULT 9

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748392
1,4-alpha-glucan branching enzyme protein isoform SBE2.2 precursor - Arabidopsis thaliana
N:Alternate names: protein P17C15.70
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jun-2000
C:Accession: T48392
R:Bevan, M.; Pohl, T.; Weisenegger, T.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Lemcke, K.;
submitted to the Protein Sequence Database, March 2000
A:Reference number: Z24492
A:Accession: T48392
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-805 <BEV>
A:Cross-references: EMBL:AL162506
A:Experimental source: cultivar Columbia; BAC clone P17C15
C:Genetics:
A:Map position: 5
A:Intons: 42/1: 81/3; 142/2; 175/2; 189/3; 209/3; 236/3; 275/3; 303/3; 344/2; 384/2; 42
A:Note: P17C15.70
C:Superfamily: 1,4-alpha-glucan branching enzyme

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```

Query Match      78.1%; Score 3258; DB 2; Length 805;
Best Local Similarity 76.6%; Pred. No. 6.3e-237;
Matches 584; Conservative 75; Mismatches 71; Indels 32; Gaps 4;

```

```

QY      18 AAAQPEELQIPE-----DIEBQFAVNMGGTLEKLEBSPTQGIYETITDG 64
Db      59 AIAASEKVLVPMDDDDPRGFSQIFDLESQTMEX-----TEAVRTEDQIMNV----- 105
QY      65 VTGKVELVVGKRRVYKPGDQGIYEIDPTLKDFRSHLDYRSEYRIRAAIDQHEGG 124
Db      106 ----VVER--GVKPRIVPPRODGKTIYEIDPMLKTYNNHLDYRGQYKLAIEIDKYG 159
QY      125 LEAFSRGKELGFTSAEGITYREMAPGASALVGFNNMNPADMTRTDYGWEIFL 184
Db      160 LEAFSRGKELGFTSRDAGITIRMAAGAKAASLIGDENMNSNADIMTRNBFGWELFL 219
QY      185 PNNADGSPALPHGRKVKIAMDTPSGVKSISAMTKFSVQAGEIPFNQIYDDPPEEKY 244
Db      220 PNNYDGPALPHGRKVKIAMDTPSGIKDISIPAMTKFSVQAGEIPFNQIYDDPPEEKY 279
QY      245 FOHPQKRPSPILRYESHIGMSPEPKINSYANFRDEVLPRIKLGYAVAOIMAOESY 304
Db      280 FKHPQKRPSPILRYEYHVGMSSTBPWNTYANFRDVLPRIKLGYAVAOIMAOESY 339
QY      305 YASGKYVITNFASSRFQPEDEKSLIDRAHEGLVLMIDIVSHSSNNLTDLGNGFDG 364
Db      340 YASGKYVITNFASSRCGTPEELKSLIDRAHEGLVLMIDIVSHASKNTLDGLNMFPG 399
QY      365 TDHYHFHGGRGHMMWDSRLFNYSWEVLAFLLSNAWMLDEYKFDPRFPQVTSMMYT 424
Db      400 TDHYHFHGGRGHMMWDSRLFNYSWEVLAFLLSNAWMLDEYKFDPRFPQVTSMMYT 459

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QY      425 HHGLQMTFTNGYGEYFEGATVDVAVYVLMVNDLHGHLPAVSGEDVSGMFTFCIPV 484
Db      460 HHGLSVGTGYTEYFGLIEDVDVANVLMVNDMHLGLYEAITVGEDVSGMFTFCIPVQ 519
QY      485 DGVGVFDYRLHMAADKMTIELLKQSDSEKMDIYHTLTNRRWLEKCVYAESHDQALVG 544
Db      520 DGVGVFDYRLHMAADKMTIELKKRDEDMQGDIIYTLNRRWSEKISYAESHDQALVG 579
QY      545 DKTIAFWLMDKMYDPMALDRPSTPRIDRGIALHKKMRLVTMGLGEGYLPMGNBGRHP 604
Db      580 DKTIAFWLMDKMYDPMALDRPSTPRIDRGIALHKKMRLVTMGLGEGYLPMGNBGRHP 639
QY      605 EWIDPFRGPOTLPTGKVLPGNNNSYDKCRFRFDLGADFLRYHGMQEPDQAMHLEEKY 664
Db      640 EWIDPFRGEBRLDGSVTPGNNSYDKCRFRFDLGADFLRYHGMQEPDQAMHLEEKY 699
QY      665 FMTSEHQVSRKHEEDKVIIFERGDVLFVFNFWMSNPFYRVGCSPPGKYKVALDSDDA 724
Db      700 FMTSEHQVSRKHEEDKVIIFERGDVLFVFNFWMSNPFYRVGCSPPGKYKVALDSDDA 759
QY      725 LFGGFSRLDHDVDYFTTEHPHNDPRSPFSVYTPSRATVYVAL 766
Db      760 LFGGFSRLDHDVDYFTTEHPHNDPRSPFSVYTPSRATVYVAL 801

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RESULT 10

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707743
probable 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) isoform II - potato (fragment)
N:Alternate names: starch branching enzyme II
C:Species: Solanum tuberosum (potato)
C:Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000
C:Accession: T07743
R:Larsson, C.T.; Khoshnoodi, J.; Ek, B.; Raak, L.; Larsson, H.
Plant Mol. Biol. 37, 505-511, 1998
A:Title: Molecular cloning and characterization of starch-branching enzyme II from pot;
A:Accession: T07743
A:Reference number: Z16110; M01D:98278379; PMID:96117817
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-830 <LAR>
A:Cross-references: EMBL:AJ000004; NID:92764395; PID:CA03846.1; PID:92764396
A:Experimental source: cv. Amanda
A:Gene: Sbe-II
C:Function:
A:Description: catalyzes the transglycosylation of a terminal segment of a 1,4-alpha-D-
A:Pathway: glycogen/starch biosynthesis
C:Superfamily: 1,4-alpha-glucan branching enzyme
C:Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

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Query Match      76.9%; Score 3207; DB 2; Length 830;
Best Local Similarity 72.7%; Pred. No. 4.6e-233;
Matches 587; Conservative 83; Mismatches 89; Indels 48; Gaps 6;

```

```

QY      2 ATPAVSGATL--GVARPPAAQPEELQIPE-----DIEBQFAVNMGGTLEKLEBSPTQGIYETITDG 37
Db      12 STVAASGKVLVPGTQSDSSSTDCPEFTETSPENSASTDVDSSTHEASQIKTENDDV 71
QY      38 ---VNMGTGTAE-----KLESSEPTQGIYETITDGVTGKVELVVGKRRV 81
Db      72 EPSSDLVGSVEELDPASSIQLOEGGKLESKTLNTEETIIDSDFIRE-----RGI 123
QY      82 PKPGDQKVIYEIDPTLKDFRSHLDYRSEYRIRAAIDQHEGGLEAFSRGKELGFTRSA 141
Db      124 PPGGIGQKIYEIDPLTNRQHLDYISQYKTLREAIIDKXEGGLEAFSRGKELGFTRSA 183
QY      142 EGITYREMAPGASALVDFNNMNPADMTWTDYGEWEIFLNNADGSPALPHGRKVK 201
Db      184 TGIYREMAPGASALVIDFNNMNPADMTWTDYGEWEIFLNNADGSPALPHGRKVK 243
QY      202 IMNDPSSGYKDSISAMIKESVQAGEIPFNQIYDDPPEEKYFOHPQKRPESLRYES 261

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Db 244 IRMDTSGVSDSIIPAMINYSQLPDELIPNGIYDDPEEERYIFQHPKPKSRIRYES 303
 Qy 262 HIGMSSPEPKINSYANFRDEVLPRIKLGYNAVOIMAIQEHSYIASFGYHTNFPAPSSR 321
 Db 304 HIGMSSPEPKINSYANFRDEVLPRIKLGYNAVOIMAIQEHSYIASFGYHTNFPAPSSR 363
 Qy 322 FGRPEDLKSLIDRAHEGLIVLMDIVSHSNNLTDLNGSDGTDTHFHGGPRGHMMW 381
 Db 364 FGRPEDLKSLIDRAHEGLIVLMDIVSHSNNLTDLNGSDGTDTHFHGGPRGHMMW 423
 Qy 382 DSELPFYGSGWEVLRFLISNARMWLEEKYKFDGFRDGYTSMYTHHGLQMTFTGNYGEYFG 441
 Db 424 DSELPFYGSGWEVLRFLISNARMWLEEKYKFDGFRDGYTSMYTHHGLQMTFTGNYGEYFG 483
 Qy 442 PATDVAVVYLMVNDLIHGLHPDVAISIGEDVSGMPTFCIPVDGSGFDYRLHMAVADK 501
 Db 484 LATDVAVVYLMVNDLIHGLHPDVAISIGEDVSGMPTFCIPVDGSGFDYRLHMAVADK 543
 Qy 502 WTELLKQSDBSWKMGGDIVHTLTNRRLMEKCVTAESHQALVGDKTAFWLMKDMYDFM 561
 Db 544 WTELLKQSDBSWKMGGDIVHTLTNRRLMEKCVTAESHQALVGDKTAFWLMKDMYDFM 603
 Qy 562 ALDRPSTPRIDRGIALHKMRLVTMGLGEGYLNFMGNEFGHPMIDFPFRGPQTLPTGKY 621
 Db 604 ALDRPSTPRIDRGIALHKMRLVTMGLGEGYLNFMGNEFGHPMIDFPFRGPQTLPTGKY 663
 Qy 622 LPGNNSYDKCRRRFDLGDADFLRYHGMQEPDQAMQHLBEKXYGEMTSEHQYVSRKHEDKV 681
 Db 664 IPGNQSYDKCRRRFDLGDADFLRYHGMQEPDQAMQHLBEKXYGEMTSEHQYVSRKHEDKV 723
 Qy 682 VIFEEGDLVFNFMNSNFEDYRVGCSRPGRKXVALDSDDALFGGSRSLDHDVDYTTT 741
 Db 724 VIFEEGDLVFNFMNSNFEDYRVGCSRPGRKXVALDSDDALFGGSRSLDHDVDYTTT 783
 Qy 742 EHPDNRPRSFSYVTPSRATVAVYALTE 768
 Db 784 EGVYDPRPSIMVYABSRATVAVYALVD 810

RESULT 11
 B84780
 starch branching enzyme II [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 17-May-2002
 C:Accession: B84780
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Unayam, L.; Tallon, L.;
 Ems, D.; Niernann, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; WUID:20083487; PMID:10617197
 A:Accession: B84780
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-858 <STO>
 A:Cross-references: GB:AE002093; NID:G4561160; PIDN:AAD24644.1; GSPDB:GN00139
 C:Map position: 2
 C:Superfamily: 1,4-alpha-glucan branching enzyme

Query Match 75.7%; Score 3155; DB 2; Length 858;
 Best Local Similarity 75.2%; Pred. No. 4e-229;
 Matches 561; Conservative 90; Mismatches 79; Indels 16; Gaps 3;
 Qy 23 EELQIPEDIEBOGFAENMTGTAELKLESSPTQGIIVETINDGVTKGVKELVGEKPRVVP 82
 Db 109 EEAQETETL-DQSAISTSGSISYKEPFAKMSHV-----DQEVGQ-RKIP 152
 Qy 83 KPQDQKIVEIDPTLDFRSHLDYRSEYVRIRAPADIDQHEGGLAFAFGYKGLGFTSAAE 142
 Db 153 PGDQGRIVDIDPMANSHRHLIDYRGOYKLEEDIDKNGGLEAFRGYEIIFGFTSAAE 212

Qy 143 GITYREKAPGASALVLVGFENNMMNPNADMTNDYGVWEIPLNNMADGSPALPHGSRVKI 202
 Db 213 GITYREKAPGASALVLVGFENNMMNPNADMTNDYGVWEIPLNNMADGSPALPHGSRVKI 272
 Qy 203 RMDTSGVSDSIISAMKFPVOAPGEIPFNGIYDDPEEERYIFQHPKPKSRIRYESH 262
 Db 273 RMDTSGVSDSIIPAMINYSQLPDELIPNGIYDDPEEERYIFQHPKPKSRIRYESH 332
 Qy 263 IGMSSPEPKINSYANFRDEVLPRIKLGYNAVOIMAIQEHSYIASFGYHTNFPAPSSR 322
 Db 333 VGMSTPEPKINSYANFRDEVLPRIKLGYNAVOIMAIQEHSYIASFGYHTNFPAPSSR 392
 Qy 323 GTPPEDLKSLIDRAHEGLIVLMDIVSHSNNLTDLNGSDGTDTHFHGGPRGHMMW 382
 Db 393 GTPPEDLKSLIDRAHEGLIVLMDIVSHSNNLTDLNGSDGTDTHFHGGPRGHMMW 452
 Qy 383 SELPFYGSGWEVLRFLISNARMWLEEKYKFDGFRDGYTSMYTHHGLQMTFTGNYGEYFG 442
 Db 453 SELPFYGSGWEVLRFLISNARMWLEEKYKFDGFRDGYTSMYTHHGLQMTFTGNYGEYFG 512
 Qy 443 ATDVAVVYLMVNDLIHGLHPDVAISIGEDVSGMPTFCIPVDGSGFDYRLHMAVADK 502
 Db 513 ATDVAVVYLMVNDLIHGLHPDVAISIGEDVSGMPTFCIPVDGSGFDYRLHMAVADK 572
 Qy 503 IELLKQSDBSWKMGGDIVHTLTNRRLMEKCVTAESHQALVGDKTAFWLMKDMYDFM 562
 Db 573 IELLKQSDBSWKMGGDIVHTLTNRRLMEKCVTAESHQALVGDKTAFWLMKDMYDFM 632
 Qy 563 LDRPSTPRIDRGIALHKMRLVTMGLGEGYLNFMGNEFGHPMIDFPFRGPQTLPTGKY 622
 Db 633 VDRQTPPRIDRGIALHKMRLVTMGLGEGYLNFMGNEFGHPMIDFPFRGPQTLPTGKY 692
 Qy 623 LPGNNSYDKCRRRFDLGDADFLRYHGMQEPDQAMQHLBEKXYGEMTSEHQYVSRKHEDKV 682
 Db 693 AGNNSYDKCRRRFDLGDADFLRYHGMQEPDQAMQHLBEKXYGEMTSEHQYVSRKHEDKV 752
 Qy 683 IIFEEGDLVFNFMNSNFEDYRVGCSRPGRKXVALDSDDALFGGSRSLDHDVDYTTT 742
 Db 753 IIFEEGDLVFNFMNSNFEDYRVGCSRPGRKXVALDSDDALFGGSRSLDHDVDYTTT 812
 Qy 743 EHPDNRPRSFSYVTPSRATVAVYALTE 768
 Db 813 EGVYDPRPSIMVYABSRATVAVYALVD 838

RESULT 12
 S65045
 1,4-alpha-glucan branching enzyme (BC 2.4.1.18) isoform SB2.1 precursor - Arabidopsis
 thaliana
 N:Alternate names: starch branching enzyme 2.1
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 22-Nov-1996 #sequence_revision 22-Nov-1996 #text_change 18-Jun-1999
 C:Accession: S65045
 R:Fisher, D.K.; Gao, M.; Kim, K.N.; Boyer, C.D.; Guiltinan, M.J.
 Plant Mol. Biol. 30, 97-108, 1996
 A:Title: Two closely related cDNAs encoding starch branching enzyme from Arabidopsis th
 A:Reference number: S65045; WUID:196197401; PMID:8616246
 A:Accession: S65045
 A:Molecule type: mRNA
 A:Residues: 1-854 <FRS>
 A:Cross-references: EXBL:U18617; NID:G619938; PIDN:AAB03099.1; PID:G619939
 A:Note: only a part of the coding sequence is given
 C:Genetics:
 A:Genome: nuclear
 C:Function:
 A:Description: catalyzes the transglycosylation of a terminal segment of a 1,4-alpha-D-
 A:Pathway: glycogen/starch biosynthesis
 A:Note: final step in biosynthesis of glycogen or amylopectin
 C:Superfamily: 1,4-alpha-glucan branching enzyme
 C:Keywords: chloroplast; glycogen/starch biosynthesis; glycosyltransferase; hexosyltran
 F:1-47/Domains: transactin (chloroplast) #status predicted <TNP>
 F:148-854/Product: 1,4-alpha-glucan branching enzyme isoform SB2.1 #status predicted <M

Best Local Similarity 74.8%; Pred. No. 1.3e-227;
Matches 558; Conservative 91; Mismatches 81; Indels 16; Gaps 3;

```

QY 23 EEIQIPDIEQIAEVMVTGGTAKLSSSEPTQGIETITDGVTKGVKELVVGEXPRVP 82
DB 105 EEAQETITL-DQISALSTSGSISKEDPAKSHSV-----DQEVGQ--RKIP 148
QY 83 KPDDGQKIVEIDPTLKDPRSHLDYRSEYRRIRAAIDHSGGLEAFSGYEKLGFTRSAE 142
DB 149 PPDDGKRIYIDPDLNHSRNLDIRYGGYRKLREBIDNKGGLFAFSRGEIFGFTRSAT 208
QY 143 GTTYREAPAGASALVGDFFNNMNPMDTYMRDDYGVWEILPNNADSPALPHSRVKI 202
DB 209 GITYREAPAGAKASLIGDFNNMNAKSDVMAKDFGWEILPNNADSPALPHSRVKI 268
QY 203 RMDTPSGVDSISAMIKFSVQAPGEIPNGIYDPEEEKYVFCHPQKRPESLRITYSH 262
DB 269 RMDTPSGIKSIPAMIKSVQPPGEIIPNGIYDPEEDKKAFAKPRKPKTSIRITYSH 328
QY 263 IGNSPEPKINSYANFDEVLPRIKLGYNAVQIMAIQESHVYASFGYHVTNFEAPSSRF 322
DB 329 VGMSSTPKINTYANFRDVLPRIKLGYNAVQIMAIQEHAYVASFGYHVTNFEAPSSRF 388
QY 323 GTPEBDKSLIDRAELGLVMDIVHSHSNNTLDGLNGFDGDTNHYHGGRRGHMMMD 382
DB 389 GTPDDKSLIDKAEHLGLVMDIVHSHSNNTLDGLNGFDGDTNHYHGGRRGHMMMD 448
QY 383 SRLFNYSWEVLRFLISNARWMLSEYKFDGPRFDGVTSMNTYTHGLQMTFTNGSEYGF 442
DB 449 TRLENYGSWEVLRFLISNARWMLSEYKFDGPRFDGVTSMNTYTHGLQMTFTNGSEYGF 508
QY 443 ATDVDAVYVYMLVNDLHGLHPDAVSGEDVSGMPTFCIPVDGVDYRLLMAVADKW 502
DB 509 STDVDAVYVYMLVNDLHGLHPDAVSGEDVSGMPTFCIPVDGVDYRLLMAVADKW 568
QY 503 IELLKQSDSKMGQDVIYHNTNRRLKCYTAAESHDAVNDKTIAPFLMDKMDYDEKA 562
DB 569 IELLKQSDSKMGQDVIYHNTNRRLKCYTAAESHDAVNDKTIAPFLMDKMDYDEKA 628
QY 563 LDRPSTPICHGIALHKMIRLYVTWGLGEGYLNFGNFGHPHMTIDPPRPOTLPTGKYL 622
DB 629 VDRQATPRVDGIALHKMIRLYVTWGLGEGYLNFGNFGHPHMTIDPPRPOTLPTGKYL 688
QY 623 PGNNSYDKCRRRFDLGDADFLRYHGMQEFDAQMHLEEKYFMTSEHOYVRKHEDEKY 682
DB 689 AGNNSYDKCRRRFDLGDADFLRYHGMQEFDAQMHLEEKYFMTSEHOYVRKHEDEKY 748
QY 683 IIFERGDVYFVNFPMWSNFPDYRGGSPGKRYKALDSDDDLFGGFSRLDHDVYFTE 742
DB 749 IIFERGDVYFVNFPMWSNFPDYRGGSPGKRYKALDSDDDLFGGFSRLDHDVYFTE 808
QY 743 HPNDNRPSFSYTPSRVAVVALTE 768
DB 809 GRHDDRPFCSFWYAFCRVAVVALTE 834

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RESULT 13

T06578
1,4-alpha-glucan branching enzyme (EC 2.4.1.18) sbel precursor - wheat
N/Alternate names: starch branching enzyme I
C/Species: Triticum aestivum (common wheat)
C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 20-Jun-2000
C/Accession: T06578
R:Chibbar, R.N.
submitted to the EMBL Data Library, April 1997
A/Reference number: Z15772
A/Accession: T06578
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-830 <CH1>
A/Cross-references: EMBL:Y12320; PIDD:CAA72987.1
A/Experimental source: cv. Felder; kernels at 12 days post-anthesis
C/Genetics:

A/Gene: Sbel
C/Function:
A/Description: catalyzes the transglycosylation of a terminal segment of a 1,4-alpha-D-
A/pathway: glycogen/starch biosynthesis
C/Superfamily: 1,4-alpha-glucan branching enzyme
C/Keywords: amyloplasi; glycogen/starch biosynthesis; glycosyltransferase; hexosyltram
F.1-61/Domain: transit peptide (amyloplasi) #status predicted <TMP>
F.62-830/Product: 1,4-alpha-glucan branching enzyme sbel #status predicted <MAT>

Query Match 52.6%; Score 2193.5; DB 2; Length 830;
Best Local Similarity 55.7%; Pred. No. 9.4e-157;
Matches 408; Conservative 104; Mismatches 174; Indels 47; Gaps 9;

```

QY 51 SEPTQGIETITDGVTKGVKELVVGEXPRVPKPGQOKIYEIDPTLKDPRSHLDYRSE 110
DB 63 SAPRDYTMATADG-----VGDLP-----IYDDPKFAGKEHSTYMKK 102
QY 111 YRIRAPAIQHEGGLBAPFGRYEKLGFTSAEGITYREMAPGASALVGDFFNNMNPAD 170
DB 103 YLDQKHSIEKHGGLBEPFSKGYLKFGINTENDATVREMAPAMDADLIGDFNNMNSGH 162
QY 171 TWTRDDYGVWEILPNNADGSPALPHGSRVKIMDTPSGY-KDSISAMIKFSVQAPGEI- 228
DB 163 RMTKMDYGVWSIRI-SHVGKFPALPHNSKYKFFHRDGLVMDVRVPAMIRVATPDASFG 221
QY 229 -PENGITYDPEEEKYVFCHPQKRPESLRITYSHIGNSPEPKINSYANFRDEVLPRIK 287
DB 222 APDGVHMDPPSGERYVFKHPRKPDAPRIYEAHVMSGKEPEVSTYREPADVLPRIK 281
QY 288 RUCYNAVQIMAIQESHVYASFGYHVTNFEAPSSRFCTPEBDKSLIDRAELGLVMDIV 347
DB 282 ANNTYNAVQIMAIQESHVYASFGYHVTNFEAPSSRSCTPEBDKSLVDAKSLGLRLMDV 341
QY 348 HSHSNNTLDGLNGFD--GTDTHYHGGRRGHMMDSRLFNYSWEVLRFLISNARW 404
DB 342 HSHSNNTLDGLNGFDVQNTQESYFPTGGRGYKMLDSRLFNYSWEVLRFLISNARW 401
QY 405 LBEYKFDGPRFDGVTSMNTYTHGLQMTFTNGYGFPGATVDVAVYVYMLVNDLHGLAP 464
DB 402 MDEFMFDGPRFDGVTSMNTYTHGLQMTFTNGYGFPGATVDVAVYVYMLVNDLHGLAP 461
QY 465 DAVISGEDVSGMPTFCIPVDGVDYRLLMAVADKWIELKQSD-SWKGQDVIHFLT 523
DB 462 EATVVAEDVSGMPTFCIPVDGVDYRLLMAVADKWIELKQSD-SWKGQDVIHFLT 521
QY 524 NREMLEKCVTAAESHDAVNDKTIAPFLMDKMDYDEKALDSDDDLFGGFSRLDHDVYFTE 583
DB 522 NREMLEKCVTAAESHDAVNDKTIAPFLMDKMDYDEKALDSDDDLFGGFSRLDHDVYFTE 581
QY 584 VTMGLGEGYLNFGNFGHPHMTIDPPRPOTLPTGKYLPGNNSYDKCRRRFDLGDADF 643
DB 582 IYVALGSDGYLNFGNFGHPHMTIDPPR-----EGNNSYDKCRRRFDLGDADF 630
QY 644 LRYHGMQEFDAQMHLEEKYFMTSEHOYVRKHEDEKVIIFERGDVYFVNFPMWSNFP 703
DB 631 LRYHGMQEFDAQMHLEEKYFMTSEHOYVRKHEDEKVIIFERGDVYFVNFPMWSNFP 690
QY 704 DYRVGSRPGKRYKALDSDDDLFGGFSRLDHDVYFTE-----EHPNDNRPSFSY 755
DB 691 GYKYGCDLPGKRYKALDSDLMLFGHGRVADNDHFTSPBGVPGVETNENRPNFSKIL 750
QY 756 TPSTAVVALTE 768
DB 751 SPSTAVVALTE 763

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RESULT 14

T07824
1,4-alpha-glucan branching enzyme (EC 2.4.1.18) I (clone sbel1) - potato (fragment)
C/Species: Solanum tuberosum (potato)
C/Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000
C/Accession: T07824
R:Koshnoodi, J.; Blennow, A.; Ek, B.; Raek, L.; Larsson, H.

Tue Apr 20 10:02:30 2004

us-09-508-377-12.rpr

Page 10

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Db 432 YFSLDUDVDALVYWMANHLHKLLEFATVAEDVSGMPVLCRPVDEG3GVGDFPRLAMAI 491
QY 499 ADKWIIEJLK-QSDESKKGGDIYHTLTNRRLMEKCTVYAESHDQALVGDKTIAFWLMDKM 557
Db 492 PDRWIDYLNKEDRKWSNSEIVQTLNRRYTEKCIAYASHDQIVGDKTIAFLMDKEM 551
QY 558 YDFVALDRPSTPRIDRGIALHQMIRLVTMGLGEGYLNFMGNEFGHPENIDFPFGPQTLP 617
Db 552 YTGMSDLOPASPTINRGIALQKMHFTMALGGDGLNFMGNEFGHPENIDFP----- 605
QY 618 TGKVLPGNNNSYDKCRRRFDLGADFLRYHGMQEPDQAMQHLLEKYGFWTSZHOYVSRKA 677
Db 606 -----EGNWSYDKCRQMSLVDTDLRYKYNNAFDQAMNALLEEFSSFLSSKQIVSDMN 660
QY 678 EEDKVIIFERGDVVFENFHMNSFPDYRVGGRPKYKVALDSDDALFGFSRLDHDVD 737
Db 661 EKDKVIVFERGDVVFENFHMNTYKGYKVGCDLPGKIRVALDSDALVFGHGRVGHADV 720
QY 738 YFTT-----EHPDNRPRSFSVYTPSRITAVY 764
Db 721 HFTSPBGMPSVPEITFNNRPNNSFKVLSPPRTCVAY 755
```

Search completed: April 15, 2004, 08:38:41
Job time : 24 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 15, 2004, 08:35:15 ; Search time 18 Seconds
(without alignments)

2221.660 Million cell updates/sec

Title: US-09-508-377-12

Perfect score: 4169

Sequence: 1 MATFVSGATLGVARRPAAA.....PRFSVYTPSRVAVYALTE 768

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3342	80.2	799	1	GLGB_MAIZE
2	2166.5	52.0	820	1	GLGB_ORISA
3	2140	51.3	702	1	GLGB_HUMAN
4	2122.5	50.9	861	1	GLGB_SOLTU
5	1795.5	43.1	704	1	GLGB_YEAST
6	628	15.1	715	1	GLGB_VIBVU
7	624	15.0	773	1	GLGB_SYNP7
8	620	14.9	755	1	GLGB_VIBPA
9	592.5	14.2	666	1	GLGB_NITRU
10	579	13.9	734	1	GLGB_NITRU
11	576	13.8	762	1	GLGB_NITRU
12	574	13.8	737	1	GLGB_NITRU
13	573	13.7	770	1	GLGB_SYNP3
14	571.5	13.7	637	1	GLGB_OCEIH
15	568.5	13.6	731	1	GLGB_COREF
16	568	13.6	766	1	GLGB_SYNEL
17	564.5	13.5	741	1	GLGB_CORGL
18	562	13.5	754	1	GLGB_ANMSP
19	558	13.4	730	1	GLGB_HARIN
20	557	13.4	730	1	GLGB_PASMU
21	555.5	13.3	734	1	GLGB_AGRU
22	554	13.3	727	1	GLGB_YERPE
23	553.5	13.3	728	1	GLGB_ECOLI
24	552.5	13.3	728	1	GLGB_SHIFL
25	550.5	13.2	705	1	GLGB_DEIRA
26	550.5	13.2	728	1	GLGB_ECO57
27	549.5	13.2	630	1	GLGB_AQUAE
28	548.5	13.2	728	1	GLGB_ECOL6
29	548.5	13.2	728	1	GLGB_SALTI
30	548.5	13.2	728	1	GLGB_SALTI
31	548	13.1	725	1	GLGB_AGRU5
32	544.5	13.1	721	1	GLGB_BROWA
33	541.5	13.0	621	1	GLGB_RHOWR

34	540.5	13.0	634	1	GLGB_LACGL	O890j1 lactobacill
35	540.5	13.0	666	1	GLGB_BACCL	P30537 bacillus ca
36	540	13.0	639	1	GLGB_BACCL	P30538 bacillus sc
37	538.5	12.9	724	1	GLGB_XANAC	O8p13 xanthomonas
38	537	12.9	732	1	GLGB_PSEAR	O91w2 pseudomonas
39	535.5	12.8	731	1	GLGB_MYCBO	P59816 mycobacteri
40	530.5	12.7	664	1	GLB2_GLOBE	O8xx15 clostridium
41	530	12.7	731	1	GLGB_ERWCH	O895cs erwina chr
42	525.5	12.6	731	1	GLGB_MYCTU	O10625 mycobacteri
43	522.5	12.5	724	1	GLB1_XANCP	O8pe48 xanthomonas
44	521	12.5	639	1	GLGB_BUTFI	P30539 butyrivibri
45	520	12.5	737	1	GLGB_BIFLO	O89510 bifidobacte

ALIGNMENTS

RESULT 1
GLGB_MAIZE STANDARD; PRT; 799 AA.
ID GLGB_MAIZE
AC Q08047;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE 1,4-alpha-glucan branching enzyme IIB, chloroplast precursor
DE (EC 2.4.1.18) (Starch branching enzyme IIB) (O-enzyme).
GN SBE1.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 58-65.
RC STRAIN=cv. M64A X 182E; TISSUE=Endosperm;
RX MEDLINE=94105320; PubMed=8278524;
RA Fisher D.K., Boyer C.D., Hannah L.C.;
RT "Starch branching enzyme II from maize endosperm.";
RL Plant Physiol. 102:1045-1046(1993).
RN [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 248-271 AND 305-315.
RC STRAIN=cv. B73; TISSUE=Endosperm;
RX MEDLINE=95152344; PubMed=7849565;
RA Guan H.P., Baba T., Preiss U.;
RT "Expression of branching enzyme II of maize endosperm in Escherichia coli.";
RL Cell. Mol. Biol. 40:981-986(1994).
CC - FUNCTION: Catalyzes the formation of the alpha-1,6-glucosidic linkages in glycogen by scission of a 1,4-alpha-linked oligosaccharide from growing alpha-1,4-glucan chains and the subsequent attachment of the oligosaccharide to the alpha-1,6 position.
CC - CATALYTIC ACTIVITY: Formation of 1,6-glucosidic linkages of starch.
CC - PATHWAY: Starch biosynthesis; third step.
CC - SUBUNIT: Monomer (By similarity).
CC - SUBCELLULAR LOCATION: Chloroplast; Amyloplast.
CC - SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
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CC EMBL; L08065; AAA18571.1; -
CC PIR; T02981; T02981.
CC MatedDB; 63943; -
CC InterPro; IPR006047; Alpha amyl cat.
CC InterPro; IPR004193; Glyco_hydro_13N.
CC Pfam; PF00128; alpha-amylase; 1.

DR Pfam, PF02922; isoamylase N; 1.
 KW Glycogen biosynthesis; Starch biosynthesis; Transferase;
 KM Glycosyltransferase; Amyloplast; Chloroplast; transit peptide.
 FT TRANSIT 1 57 CHLOROPLAST (AMYLOPLAST).
 FT CHAIN 58 799 1,4-ALPHA-GLUCAN BRANCHING ENZYME 11B.
 FT ACT_SITE 341 341 BY SIMILARITY.
 FT ACT_SITE 376 376 BY SIMILARITY.
 FT ACT_SITE 381 381 BY SIMILARITY.
 FT ACT_SITE 445 445 BY SIMILARITY.
 FT ACT_SITE 447 447 BY SIMILARITY.
 FT ACT_SITE 502 502 BY SIMILARITY.
 FT ACT_SITE 569 569 BY SIMILARITY.
 FT ACT_SITE 570 570 BY SIMILARITY.
 SQ SEQUENCE 799 AA; 90517 MW; 0B44DE03778B087A C6C64;

Query Match 80.2%; Score 3342; DB 1; Length 799;
 Best Local Similarity 78.4%; Pred. No. 3.1e-239;

Matches 608; Conservative 67; Mismatches 79; Indels 22; Gaps 4;

4 PAVSGATLV-----APPAAQPEELQIPEDIEQTEVNMGTGTAKESSS----- 52
 35 FLTRGARVCGSGTHGAMRAAAAKAVVPEGEND-----GLARADSAQFQDEL 85
 53 PFGQIVETIDGVYKVKELVVGKPRVYKPGDQKQIYEIDPTLKDRSHLDYRSEYR 112
 86 EVDISEETCGA--GVADAQALNRVAVPPSDQKIFQIDPMIQKTHLEYRSLYR 143
 113 RIRAIIDQHEGGLAEFGRGYEKLGFTRSAEGITREMAPGAASALYVDPMNMENADTM 172
 144 RINSIDIEHGGLEAFERSYKFGFNASABEGITREMAPGAASALYVDPMNMENADTM 203
 173 TRDDYGVWEIFLPNNADGSPAIPIHOSRYKIMDTSSGYKDSISATIKSVQAPGPIPN 232
 204 SKNEFGWEIFLPNNADGSPAIPIHOSRYKIMDTSSGYKDSISATIKSVQAPGPIPN 263
 233 IYDPRPEEKVYKPGHOKPESLRIRYSHIGMSPEPKINSYAFRDEVLPRIKRLGN 292
 264 IYDPRPEEKVYKPGHOKPESLRIRYSHIGMSPEPKINSYAFRDEVLPRIKRLGN 323
 293 AVQIMAIQEHSSYASFGYHVTNFFAPSSRFPTEDLKSLIDRAHELGLVMDIVSHSS 352
 324 AVQIMAIQEHSSYASFGYHVTNFFAPSSRFPTEDLKSLIDRAHELGLVMDIVSHSS 383
 353 NNTLDGLNGFGDTTHYHGGPRGHMWDRLFNYSGEVLRFLLSNARWMLSEYKFG 412
 384 NNTLDGLNGFGDTTHYHGGPRGHMWDRLFNYSGEVLRFLLSNARWMLSEYKFG 443
 413 FRFGVTSMTYTHGLQMTFTGNVYGFATDVAVVYLMVNDLHGLHDAVSGSD 472
 444 FRFGVTSMTYTHGLQMTFTGNVYGFATDVAVVYLMVNDLHGLHDAVSGSD 503
 473 VSGMPTFCIPYDGVGVDFYRLMAVADKMIELKQSDSAPKMGDIVHTLNRMLEKY 532
 504 VSGMPTFCIPYDGVGVDFYRLMAVADKMIELKQSDSAPKMGDIVHTLNRMLEKY 563
 533 TYASSHDQALVGDKTIATFWMKDMYDFALDRPSTPTIDRGIALHKMRLITMGSGSG 592
 564 TYASSHDQALVGDKTIATFWMKDMYDFALDRPSTPTIDRGIALHKMRLITMGSGSG 623
 593 YLNFNGNFGHEMIDFPRGPOTLPTGKVLPGNNNSYDKCRSRFDLGDADFLRYHQMF 652
 624 YLNFNGNFGHEMIDFPRGPOTLPTGKVLPGNNNSYDKCRSRFDLGDADFLRYHQMF 683
 653 DOAMQHELEKYGFMTEHQYVSRKHEEDKVIIFERGDLVFNFMHNSFPDYRVGCSR 712
 684 DOAMQHELEKYGFMTEHQYVSRKHEEDKVIIFERGDLVFNFMHNSFPDYRVGCSR 743
 713 GKIKVALSDDLFGGFSRLDHDVYFTTEHPHNDNPRFSVYTPRTAVVYALTE 766
 744 GYKRVVLDSDAQLFGGFSRIHHAHEFTADCSHNDNPRFSVYTPRTAVVYALTE 799

GLGB_ORYSA
 ID ID GLGB_ORYSA STANDARD; PRT; 820 AA.
 AC 001011-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) (Starch branching enzyme) (Q-enzyme).
 GN SBE1.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eriocaulaceae; Oryzaceae; Oryza.
 OC NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Japonica; TIGR=Endosperm;
 RA Nakamura Y., Yamamoto H.;
 RT "Nucleotide sequence of a cDNA encoding starch-branching enzyme, or O-enzyme I, from rice endosperm."
 RL Plant Physiol. 99:1265-1266(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=9320482; PubMed=8455548;
 RA Kawasaki T., Mizuno K., Baba T., Shimada H.;
 RT "Molecular analysis of the gene encoding a rice starch branching enzyme."
 RL Mol. Gen. Genet. 237:10-16(1993).
 RL 1- FUNCTION: Catalyzes the formation of the alpha-1,6-glucosidic linkages in glycogen by scission of a 1,4-alpha-linked oligosaccharide from growing alpha-1,4-glucan chains and the subsequent attachment of the oligosaccharide to the alpha-1,6 position.
 CC 1- CATALYTIC ACTIVITY: Formation of 1,6-glucosidic linkages of starch.
 CC 1- PATHWAY: Starch biosynthesis; third step.
 CC 1- SUBUNIT: Monomer.
 CC 1- SUBCELLULAR LOCATION: Chloroplast; amyloplast.
 CC 1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
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 CC EMBL: D10752; BAA01584.1; --
 CC EMBL: D10838; BAA01616.1; --
 DR Gramene; Q01401; --
 DR InterPro; IPR006047; Alpha_amy1_cat.
 DR InterPro; IPR004193; Glyco_hydro_13n.
 DR Pfam; PF00128; alpha-amyase; 1.
 DR Pfam; PF02922; isoamylase N; 1.
 KW Starch biosynthesis; Transferase; Glycosyltransferase; Amyloplast; Chloroplast.
 FT MOD_RES 1 1 BLOCKED.
 FT ACT_SITE 300 300 BY SIMILARITY.
 FT ACT_SITE 335 335 BY SIMILARITY.
 FT ACT_SITE 340 340 BY SIMILARITY.
 FT ACT_SITE 407 407 BY SIMILARITY.
 FT ACT_SITE 409 409 BY SIMILARITY.
 FT ACT_SITE 464 464 BY SIMILARITY.
 FT ACT_SITE 533 533 BY SIMILARITY.
 FT ACT_SITE 533 533 BY SIMILARITY.
 FT CONFLICT 13 13 P -> A (IN REF. 2).
 FT CONFLICT 715 753 VGHVDHFTSPGEMGVEITNNRPNNSFKULSPRTCV -> LAMMWITSRLPRECEYKQISTALTLSKSPRPV (IN REF. 2).
 SQ SEQUENCE 820 AA; 93262 MW; A687CE9396F59DF C6C64;

Query Match 52.0%; Score 2166.5; DB 1; Length 820;
 Best Local Similarity 57.8%; Pred. No. 2.9e-152;

[illegible]

	-	FUNCTION:	Required for sufficient glycogen accumulation. The alpha 1-6 branches of glycogen play an important role in increasing the solubility of the molecule and, consequently, in reducing the osmotic pressure within cells.
	-	CATALYTIC ACTIVITY:	Formation of 1,6-glucosidic linkages of glycogen.
	-	PATHWAY:	Glycogen biosynthesis; third step.
	-	SUBUNIT:	Monomer.
	-	TISSUE SPECIFICITY:	Highest levels found in liver and muscle.
	-	DISEASE:	Defects in GBE1 are the cause of glycogen storage disease IV (GSD-IV) [MIM:232500]; also known as Andersen's disease. GSD-IV is a rare form of glycogenosis characterized by the accumulation of abnormally structured glycogen that results in early onset hepatic cirrhosis, cardiac arrest and neuromuscular diseases. Most children with this condition die before two years of age. No treatment apart from liver transplantation has been found to prevent progression of the disease.
	-	SIMILARITY:	Belongs to family 13 of glycosyl hydrolases.
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DR	EMBL;	L07956;	AAS8642.1; --
DR	PIR;	A46075;	A46075.
DR	GeneW;	GNCGN;	4180; GBE1.
DR	GK;	O04446;	--
DR	MIM;	607839;	--
DR	NM_;	232500;	--
DR	GO;	GO:0003884;	F.1.4-alpha-D-glucose branching enzyme activity; TAS.
DR	GO;	GO:0006091;	P:energy pathway; TAS.
DR	GO;	GO:0005977;	P:glycogen metabolism; TAS.
DR	InterPro;	IPIR006047;	Alpha-amyl cat.
DR	InterPro;	IPIR004193;	Glyco_hydro_13n.
DR	Pfam;	PF00128;	alpha-amylase; 1.
KX	Pfam;	pf09222;	isomylase_N; 1.
KW	Glycogen biosynthesis;	Transferase;	Glycosyltransferase;
KW	Glycogen storage disease.		
FT	ACT SITE	251	BY SIMILARITY.
FT	ACT SITE	286	BY SIMILARITY.
FT	ACT SITE	291	BY SIMILARITY.
FT	ACT SITE	355	BY SIMILARITY.
FT	ACT SITE	357	BY SIMILARITY.
FT	ACT SITE	412	BY SIMILARITY.
FT	ACT SITE	480	BY SIMILARITY.
FT	ACT SITE	481	BY SIMILARITY.
SEQUENCE	702 AA;	80443 MW;	4DF3AABD365A8FE3 CRC64;
Query Match	51.3%;	Score 2140;	DB 1; Length 702;
Blast Local Similarity	57.5%;	Pred. No. 2.le-150;	
Matches	Conservative 102;	Mismatches 170;	Indels 16; Gaps 5;
QY	89	KIYEIDPFLPKPRSHLDVRYSEBRRIRAPADQHGGGLAFSGRGYEKLGFTRSAEGITF-R	147
Db	30	RLLIEDPLRKYYAVNDPFRKYKFQLIKNGENGGDIKRGEISGVHRCADGGLYSK	89
QY	148	EWAPCAHSALVGDPNNMNPNVAQTMDTDGYCVMEIFLPNNAAGSPALPHGRVKVIKDTP	207
Db	90	EWAPCAHEVFPLTGJENGWNPPSYEKKDLDYCKMLLYIPKPKNCSVLVPHGSKLVVTISK	149
QY	208	SG-YVDSTIAWKTSVOAPEIIPPNGRIYGVEPEEKVYFCQPQRPSRLTYESHIGMS	266
Db	150	SGELTRYISPAAKVYREGDNVNATDMWD--EHSEYFKISRKRKRSLRTIYESHOIS	207
QY	267	SPEPKINSYPANRDENVLRIRLGAYNAVQVLAIOESHYSAFGYVTVNFPASSRFGTPE	326
Db	208	SHEGVSASYKFAKTONTVLRPKGIGNCQLMAIMEHAHVYAFFGYOITSFFAASSRGYTFE	267
QY	327	DKSITPAHETCI I Y MDTHSSSNNTT DCT NGPGSTDPHYHHGGGRGHMMNMDSIE F	386

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DB      268 ELQELVDTHASHWITVLLDVVSHASKASDGLNMFDCGSCYHSGRGTGHDMDSRLLF 327
QY      387 NYGSMWEVLRLSNNAWMLBEYKFDGFRPDGVTSMTYTHGLQMTFTNGYGEYFGFATDV 446
DB      328 AYSWSEVLRLSNIRWMLBEYRFDGRFGVTSMLYHHGVGGGSGDYSEYFGLQVDE 387
QY      447 DAVVYLMVNDLHGLHPDVAISGEDVSGMPTFCIPYPDGVGVGDYRLNMAVADKMTIEL 506
DB      388 DALTYLMLANHLVHTLCPCDSITTAEDVSGMPALCSPISQGGGGRYRLNMAIPDKMQL 447
QY      507 KO-SDSWMKGDIVHTLTLNRWLEKCVTAESHDOALVGDITAFMLDKMDKMFMALDR 565
DB      448 KERKEDDMNGDVIYTLNRRYLEKCIAYESHDOALVGDKSLAFMLDMAMTMMSLVT 507
QY      566 PSTPRIDRGIALHKMIRLVMTMGLGEGYLNFMGNEFGHPENIDPPRGQTLPTGKVLPGN 625
DB      508 PFTPVIDRGIQHMKMIRLITHTGEGYLNFMGNEFGHPENIDPPR-----KGN 556
QY      626 NNSYDKCRRRFDLGDADFLRYHGMQEPDQAMQHLEKKGFWTSEHQYYSRKHEEDKVIIF 685
DB      557 NESHYARROFHLTDLLRYKFLNFRDNRNLEERYGWLAAQAVYSEKHEGKILAF 616
QY      686 ERDDIVAVENFMHNSFPDYRVGSGRGKYKVALDSDDALFGFSRLDHDYDPTTEHPH 745
DB      617 ERAGLFTFNFHPSKSTYDTRVGTALPEKFKIVLSDAAYGGHORLDHSTDFSEAPEH 676
QY      746 DNRPSFSVYTPSRTAVY 763
DB      677 NGRPYSLVYIIPSRVALI 694

RESULT 4
GLGB_SOLUTU STANDARD; PRT; 861 AA.
AC P30932;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE 1,4-alpha-glycan branching enzyme (EC 2.4.1.18) (Starch branching
  enzyme) (O-enzyme).
DE SBE1 OR SBE.
OS Solanum tuberosum (Potato).
OC Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
  OC lamiales; Solanales; Solanaceae; Solanum.
OC NCBI_Taxid=4113;
OX RN
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Diabella;
RX MEDLINE=94105324; PubMed=8278528;
RA Poulsen P., Krelberg J.D.;
RT "Starch branching enzyme cDNA from Solanum tuberosum.";
RL Plant Physiol. 102:1053-1054 (1993).
RN [2]
RP SEQUENCE OF 279-527 FROM N.A.
RC STRAIN=cv. Desiree; TISSUE=Tuber;
RX MEDLINE=92079917; PubMed=1745241;
RA Kossmann J., Visser R.G.F., Mueller-Roeber B., Willmitzer L.,
  RA Sonnwald U.;
RT "Cloning and expression analysis of a potato cDNA that encodes
  branching enzyme: evidence for co-expression of starch biosynthetic
  genes.";
RL Mol. Gen. Genet. 230:39-44 (1991).
CC -1- FUNCTION: Catalyzes the formation of the alpha-1,6-glucosidic
  linkages in glycogen by scission of a 1,4-alpha-linked
  oligosaccharide from growing alpha-1,4-glucan chains and the
  subsequent attachment of the oligosaccharide to the alpha-1,6
  position.
CC -1- CATALYTIC ACTIVITY: Formation of 1,6-glucosidic linkages of
  starch.
CC -1- PATHWAY: Starch biosynthesis; third step.
CC -1- SUBUNIT: Monomer.

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CC -1- SUBCELLULAR LOCATION: Chloroplast; amyloplast.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
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-----
CC DR EMBL; X69805; CAA49463.1; -.
CC DR PIR; S34730; S34730.
CC DR InterPro; IPR006047; Alpha_amyl_cat.
CC DR InterPro; IPR004193; Glyco_hydro_13n.
CC DR Pfam; PF00128; alpha-amylase; 1.
CC DR Pfam; PF02922; Isoamylase N; 1.
CC DR Starch_biosynthesis; Transferrase; Glycosyltransferase; Amyloplast;
  KW Chloroplast.
FT ACT_SITE 320 320 BY SIMILARITY.
FT ACT_SITE 355 355 BY SIMILARITY.
FT ACT_SITE 360 360 BY SIMILARITY.
FT ACT_SITE 427 427 BY SIMILARITY.
FT ACT_SITE 429 429 BY SIMILARITY.
FT ACT_SITE 484 484 BY SIMILARITY.
FT ACT_SITE 553 553 BY SIMILARITY.
SQ SEQUENCE 861 AA; 99083 MW; F3D519AC7C1BBF2 CRC64;

Query Match 50.9%; Score 2122.5; DB 1; Length 861;
Best Local Similarity 55.8%; Pred. No. 5,7e-149;
Matches 400; Conservative 97; Mismatches 189; Indels 31; Gaps 8;

QY 44 TAKLESSPPTGIVETIDGVTK-----GKELVGEKRVVPKPGDGK-----LY 91
DB 40 TGLKFGSQRSMDISTPKSRVAKDERMKSSAISAVLTNDNGMALBEDVKENTIGLL 99
QY 92 EIDPTLKDFRSHLDVYSEYRIRAAIDHGGLEAFSRGYEKLGFRSAGITRYEMAP 151
DB 100 NIDPTLEPLDLHRHMKRYVDQKMLIEKYEGLPEPAQYLRKGFREDDCIYREWAP 159
QY 152 GAHSAALVQDFNNWPNADMTPTDDYGVWEIPLPNADSGPALPHGSRVYKRMTPSGV- 210
DB 160 AAQEDDEVIGDFNMGNSNMHMEKDOFQVWSIRIP-DVDSKRVIPHNSRVKRFYHGNGW 218
QY 211 KQISAMIKFSVQAQGEI--PFGIYDPEEEKYVQCHQOPKRPESIRIYESHIGMSSP 268
DB 219 VDIRIPMIKATADATFPAAPYDGVWDPPSERYHKYRPPRPAPRIYEAHVGSSS 278
QY 269 EPKINSYANFRDEVLPRIKRAGYNAVOIMAIOESHYYASFQYHVTNPPAPSSRFGTPEDL 328
DB 279 EPRVNSYREPADVLPRIKANNVTQVLAIMEHSYGSFGYHVTNPPAVSSRYGNPDL 338
QY 329 KSLIDRAHELGILVMDIVSHSSNNTLDGNGD---GDTYHFGGPRGHMMWDSRL 385
DB 339 KYLIDKXASLGLOVLDVVVSHASNNVTDGNGFDIQGSGQSESYFHAERGGYHKLWDSRL 398
QY 386 FNYGSMWEVLRLSNNAWMLBEYKFDGFRPDGVTSMTYTHGLQMTFTNGYGEYFGFATDV 445
DB 399 FNYANWEVLRLSNLRWMLBEYVFDGRFGDITSMLYHHGIMNGFQGNVEYSEATD 458
QY 446 VDAVVYLMVNDLHGLHPDVAISGEDVSGMPTFCIPYPDGVGVGDYRLNMAVADKMTIEL 505
DB 459 VDAVVYLMANLHKLIFPAITVAEDVSGMPGLGRPVEGIGIDYRLNMAIPDKMIDY 518
QY 506 LK-QSDSWMKGDIVHTLTLNRWLEKCVTAESHDOALVGDITAFMLDKMDKMFMALDR 564
DB 519 LKNNKNDWMSKQETSLNRRYLEKCIAYESHDOALVGDITAFMLDKMYSIGMSCL 578
QY 565 RPSRPRIDRGIALHKMIRLVMTMGLGEGYLNFMGNEFGHPENIDPPRGQTLPTGKVLPG 624
DB 579 TDASPVVDRGIALHKMIRLFFTMALGSGYLNFMGNEFGHPENIDPPR-----EG 627
QY 625 NNSYDKCRRRFDLGDADFLRYHGMQEPDQAMQHLEKKGFWTSEHQYYSRKHEEDKVIIF 684

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DB 628 NMWYXKCRGOWMLADSEHLRYKFMNAPDRAMNSLDEKFSPLASGKQIVSSMDDNKVVV 687
QY 685 FERGDVLFVFNPFWMNSFPFIRYVGCSPKGYKVALDSDDDALFGFSLDHDVDFTT 741
DB 688 FERGDVLFVFNPFWMNSFPFIRYVGCSPKGYKVALDSDDDALFGFSLDHDVDFTT 744

RESULT 5
GLGB_YEAST
ID GLGB_YEAST STANDARD; PRT; 704 AA.
AC P32775;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) (Glycogen branching
enzyme).
GN GLC3 OR YEL011W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=92340578; PubMed=1634552;
RA Thon V.J., Vigneron-Lesens C., Marianne-Pepin T., Montreuil J.,
RA Decq A., Rachez C., Ball S.G., Cannon J.F.,
"Coordinate regulation of glycogen metabolism in the yeast
Saccharomyces cerevisiae. Induction of glycogen branching enzyme."
RA J. Biol. Chem. 267.15224-15228 (1992).
RL [2]
RN SEQUENCE FROM N.A.
RX STRAIN=S288C / AB972;
RA Dietrich F.S., Mulligan U.T., Hennessey K.M., Yelton M.A., Allen E.,
RA Araujo R., Aviles E., Berno A., Brennan T., Carpenter J., Chen E.,
RA Cherry J.M., Chung E., Duncan M., Guzman E., Hartzell G.,
RA Huntley-Smith S., Hyman R.W., Kayser A., Komp C., Laehkari D., Lew H.,
RA Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P.,
RA Oh C., Patel P.X., Roberts D., Sehl P., Schramm S., Shogren T.,
RA Smith V., Taylor P., Wei Y., Botstein D., Davis R.W.,
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome V."
RL Nature 387.78-81 (1997).
CC -1- CATALYTIC ACTIVITY: Formation of 1,6-glucoacidic linkages of
glycogen.
CC -1- PATHWAY: Glycogen biosynthesis; third step
CC -1- DEVELOPMENTAL STAGE: EXPRESSED DURING THE TRANSITION BETWEEN THE
MAXIMAL GLYCOGEN ACCUMULATION.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
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CC -----
CC EMBL: M76739; AAA34632.1; -.
CC EMBL: U18530; AAB64488.1; -.
CC PIR: S50448; S50448.
CC Germonline: 139015; -.
CC SGD: S0000737; GLC3.
CC GO: GO:0003844; F.1.4-alpha-glucan branching enzyme activity; IGI.
CC GO: GO:0005977; P:glycogen metabolism; IMP.
CC InterPro: IPR006047; Alpha_amyl_cat.
CC InterPro: IPR004193; Glyco_hydro_13N.
CC Pfam: PF00126; alpha-amylase; 1.
CC Pfam: PF02922; isoamylase_N; 1.
CC Glycogen biosynthesis; Transferase; Glycosyltransferase.
CC ACT SITE 248 248
CC ACT SITE 283 283
CC BY SIMILARITY.
CC ACT SITE 283 283
CC BY SIMILARITY.

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FT ACT SITE 288 288 BY SIMILARITY.
FT ACT SITE 354 354 BY SIMILARITY.
FT ACT SITE 356 356 BY SIMILARITY.
FT ACT SITE 417 417 BY SIMILARITY.
FT ACT SITE 485 485 BY SIMILARITY.
FT ACT SITE 486 486 BY SIMILARITY.
FT ACT SITE 564 564 BY SIMILARITY.
FT CONFLICT 564 564 S -> T (IN REF. 1).
SQ SEQUENCE 704 AA; 8115 MW; 9C227E107B825F27 CRC64;

Query Match 43.1%; Score 1795.5; DB 1; Length 704;
Best Local Similarity 51.4%; Pred. No. 6,6e-125;
Matches 367; Conservative 105; Mismatches 199; Indels 43; Gaps 17;

QY 84 PDDGQKIYEIDPTLDFRSHL-DYRYS-...YRIRALIDQEGGLEAFSR-GYEKLGF 137
DB 5 PDNVGAVEFDFMLKPFADVLSEERYLADKMLYDITHAFPDGSGYQSLKFPADSKSYGL 64
QY 138 TRSAR--GITYREMAPGASALVGPNNWNPNA-DTMRDDYGVWEIFLPNNADGSPAI 194
DB 65 HANPRTKELTYKEMAPNARAFVGFNNWDTTSHLKNKNDGNTTLHPLENGFPAI 124
QY 195 PHGRSVKIRMDTPSGVK-DSISAWIKFSVQAPGEI-----PNGIYDPPDEEKYVFOH 247
DB 125 PHDSKIKVFIIPDGSKIRFLPAMITRATOPSKETSKQFGPAVEGRWNP--ENPYEFVH 182
QY 248 POPKPE--SLRIYESHIGSSPEPKINSYANFRDEVLEIRIKLGYNAVOIMAIQHSY 304
DB 183 PPKPSESVDLSRIYEAHAGVISPEPKITYKFTKVLPRIKYLGDAIQMAIMHAY 242
QY 305 YASFGYHTVTFAPSPRFGTPEDLKSLIDRAHELGLIYVMDIYSHSSNNTDGLNGPDG 364
DB 243 YASFGYHTVTFAPSPRFGTPEDLKSLIDRAHELGLIYVMDIYSHSSNNTDGLNGPDG 302
QY 365 TDTHYFHF--GGPRGHMMWDSRLFNYSWEVLRFLLSNARWMBEYKDFGFRPDGYSMM 422
DB 303 SHQYFHSISGSGHEPLDWSRLFNYSWEVLRFLLSNARWMBEYKDFGFRPDGYSMM 362
QY 422 YTHHGLQW--FTTGNAGEYFG--FATDVAVYVLMVNDLIQLHBD-AVSIQEDVSGM 476
DB 363 VYHNGVAGAGSSGQDYNELSRDSFVDEHALYVLMVNDLIQLHBD-AVSIQEDVSGM 422
QY 477 PFFCIPVDPGSGVGFDRLLMAVADKVIILIKQ--SDSSWKKGDIYHTITRNMLEKCTYA 535
DB 423 PFLCIPRISIGTGFDRLLMAVADKVIILIKQ--SDSSWKKGDIYHTITRNMLEKCTYA 482
QY 536 ESHDQALVGDKTLAFPLMDKDY--DEMALDRPSTPRIDRGIALHKMRLVTMGSGEGYL 594
DB 483 ESHDQALVGDKTLAFPLMDKDY--DEMALDRPSTPRIDRGIALHKMRLVTMGSGEGYL 541
QY 542 NNEGNEFGHPWLDPEFN-----VNGGSYKARARQFLADDPRLRYQNLNEBDR 590
DB 595 NNEGNEFGHPWLDPEFN-----VNGGSYKARARQFLADDPRLRYQNLNEBDR 541
QY 655 AMQHLLEKYGFMSTSEHQYVSRKHEDEKVIIFEGDVLVFNFMKNSFFDYRVCCSPGK 714
DB 591 SMQLEKRRKNTKQAVYSLKHEGDKMVFEEENMLFIFFNFPNTSYSDYRVVEKAGT 650
QY 715 YKVALDSDDALFGFSLDHDVDFTTTTPHDBRPSPFSYVTSRATVYVALTE 768
DB 651 YKVALDSDDALFGFSLDHDVDFTTTTPHDBRPSPFSYVTSRATVYVALTE 704

RESULT 6
GLGB_YIBVU
ID GLGB_YIBVU STANDARD; PRT; 715 AA.
AC Q8D9F0;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) (Glycogen branching
enzyme) (BE) (1,4-alpha-D-glucan:1,4-alpha-D-glucan 6-glucosyl-
transferase).
GN GLGB OR VV21252.

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 CC
 CC EMBL; M1544; AAB39038.1; -
 DR PIR; J00550; J00550.
 DR HAMAP; MF_00685; -; 1.
 DR InterPro; IPR006047; Alpha_amyl_cat.
 DR InterPro; IPR006407; GLGB.
 DR InterPro; IPR004193; Glyco_hydro_13N.
 DR Pfam; PF00128; alpha-amylase; 1.
 DR Pfam; PF02922; isoamylase N; 2.
 DR TIGRFAMs; TIGR01515; branching_enzyme; 1.
 DR Glycogen biosynthesis; Transferrase; Glycosyltransferase.
 KM
 FT INIT_MET 0
 FT ACT_SITE 334 334 BY SIMILARITY.
 FT ACT_SITE 369 369 BY SIMILARITY.
 FT ACT_SITE 374 374 BY SIMILARITY.
 FT ACT_SITE 437 437 BY SIMILARITY.
 FT ACT_SITE 439 439 BY SIMILARITY.
 FT ACT_SITE 492 492 BY SIMILARITY.
 FT ACT_SITE 559 559 BY SIMILARITY.
 FT ACT_SITE 560 560 BY SIMILARITY.
 SQ SEQUENCE 773 AA; 89063 MW; 52BA117CA337BF57 CRC64;

Query Match 15.0%; Score 624; DB 1; Length 773;
 Best Local Similarity 24.9%; Pred. No. 3.5e-38;
 Matches 198; Conservative 111; Mismatches 249; Indels 238; Gaps 32;

75 GKKPRVVPKPGDQKYEI-DPTLKDRSHLDVRSYRRIRAIIDHGGLEAFSGYE 133
 DB 97 GERERITYPD-----YAFRSPLITDIDIL-FAEGNHRI-----YE 132
 134 KLGF-----TRSAGITREWAPGASALYGDENNPNADDTMRDYGVWEIPLP- 185
 133 KGAHPCELENVAGVAFVAPASRNNVSIIGDFSMQGRKKHARRSGIETLPELTIV 192
 186 -----NNAOC---SPALPHGRVYKIMDPTEGVCDSISAMIKFSVQAGEIIPNGIT 234
 193 GAAYKEIKNYDGHIEKSDPYGQDEVRRKTSIVADL----- 231
 235 YDPPEEKYVF-----QHPOKRPESLRIRIESHIG-----MSSPEPK 271
 232 -----DRITWGADMLERRRHOEPLR-QPISVTEVHSGSMHAASDAIATDAQCKPLP 284
 272 IN-----SYANFDEVLPRIRLGNAYQVIAIOESHYSYASFGYVNTFFAPSS 320
 285 VPADILKPGARFLTYRELADRLIPYVDLQSHIELPIAHPPDGGMGVQVTGYVATS 344
 321 RRGTEPDKSLIRPAHELGLVLMYVSHSSNNYLDGLANGFDGTDTHYFHGPRGHHMM 380
 345 RGSPPEDFMFVVRCHONGIGVILDWPGHFKPGG-HGLAFDGTTHYEHADSQGEHRE 403
 381 WPSRLFNYSWSEVLRFLLSNARWKLSEYKDPGFPDDGVTSMNYHHGLOMFTGNVYGEY- 439
 404 WGLTVNNGGHEVRANFLAANALFWFDKXHTDGIKIVDAVASMLY-----LTYNRKEGWT 457
 440 ---FGFATDVAVVYLYLVNDLHGHPDAVSGEDVSGMPTFCIPYDDGVGVFDYRLHM 496
 458 PNEYGGRRENIEADFLRQVNHILFSYFGALSIABESGSMWVMPYVGLGFTLK--- 514
 497 AVADKTIELLKQDSWKMGDIYHTLNNRRRLKCKVYABSHD---QALVDDKTIAPFLM 553
 515 -----WNMG-----WMHMDLYFMSDPWRFQHNQNVTFISIVYA 548
 554 DKDMYDFMALDRSPSTRIDRGIALHKRIYLTVMGLGGE-----GYL----- 594

595 NFMNGEPHPEMIDPPRGQTLPTGKVLFGNNNSYDKCRRRFDLGNDF--LRY--HGM 649
 DB 600 LFMGMEFG--QWAEW-----NWV-----GDLEMTLLQYEPHQGL 631
 650 QEPDQAMHLEKRYEPMTSE-----HOYVS---RKHEEDKVIIFERGD 690
 DB 632 KQFVQDLNHLTRMAPALYSEDCNQAGFEWIDCSDNHNSIVSFTRRHESDRP-----L 684
 691 VFVFNFMNSHFDRVGCSPRGKYKVALDSDDALFGGFSRLDHDVDPYPTTEHPHNRPR 750
 DB 685 VVVCNF-TPQRAHARIGVPVAGFYREINSDABSYG-SNMGNLGKXTDEWSCHNRPF 742
 751 SPSVYTPSRITAVVAL 766
 DB 743 SLIDLPLPVLTLVLEL 758

RESULT 8
 GLGB_VIBPA STANDARD; PRT; 755 AA.
 ID GLGB_VIBPA
 AC Q87FR0;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) (Glycogen branching
 DE enzyme) (BE) (1,4-alpha-D-glucan:1,4-alpha-D-glucan 6-glucosyl-
 DE transferase).
 GN GLGB OR VPAL618.
 OS Vibrio parahaemolyticus.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrrio.
 OX NCBI_TaxID=670;
 RN [1]
 RC STRAIN=RMD 2210633 / Serotype O3:K6;
 RX MEDLINE=22508454; PubMed=12620739;
 RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
 RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
 RA Yasunaga T., Honda T., Shingawa H., Hattori M., Iida T.;
 RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
 RT distinct from that of V. cholerae.";
 RL Lancet 361:743-749 (2003).
 CC -!- FUNCTION: Catalyzes the formation of the alpha-1,6-glucosidic
 CC linkages in glycogen by scission of a 1,4-alpha-linked
 CC oligosaccharide from growing alpha-1,4-glucan chains and the
 CC subsequent attachment of the oligosaccharide to the alpha-1,6
 CC position (By similarity).
 CC -!- CATALYTIC ACTIVITY: Formation of 1,6-glucosidic linkages of
 CC glycogen.
 CC -!- PATHWAY: Glycogen biosynthesis; third step.
 CC -!- SUBUNIT: Monomer (By similarity).
 CC -!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
 CC
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 CC
 CC EMBL; AP005089; BAC62961.1; -
 DR HAMAP; MF_00685; -; 1.
 DR InterPro; IPR006047; Alpha_amyl_cat.
 DR InterPro; IPR004193; Glyco_hydro_13N.
 DR Pfam; PF00128; alpha-amylase; 1.
 DR Pfam; PF02922; isoamylase N; 1.
 DR Glycogen biosynthesis; Transferase; Glycosyltransferase;
 KM Complete proteome.
 FT ACT_SITE 330 330 BY SIMILARITY.
 FT ACT_SITE 365 365 BY SIMILARITY.

FT ACT_SITE 433 433 BY SIMILARITY.
FT ACT_SITE 435 435 BY SIMILARITY.
FT ACT_SITE 488 488 BY SIMILARITY.
FT ACT_SITE 555 555 BY SIMILARITY.
FT ACT_SITE 556 556 BY SIMILARITY.
SQ SEQUENCE 755 AA; 87504 MW; 8F052368B657D79 CRC64;

Query Match 14.9%; Score 620; DB 1; Length 755;
Best Local Similarity 25.0%; Pred. No. 6.6e-36;
Matches 193; Conservative 133; Mismatches 273; Indels 174; Gaps 30;

QY 71 ELVVGKPRV-VKPKDGGKTY--EIDPTLKFRSHLDYR-----YSEYR 112
DB 78 ELVNGEPVALERDSDSGFLKQGRDLHLYLADVDMVNEQIIDDYQYHNIYGEYE 137
QY 113 RIRALIDQHE--GGLPFSRGYKLGFTSAGGITYREMAPGASALVGDENNANNA 169
DB 138 HLHTPKDMYHMGAAHFTLERGGENI-----SGVRFVYAPHASAVSLVGCFFNQMDGR 191
QY 170 DMTTRDDYGVWEIFLNNADGSPALPHGSRKIMDPS--GVKDSISAMIKFSVQAPGE 227
DB 192 HPMQRDLGYGWIWGIPT-----PGLRSGVQYKFLKGNHGLPRKQDPWGFYSQYFS- 243
QY 228 IPFNGIYDPRPEEKYVFOHPQ-----PKRPSRLRYESHIGMSPEPKINSYANFR- 279
DB 244 --FASTYD--HKRYQMDAKMKNRAVTCRDEALSYELHAGSWKRDGK-GDFLNYRE 297
QY 280 --DEVLEIRIKLGNVAVQIAIQSHSYASFGHYTNFPAPSGRPTGTEDLKSLIDRAHE 337
DB 298 LABQLVYLVDMGYTHVLMFVSHRPFSGSWGQPVGFAPTSRYSQSDDFEFVDACHQ 357
QY 338 LGLVLMYDIHSHSNNTLDLNFQDGTTHYFGSGPHHMMMSRLFNYSMEVLEPL 397
DB 358 AGGIVVLDWVPAHPSPDD--HGLANFDGTLPHDPDRHGHODMNSYIYDLREHVRFL 416
QY 398 LSNARWMLSEYKFGFDPDVTSMYTHHGLQMTFTGNYGEYF--GFADVDVAVVYLM 453
DB 417 VSNRLYVFEQGHIDGIRVDAVASMLY-----LDVSRSHDQVPRVDGNNENYDALTLK 470
QY 454 LVNDLHGLHPDAVISIGDVSGMPTFCIPVDGQGVGPYRLHMAVADKRIELKQSDSW 513
DB 471 MNNEEVYKHPFNAMTIAEESTAFPGVSAPTFWGGIGFGFKNMWG--WM--HDSLSY 522
QY 514 KMGDIYVTLNRRRLKLVTAE-----SHDQALGDKTI-----APFLMDKM-- 557
DB 523 VKEDPRVHKVHNHTTTPPLVYAHSENYVLSHSDVVGKGSINHKMRDEDEQOQANLA 582
QY 558 --YDFMADRPSTPRIDRGIALHKMIRLVTMGLGSGYVNFNGNEFGH--PEWIDFRPGPOT 615
DB 583 YYGIM-----YQGPGR-KLNFMAELIGQTEW-- 608
QY 616 LPTGKVLPGNNNSYDKCRRPDLGDADLRLYHGMQEPDQAMQHLEKYGFMSSHOYVR 675
DB 609 -----NHDDQLQWFL--EYERHOGVQKLMEDLNLHLYRNEAM----- 644
QY 676 KHEED-----KVIIFER--GDLVFVNFMMSNPFYRGSGSRPGY 715
DB 645 --HDDCCVPAGIEWRLQDADASILAHKISKEGELLITNTTPVPHHEFRIGVPRVQY 703
QY 716 KVALDSDALFGG--FSRLDHVDVYFTTEHPHNRPRSPSVYTPSATAVVYAL 766
DB 704 ELLANTDSKRGSGSPKYL--TSVKTREKVESBSLPGSLLELLPLSTVTFYKL 753

RESULT 9
GLGB_VIBCH
ID_GLGB_VIBCH STANDARD; PRT; 666 AA.
AC Q9KNE8;
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DT 1-4-alpha-glycan branching enzyme (EC 2.4.1.18) (Glycogen branching

DE (transferase).
GN GLGB OR VCA0016.
OS *Vibrio cholerae*.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; *Vibrio*.
OX NCBI_TaxID=666;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=El Tor N16961 / Serotype O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.P., Eissen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bae S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Uterback T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Frazer C.M.,
RT "DNA sequence of both chromosomes of the cholera pathogen *Vibrio*
RT cholerae".
RL Nature 406:477-483 (2000).
CC -1- FUNCTION: Catalyzes the formation of the alpha-1,6-glucosidic
CC linkages in glycogen by scission of a 1,4-alpha-linked
CC oligosaccharide from growing alpha-1,4-glycan chains and the
CC subsequent attachment of the oligosaccharide to the alpha-1,6
CC position (by similarity).
CC -1- CATALYTIC ACTIVITY: Formation of 1,6-glucosidic linkages of
CC glycogen.
CC -1- PATHWAY: Glycogen biosynthesis; third step.
CC -1- SUBUNIT: Monomer (by similarity).
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC
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CC
CC EMBL: AE004345; AAP95930.1; --
CC PIR: D82511; D82511.
CC TIGR: VCA0016; --
CC HAMAP: MF_00685; atypical; 1.
CC InterPro: IPR006047; Alpha_amyl_cat.
CC InterPro: IPR006407; GLGB.
CC InterPro: IPR004193; Glyco_hydro_13N.
CC Pfam: PF00128; alpha-amylase; 1.
CC Pfam: PF02922; isoamylase; 1.
CC DR TIGRGRAMS: TIGR01515; branching_enzym; 1.
CC KW Glycogen biosynthesis; transferase; Glycosyltransferase;
CC complete proteome.
CC FT ACT_SITE 240 240 BY SIMILARITY.
CC FT ACT_SITE 275 275 BY SIMILARITY.
CC FT ACT_SITE 280 280 BY SIMILARITY.
CC FT ACT_SITE 343 343 BY SIMILARITY.
CC FT ACT_SITE 345 345 BY SIMILARITY.
CC FT ACT_SITE 398 398 BY SIMILARITY.
CC FT ACT_SITE 465 465 BY SIMILARITY.
CC FT ACT_SITE 466 466 BY SIMILARITY.
SQ SEQUENCE 666 AA; 77095 MW; BA538EBD93D9868 CRC64;
Query Match 14.2%; Score 592.5; DB 1; Length 666;
Best Local Similarity 25.4%; Pred. No. 6e-36;
Matches 171; Conservative 122; Mismatches 238; Indels 143; Gaps 25;


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QY 225 PGEIPIFNGIYDDPPEEKYFQ---HPQ---KREPSLRIYSHIGWSPPEKINSYAN 277
D 152 PS---FAVITYD---HRRYQWQDTAMQGRPVTEKRKQALSFYELHYG-SWKGENSEFELN 204
QY 278 FR---DEVLPRIKELGYNAVOJMALIOESHYASFGYHVTNFFAPSSRFQPEDLKSLDR 334
D 205 YRELADQVPEYLVENGYHVELMPVAHEHPFGYSWGQVGLFAPTSRYSQSPDFKIFVDL 264
QY 335 AHELGLVLMIDIVHSHSNNTLDGLNGFGDGTTHYHFGPGRGHMMWDSRLFYNGSEVL 394
D 265 CHQAGIGVLDVNPVPHFSPDS-HGLANFQGTPLFHPDPRGRGHQDMNSIYVLDGHEHR 323
QY 395 RFLLSNARWLEBYKXFGDFRFGVTSMTYTHGLQMTFTGNVGEYF---GFATDVAVY 450
D 324 RFLVANAUYFEMFHDIGIRYDAVASMLY-----LDYRSRDQMTPNVDGGRNVDALA 377
QY 451 YLMVNDLHGHHPDAVSGEDVSGMPTCIPYPDGCVGFDRYLAHNAVADKMIELKQSD 510
D 378 TFKMNNBZYKFPFPAAMTIAESTAPGVSAPTFMGGLGFGFKMNGMMHDSLSYKE-- 435
QY 511 ESMKMGDIYHTLTJNRWLEKCTYA-----ESHQALVGDXTAF-----WLMDKD 556
D 436 -----DVRHRYHNTLTPLLIYASENYVLSLSDDEVYGRSLMYKMPGDEMQOTAN 469
QY 557 MYDFMALDRPSTPRIDRGIALHMKTRLVTMGLGEGY-----LNFMGNEFGH-PEWT 607
D 490 LRAYL-----GYMTGQPKLNFMTGLGQTAEW- 518
QY 608 DFPKGPQTLPTKVLPGNNNSYDKCRRRFDLADLRLHGMGEFPOAMHLEKYGPM 667
D 519 DHDGQLQWFLT-----QPERHAGIQLYRDLNHL---YQAO 552
QY 668 SEHQ-----YYSRKHEEDKVIIFER---GDVVFVFNFMNSFPDYRVCSSBP 714
D 553 ALHQJQDCBPRGFEWRLQDNADLSVIAHERNDEKGNVLTNTTPVPQGEFRLGVPKTK 612
QY 715 YKVALDSDALFPG 728
D 613 YRLINTAKQYNG 626
RESULT 10
GLGB_NITEU STANDARD; PRT; 734 AA.
AC 081ZU6;
D 10-OCT-2003 (Rel. 42, Created)
D 10-OCT-2003 (Rel. 42, Last sequence update)
D 10-OCT-2003 (Rel. 42, Last annotation update)
D 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) (Glycogen branching
enzyme) (BE) (1,4-alpha-D-glucan:1,4-alpha-D-glucan 6-glucosyl-
transferase).
DE GLGB OR NE029.
GN Nitrosomonas europaea.
OS Nitrosomonas europaea.
OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
OC Nitrosomonadaceae; Nitrosomonas.
OX NCBI_TaxId=915;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=ATCC 19718 / IFO 14298;
RX MEDLINE=2286410; PubMed=12700255;
RA Chain P., Lamerdin J.E., Larimer F.W., Regala W., Lao V., Land M.,
Hauer L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto L.A.,
Arciero D.M., Holmes N.G., Whitaker M.M., App D.J.;
RT "Complete genome sequence of the ammonia-oxidizing bacterium and
obligate chemolithoautotroph Nitrosomonas europaea."
RL J. Bacteriol. 185(12):2759-2773(2003).
CC -1- FUNCTION: Catalyzes the formation of the alpha-1,6-glucosidic
linkages in glycogen by scission of a 1,4-alpha-linked
oligosaccharide from growing alpha-1,4-glucan chains and the
subsequent attachment of the oligosaccharide to the alpha-1,6
position (by similarity).
CC -1- CATALYTIC ACTIVITY: Formation of 1,6-glucosidic linkages of
glycogen.
```

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CC -1- PATHWAY: Glycogen biosynthesis; third step.
CC -1- SUBUNIT: Monomer (by similarity).
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; BX321863; CAD85940.1; -.
DR HAMAP; MF_00685; -; 1.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR006407; GLGB.
DR InterPro; IPR004193; Glyco_hydro_13N.
DR Pfam; PF00128; alpha-amyase; 1.
DR Pfam; PF02922; isoamyase_N; 1.
DR SMART; SM00642; Aamy; 1.
DR TIGRFAMs; TIGR01515; branching enzym; 1.
KW Glycogen biosynthesis; Transferase; Glycosyltransferase;
KM Complete proteome.
FT ACT_SITE 308 BY SIMILARITY.
FT ACT_SITE 343 BY SIMILARITY.
FT ACT_SITE 348 BY SIMILARITY.
FT ACT_SITE 411 BY SIMILARITY.
FT ACT_SITE 413 BY SIMILARITY.
FT ACT_SITE 466 BY SIMILARITY.
FT ACT_SITE 533 BY SIMILARITY.
FT ACT_SITE 534 BY SIMILARITY.
SQ SEQUENCE 734 AA; 84101 MW; AFD8499CJA49EE4 CRC64;
Query Match 13.9%; Score 579; DB 1; Length 734;
Best Local Similarity 26.0%; Pred. No. 6.9e-35;
Matches 188; Conservative 103; Mismatches 257; Indels 176; Gaps 29;
D 106 YRYSEYRIRAIIDQHEGLBAFSGYREKLGFT---SASGITYREMAPGAHSAALVGD 161
D 115 YLFNEGRLLQ-----YHMLGAHRYRNHGCVTGRFPAVPMNERGVSGVD 159
QY 162 FNNNPNNA-DTMTDDVGVWEIPLFNNAADGSAIPHGSRVYKRMTPSGVKSISAMIK 220
D 160 FNRWDGRVYPMVNVHSGVWEIPLD-----LDEGALYKYE-----IRNFIS----- 201
QY 221 SVQAPGEI-----FNGIYVPRPE-----BEKYVFOHQ---PKRP-----ESLRIYE 260
D 202 -----GELILKTDPAATYELRPNNALPTLBQKTDKDDWIARKGMDWLAFLNITY 256
QY 261 SHIG-MSSPEPKINSYANFRDEVLPRIKRLGYNAVOJMALIOESHYASFGYHVTNFFAP 318
D 257 LHVSGMKRHPDGRFYSYHDLADHLIPYLDQMGYSHELLPISEHPLDESGVYATGYFAV 316
QY 319 GSRFTPEDLKSLDRARELGLVLMIDIVHSHSNNTLDGLNGFGDGTTHYHFGGR-GR 377
D 317 TSYGSPFAFMSFVDRCHQAGIGVILDWPAFPPDSF-SLARFDGT-ALYEHEDPRLGY 374
QY 378 HMMWDSRLFYNGSEVLAELLSNARWLEBYKXFGDFRFGVTSMTYTHGLQMTFTGNVNG 437
D 375 HHWDGTYFENGRNEVKFLLSSAHYWSAFHIDGLRVDVASMLY-----LNTSRKEG 428
QY 438 EY-----GFATDVAVVYLMVNDLHGHHPDAVSGEDVSGMPTCIPYPDGCVGFDR 493
D 429 EMLNRYGHNHNLBAILFRLALNTWVHGFPALFPAESTSWPAVSRAVYGLGLGFSMK 488
QY 494 LHMVADKWTIELKQSDSKMGKGDIVHTLTNRWLEKCTYAE-----SHDQA 541
D 489 WNMG-----WM-----NDLSYMOHDPVH---RRYHNELTFOQVAYTENFVLPLSHDEV 536
QY 542 LVGDKTIAFWLMDKQVDFMLDRPSTPRIDRGIALHMKIRLY---TWGLGEGYINFMG 598
D 537 VHGXKS-----MLDKMPGD-----GMQKFAURLRLFTYQMTCPGK-KINFMG 577
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QY 599 NEFGHP-----EWIDPFRGGQILPTGKVLPGNNNSYDKCKRRRDLDGDAFLRHHM 649
Db 578 NEFGQGEHWGVGHELDWYLLERDP-----HKG 605
QY 650 QEEPDAMQHE-----EKYGFMTSEHQVYSRKHEEDKVIIFER---GDLYVFENFHW 639
Db 606 QALTRDLNHLXINPALHEIDFFAEFGSWIDCHDQGVGSVSYGRHARDGSFVLVNLFTP 665
QY 700 NSEFFDYVGGSRFGKRYVALDSDDALGCGFSRLDHDVDYTTTEPHNRRRSBSVYPSR 759
Db 666 ILRTGYVGIPIGSSAYQEVFNSSDSIYDQG-SNAGNAKGISPTGQFMSGQPSDIITLPL 724
QY 760 TAVY 763
Db 725 AGVI 728

RESULT 11
GLGB_NEIDE STANDARD, PRT, 762 AA.
ID GLGB_NEIDE
AC QGRQIS;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) (glycogen branching enzyme) (BS) (1,4-alpha-D-glucan:1,4-alpha-D-glucan 6-glucosyl-transferase).
DE GLGB.
OS Neisseria denitrificans.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
CX NCBI_TaxID=494;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=99337488; PubMed=10407163;
RX STRAIN=ATCC 14686;
RA Buetcher V., Quanz M., Willmitzer L.;
RT "Molecular cloning, functional expression and purification of a glucan branching enzyme from Neisseria denitrificans."
RL Biochim. Biophys. Acta 1432:406-412(1999).
CC -1- FUNCTION: Catalyzes the formation of the alpha-1,6-glucosidic linkages in glycogen by scission of a 1,4-alpha-linked oligosaccharide from growing alpha-1,4-glucan chains and the subsequent attachment of the oligosaccharide to the alpha-1,6 position (By similarity).
CC -1- CATALYTIC ACTIVITY: Formation of 1,6-glucosidic linkages of glycogen.
CC -1- PATHWAY: Glycogen biosynthesis; third step.
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC -----
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CC -----
CC EMBL: AF102867; AAF04747.1; -.
DR HAMAP: MF 00685; -; 1.
DR InterPro: IPR006047; Alpha_amy1_cat.
DR InterPro: IPR006407; GLGB.
DR InterPro: IPR004193; Glyco_hydro_13N.
DR Pfam: PFO0128; alpha-amy1ase; 1.
DR Pfam: PFO2922; isoamy1ase_N; 1.
DR TIGRPFAM: TIGR01515; branching_enzym; 1.
KW glycogen biosynthesis; Transferring; Glycosyltransferase.
FT ACT_SITE 312 BY SIMILARITY.
FT ACT_SITE 347 BY SIMILARITY.
FT ACT_SITE 352 BY SIMILARITY.
FT ACT_SITE 415 BY SIMILARITY.

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Query Match	Best Local Match	Similarity	Score	DB 1	Length	DB 2
Query Match	Best Local Match	Similarity	Score	DB 1	Length	DB 2
187; Conservative	126; Mismatches	227; Indels	210; Gaps	37;		
101 RSHLDYVSEYRIRRAIDQHEG--GLEAFSRGIEKLG--FTF--SAGGITYSEWAGA	153	BY SIMILARITY.				
106 REEDDYAFG-----SALQHTDALMLEGTHLRREYETLGAHFAMDGVSQVAFWAWNA	159	BY SIMILARITY.				
154 HSAALVQDFNNMNNADTM--TRDDYGVWEIFLNP-----NADG---PAIPHG	197	BY SIMILARITY.				
160 RRVAVIEFEGWDSRRHAMREHTGNGLMDFTFPGVGLNALYKESVLDAENGIRKADYA	219	BY SIMILARITY.				
198 SRVIRKQDTPSGVDOSISAMIKFSQVAPGEIFENGIIYDDPPEBEKYVQHPQKRPSLR	257	BY SIMILARITY.				
220 FGALRLPTASVVR-----GL--PAKAAAPARBRANSVEARIS	256	BY SIMILARITY.				
258 IYESHIGNSDEPKIN--SYANFDEVLPRIFKLGGINAVOIMAIQHSYTAAPGYHTN	314	BY SIMILARITY.				
257 IYEVHLGSRNPNENNMYLTQLADELVNVMKMGFHIELPSEYFPFGSWQYQATG	316	BY SIMILARITY.				
315 FFASSRRGTGEDKSLIDRAHEHGLVYMDIVHSHSNNTLDGNGFGDGTTHFGGAP	374	BY SIMILARITY.				
317 LVAPFSRFGSDDELKALIDAAHAGISVILWVAGHPTDD--KGLNTDGT--ALYEHADP	374	BY SIMILARITY.				
375 R-GHWMWDSRLFYNGSWEVLRFLISNARWMLBEYKDEGDFRPDGYTSMTYTHGLOMTFT	433	BY SIMILARITY.				
375 REGTHQDMNTLIFYNGRENVGFLQGNALYIERGFGDIVDAVASMIYRN-----YS	428	BY SIMILARITY.				
424 GNYGEY---FGATVDVAVYLMVNDLHGLHPDANSIGEDVSGMFTFCLPVPDGGV	489	BY SIMILARITY.				
429 RKDGWIPNRXGSGENLEAIAFLRQTNALVLSKSTPGAGSFAEEST--SFADVTREAGLN	485	BY SIMILARITY.				
430 FDIYRLHMAVADKMT--ELLKQDSESKMGDIHTLNRMLEKCVT-----YAE-----	536	BY SIMILARITY.				
486 FDFKNMG--WMDTLRMYOE--DPVA--KTHHGKMTFGMMYQYSENFVPL	532	BY SIMILARITY.				
537 SHDQALVADKTI-----FWLMDKM--YDFMALDRSPRPRIIDRGIALHMRILVTVWG	587	BY SIMILARITY.				
533 SHDEVHGRKSLIGMPGDCMQGFANLAVYGF-----YG	568	BY SIMILARITY.				
588 LGEGGYLPMNGNEFGH--PEWIDFPRGPOTLPTGKVLPGNNNSYDKCRRRFDLGADFLRY	646	BY SIMILARITY.				
569 FPGKTL--FMGNEFAQGREM--NYQGG-----LDM	595	BY SIMILARITY.				
647 H-----GMGFDDAMQHL-----BEKYGFMTSEHOYVSRKHEEDVITF	685	BY SIMILARITY.				
536 HILDEAGMHKGVQDYVVDLNLHITYAHAPLYQLDDQPSGF-----EWLVADSDNSVYVF	650	BY SIMILARITY.				
686 ERGD-----LVVFNF-----HMNSFFDYVVGSGSPKXYKVALDSDDALFGGFSRLDH	734	BY SIMILARITY.				
651 EKRDAQRNRIIYISNFTPVREH-----YFQGNAPORYEILNSDRTYQG--SGIAN	702	BY SIMILARITY.				
735 DVDVYFTTEPHDNRPRSPSVYTPSRVAVY	764	BY SIMILARITY.				
703 GADITAEVPSHGKAQSLTLPP--LATVY	731	BY SIMILARITY.				
RESULT 12						
GLGB RHILQ	STANDARD;	PRT;	737 AA.			
AC 0985F4;						
DT 10-OCT-2003 (Rel. 42, Last Created)						
DT 10-OCT-2003 (Rel. 42, Last sequence update)						
DT 10-OCT-2003 (Rel. 42, Last annotation update)						
DE 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) (glycogen branching enzyme) (BE) (1,4-alpha-D-glucan:1,4-alpha-D-glucan 6-glycosyl-transferase).						

GN GLGB OR MUR7587.
 OS Rhizobium loti (Mesorhizobium loti).
 CC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 CC Phyllobacteriaceae; Mesorhizobium.
 CX NCBI_TaxId=381;
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAFF303099;
 RX MEDLINE=21082930; PubMed=11214968;
 RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
 Watanabe A., Ideasa K., Ishikawa A., Kawashima K., Kimura T.,
 Kishida Y., Kiyokawa C., Kohara M., Matsuno M., Matsuno A.,
 Mochizuki Y., Nakayama S., Nakazaki N., Shimpō S., Sugimoto M.,
 Takeuchi C., Yamada M., Tabata S.,
 RA "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 Mesorhizobium loti";
 RT DNA Res. 7:331-338(2000).
 RL
 CC -1- FUNCTION: Catalyzes the formation of the alpha-1,6-glucosidic
 CC linkages in glycogen by scission of a 1,4-alpha-linked
 CC oligosaccharide from growing alpha-1,4-glycan chains and the
 CC subsequent attachment of the oligosaccharide to the alpha-1,6
 CC position (By similarity).
 CC -1- CATALYTIC ACTIVITY: Formation of 1,6-glucosidic linkages of
 CC glycogen.
 CC -1- PATHWAY: Glycogen biosynthesis; third step.
 CC -1- SUBUNIT: Monomer (By similarity).
 CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
 CC
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 CC
 CC EMBL, AP003012; BAB54018.1; -
 CC DR HAMAP, MF_00685; -1.
 CC DR InterPro: IPR006047; Glyc_hydro_cat.
 CC DR InterPro: IPR006047; Glyc_hydro_cat.
 CC DR InterPro: IPR004193; Glyco_hydro_13N.
 CC DR Pfam: PF00128; alpha-amy1ase; 1.
 CC DR Pfam: PF02922; isoamylase N; 2.
 CC DR TIGRFAMs: TIGR01515; branching enzyme; 1.
 CC Glycogen biosynthesis; Transferrase; Glycosyltransferase;
 CC Complete proteome.
 CC
 CC FT ACT_SITE 314 BY SIMILARITY.
 CC FT ACT_SITE 349 BY SIMILARITY.
 CC FT ACT_SITE 354 BY SIMILARITY.
 CC FT ACT_SITE 417 BY SIMILARITY.
 CC FT ACT_SITE 419 BY SIMILARITY.
 CC FT ACT_SITE 472 BY SIMILARITY.
 CC FT ACT_SITE 539 BY SIMILARITY.
 CC FT ACT_SITE 540 BY SIMILARITY.
 CC FT ACT_SITE 540 BY SIMILARITY.
 CC SEQUENCE 737 AA; 82525 MW; BF8BCAID72AABAEB CRC64;
 SQ
 Query Match 13.8%; Score 574; DB 1; Length 737;
 Best Local Similarity 25.7%; Pred. No. 1,6e-34;
 Matches 182; Conservative 101; Mismatches 240; Indels 184; Gaps 27;
 91 YEIDPTLKDFRSHLDYRYS-----YRIRALDQHEGLAEFRGYKLGTRSAEGI 144
 109 YSRGVPVLGPMDD--DYIAEGSHLRLPDKLGAHYIEHEG-----ATGV 148
 145 TYREAFPGAHSAALVGDFFNNMNNATM--TRDYGVAEILFPLNADSP-----ALPHGS 198
 149 HFVWMPNKKRVSVVGDFFNDWGDGRRHTRDRDGLIEVEFLPDIGARPKYKEITIGDGV 208
 199 RYKIRMDTSGVDSISAWIKFSVQAGELPFGNIYDPPREKKYVQHPQPKPESLRI 258
 209 RLPPLKAD--PFAFSELRPAALASVAVAPPAIDWG-----DEAHNYRMNDPR--EAVSI 260
 259 YESHIG--MSSPEPKINSYANFDEVLPRIKRLGYNAVQIMALQESHSYVASFGYHVTNFF 316

DB 261 YEVAHGSQQLHDDGTGLTSLWDELADRLIPVYETGTFHLTFMPSIEHPYDBSWYQITGLY 320
 317 APSRFGTPEDLKSLIDRAHEHGLVLMDIVSHSSNNLTDLGIANGDGTTHYFHGGR- 375
 321 APSARFGDPDGFARVVDGAHARGVILLDWVAPHFPVDA--HGLAHPDGT-ALYEHADPRK 378
 376 GHHMWSRLFNYSWSEVLRFLSNARWMLSEYKPDGFRFDGYSMMYTHHGLOMTGN 435
 379 GFHPDMNTAIYNFGRREVVSFLVNNALFMAEKHYVDGLVDAVASMLY-----LAYSRK 432
 436 YGEYF-----GATVDVAIVYMLVNDLHGLHPDAVISGEDYSGMPTFCIPVDDGGVFD 491
 433 AGEWIPNEKGRRENLEAVSFLQKMKKEVGHHPGVNTIAESTSWPKVASAPVEHGLGFRG 492
 492 YRLHVAVADKWIETLLKQSDSWKMGDIVTTL-----NRMLEKCVTYA----- 535
 493 FK-----WNGFMHDTLVEYFSKEPIFRKHNNDLFRGLTYAPSENF 533
 536 --ESHQALVADKTIATWLDKMDYDEPMDRSTPRIDRGIATKMRILVTMGLEGEG 592
 534 VLPISHDEVHVGKGTLLSKMAGDDWQKF-----ATLRAYYGF-----MWGYPGKK 578
 593 YLNFPGNFRFG--HPEVIDPPRGQTLPTGKVLPGNNNSYKCRRRPDLGDADFLRYHMOE 651
 579 LL-FMGQEPFAQRREWS-----AALDMLDLFRPHRW- 612
 652 PDQAMCHLEKXGPFMTSEHQVSRKHEEDKVIIFERGLVFFVNFPM-----SNSFF-- 703
 613 --QYVADNLVLYRSKPALH--GRCEPE-----GFMLVIDSDQNSVFAW 653
 704 -----DYNVGSRPGKRYKALDSDDALFEG 728
 654 VRNAPGSPVAVISNFTVPVRDNYRVPLPKAKWREIINTDASEYGG 700
 RESULT 13
 GLGB SYN3 STANDARD; PRT; 770 AA.
 ID ID GLGB SYN3 PRT; 770 AA.
 AC P52981;
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) (Glycogen branching
 DE enzyme) (BF) (1,4-alpha-D-glucan:1,4-alpha-D-glucan 6-glucosyl-
 DE transferase).
 DE
 GN GLGB OR SLL0158.
 OS Synechocystis sp. (strain PCC 6803).
 CC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
 CX NCBI_TaxId=1148;
 RN
 RP SEQUENCE FROM N.A.
 RC MEDLINE=96127529; PubMed=8590279;
 RA Sugita M., Tabata S.,
 RA Kaneko T., Tanaka A., Sato S., Kocani H., Saruka T., Miyajima N.,
 RA "Sequence analysis of the genome of the unicellular cyanobacterium
 RT Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
 RT region from map positions 64% to 92% of the genome.",
 RL DNA Res. 2:153-166(1995).
 CC -1- FUNCTION: Catalyzes the formation of the alpha-1,6-glucosidic
 CC linkages in glycogen by scission of a 1,4-alpha-linked
 CC oligosaccharide from growing alpha-1,4-glycan chains and the
 CC subsequent attachment of the oligosaccharide to the alpha-1,6
 CC position (By similarity).
 CC -1- CATALYTIC ACTIVITY: Formation of 1,6-glucosidic linkages of
 CC glycogen.
 CC -1- PATHWAY: Glycogen biosynthesis; third step.
 CC -1- SUBUNIT: Monomer (By similarity).
 CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
 CC
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 CC or send an email to license@isb-sib.ch).

CC EMBL: D63999; BAA10073.1; --
 CC PIR: S76095; S76095. --
 CC HAMAP: MF_00685; --; 1.
 CC InterPro: IPR006047; Alpha_amy1_cat.
 CC InterPro: IPR006407; GlbB.
 CC InterPro: IPR004193; Glyco_hydro_13N.
 CC Pfam: PF00128; alpha-amy1ase; 1.
 CC Pfam: PF02922; isoamylase N; 2.
 CC TRFPMs; TIGR01515; branching_enzym; 1.
 CC Glycogen biosynthesis; Transferrase; Glycosyltransferase;
 CC Complete proteome.
 CC ACT_SITE 328 BY SIMILARITY.
 CC ACT_SITE 363 BY SIMILARITY.
 CC ACT_SITE 368 BY SIMILARITY.
 CC ACT_SITE 431 BY SIMILARITY.
 CC ACT_SITE 431 BY SIMILARITY.
 CC ACT_SITE 433 BY SIMILARITY.
 CC ACT_SITE 486 BY SIMILARITY.
 CC ACT_SITE 553 BY SIMILARITY.
 CC ACT_SITE 554 BY SIMILARITY.
 CC ACT_SITE 554 BY SIMILARITY.
 CC SEQUENCE 770 AA; 89527 MW; A435AFCAT703FA8A CRC64;

Query Match 13.7%; Score 573; DB 1; Length 770;
 Best Local Similarity 25.2%; Pred. No. 2e-34;
 Matches 191; Conservative 103; Mismatches 271; Indels 192; Gaps 26;

QY 95 PTLDFRSHLYRSEYRIRALIOHSGGLAFSGRYKLG----FTRSAGITREMA 150
 DB 107 PTLDFRSHLYRSEYRIRALIOHSGGLAFSGRYKLG----FTRSAGITREMA 148
 QY 151 PGASHAALVGDPPNNNNPNADTWTTRDDYGVWFILP-----NNADG--SPAIP 195
 DB 149 PNAANVSLDGPNNMDGLHQRKKNMVMWELFIPELVGTSYKYEIKMGEHIVYKTD 208
 QY 196 HGRVKRIMDTPSGYKDISAMIKSVQAPGEIPENGIIYDPEPEEKYVQHQRPPSS 255
 DB 209 YGFYOEVAPKTASIVAD-----LDG--YQWHDDEWLERRTSDDLKRP 249
 QY 256 LRIYESHIG---MSPEP-----KINSYANFDEVLPRIKRLGY 291
 DB 250 VSVYELHSGWLHTYVDEPVKTLHGBGVVSEWNTARFLTYVLDCLIVVELGY 309
 QY 292 NAVQIMAIQESHVYASFGYHVTNFPAPSRFGTPEDLKLIDRAHELGILVMDIVHSHS 351
 DB 310 THIELPLPAHEHFDSDSGVQVGYAFTRFSGPBDPMVFVDCHLNGGVIIDWVPGH 369
 QY 352 SNNLTLDGNGPDGDTYHYHGGPR-GHHMMQDSRLFNYSWEVYLRLLSNARWMBEYK 410
 DB 370 PKDG-HGLAFPDGTHL-YEHGDPKKEHKEWGTLLINYSGEVRFNLVANALFWPDKYH 427
 QY 411 DGFRRDGYTSMYTHHGLQMTFTGVNGEY---FGFATVDVAVYLVMDLHGLHPDA 466
 DB 428 DGMRVDAVASKYI-----LDYCREGGEVANEYGERENIEADFLRQVNVSVYTFPGI 481
 QY 467 VSIGEDVSGMPTFCIPVDPGVGFYRLMA-----VADKWIELLKQSDSWMGD 517
 DB 482 LSIASESTWPMVSWFTYVGGIGFNKKMMGNHMDLIDYSDMPWRPQFQNSITFSM-- 539
 QY 518 IVHTLTNRRLKCKVY--AESHDQALVGDXTAFMLMDKMDTDFNALDPPSPRIDRG 575
 DB 540 -----WYNHSENYMLALSHDEVVHG-KSNMLGKRPEDMOKXANVR----- 579
 QY 576 ALHKMIRLVTMGAGGGLYN-FWNGEFGH-PEW-----IDPRGQTLPTGKVL 623
 DB 580 -----ALTYVFTHPGKKTMSMEFGQSEKNWMDLEMLINLPPHQD----- 624
 QY 624 GNNNSYDKRRRFDLGDADFLRYHGMQDFDQAMQHLSE-----KYGFMTSEHQYVRKA 677
 DB 625 -----LKQFTELNHLTKNEPALYSNDFDSGGFWIDCSD 659

QY 678 ESDKVIIFERGD-----LVFVFNFMNSFFDVRVGRSGPKYKVALDSDDALFGFSR 731
 DB 660 NHHSVSFFRRKAKNSAFVYITNCF--TPQPHSHYRQVVPYPGFTELFNSDARQYGG-SN 717

QY 732 LDHVDVYFTTEPHDNRPSFSVYTPSRVAVALTE 768
 DB 718 MGNLGGKWTSEWSFHQPSYSLDCLPLSLVYLKLSQ 754

RESULT 14
 GLGB_OCEIH STANDARD; PRT; 637 AA.
 AC 08C2E8;
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) (Glycogen branching
 enzyme) (B3) (1,4-alpha-D-glucan:1,4-alpha-D-glucan 6-glucosyl-
 transferase).
 GN GLGB OR OB0406.
 OS Oceanobacillus iheyensis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
 OX NCBI_TaxId=182710;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HTE81 / DSM 14371 / JCM 11309;
 RX MEDLINE=2220767; PubMed=2235376;
 RA Takami H., Takaki Y., Uchiyama I.;
 RT "Genome sequence of Oceanobacillus iheyensis isolated from the Iheya
 RT Ridge and its unexpected adaptive capabilities to extreme
 RT environments.";
 RL Nucleic Acids Res. 30:3927-3935(2002).
 CC - FUNCTION: Catalyzes the formation of the alpha-1,6-glucosidic
 CC linkages in glycogen by scission of a 1,4-alpha-linked
 CC oligosaccharide from growing alpha-1,4-glucan chains and the
 CC subsequent attachment of the oligosaccharide to the alpha-1,6
 CC position (By similarity).
 CC - CATALYTIC ACTIVITY: Formation of 1,6-glucosidic linkages of
 CC glycogen.
 CC - PATHWAY: Glycogen biosynthesis; third step.
 CC - SUBUNIT: Monomer (By similarity).
 CC - SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
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 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC EMBL: AP004594; BAC12362.1; --
 CC HAMAP: MF_00685; --; 1.
 CC InterPro: IPR006589; Alp_amy1_cat sub.
 CC InterPro: IPR006047; Alp_amy1_cat.
 CC InterPro: IPR006407; GlbB.
 CC InterPro: IPR004193; Glyco_hydro_13N.
 CC Pfam: PF00128; alpha-amy1ase; 1.
 CC Pfam: PF02922; isoamylase N; 1.
 CC SMART: SM00642; Amy1; 1.
 CC TRFPMs; TIGR01515; branching_enzym; 1.
 CC Glycogen biosynthesis; Transferrase; Glycosyltransferase;
 CC Complete proteome.
 CC ACT_SITE 202 BY SIMILARITY.
 CC ACT_SITE 237 BY SIMILARITY.
 CC ACT_SITE 242 BY SIMILARITY.
 CC ACT_SITE 305 BY SIMILARITY.
 CC ACT_SITE 307 BY SIMILARITY.
 CC ACT_SITE 361 BY SIMILARITY.
 CC ACT_SITE 428 BY SIMILARITY.
 CC ACT_SITE 429 BY SIMILARITY.
 CC SEQUENCE 637 AA; 74651 MW; 2A5165A2556A269D CRC64;

Query Match 13.7%; Score 571.5; DB 1; Length 637;
 Best Local Similarity 25.9%; Pred. No. 2e-34;
 Matches 173; Conservative 103; Mismatches 239; Indels 153; Gaps 26;

139 RAAGCTTTEEMAPGASALVDPENNNPNADMTTR-DDYGVWEIFLPNNADSGPAIPHG 197
 32 KKRGGYFAVWMAWNAKVCVGDPMNNEESHLEKRTDGLWGCFI---ADIPASYSK 88
 198 SVYKIMDPSGVKDSISAWIKESVQAPGHPFNGIY-----YDPPEEKYV 244
 69 YHICSEDDISILKADPPATQAEKRPKASVIRPANGQWSDQWIEQRNTYD----- 141
 245 FQHPQKRPESLRITYSHIG--MSPEPKINSYANPDEVLPRIKLGYNAVQIMAIQEH 302
 142 YSSP-----ISIEVHLGTWKKTKKQFLSYRELATQOLIPYKSLGYTHIELLPINEH 194
 303 SYASRGYVNTNFAFSSRGTEDKSLIDRAHELGVLVMDIVHSHSSNNTLGLNGF 362
 195 PDRSMGYQITGYFAVTSRYGNPSDFKYFDQCHQHOIGVLDWPGHFCXODF-GLRQF 253
 363 DQTDYTFYGGPGRGHMMMDSRLEFNYSWVLEFPLSNAMWLEEKYFDPGVTSM 422
 254 DQAPLYEYDPRKSEKSKWGTLAFDYGRPVQSLINATYWLKEFHIDGLRVDAVASML 313
 423 YTHHGLQMTFTNGYGEY-----FGPATVDVAVYLMVNDLHGHPDAVSIGEDV 473
 314 YL-----NFDRYDEEKIYNTYTGSEENLEAFALFKLNKVVPSYIPGALMAEDS 363
 474 SGMPTFCIPVDPGVGDVYLMHVAADKW-ELIKQSDSKMGADIVHTLNRBW----- 527
 364 SOLPLVTAIPANKGLGNYKMNNG---WMNDLL-----SMEKESGSH---RKHNNRL 410
 528 -LEKCVYAE-----SHDQALVGDKTIAFWLMDK---DWDYFVALDRPSTPRIDRGIAL 577
 411 TSPFWTYEBNLYLPLSHDEVHSGKS---LDDKMGDDQWQQA----- 451
 578 HKMIRLVTMGLGGEY-----LNMGNBFG-HRPWIDFPRGPQTL---PTGKVLFGN 625
 452 -NLRL-----YGVYVTHPGRKVLVPMGELAQYAEWKQTEELDMHLEBYLTKGI--- 500
 626 NNSYDKCRRRFDGDDFLAYHGMQGEEDQAMQHLSEKY--GFMTSEHQYVSRKHEEDVI 683
 501 -----YHYIKNINELYQHPLELYELDHLSEGEFWIIDPHNIDQSVI 540
 684 IFEK-----GDLVFVFNFMWSNFPDYRAGCSRPGRKYVALDSDDDLFGSFSRLDHDV 737
 541 ARRRKANKRQDELITCNF-TPOVHFDYKIGVPSGSKYKEIFNDSVRFSSGQINSEGH 599
 738 YETTEHPH 745
 600 FSPFEKMH 607

RESULT 15

GLGB COREF STANDARD; PRT; 731 AA.
 ID GLGB COREF
 AC 08FO12;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) (Glycogen branching enzyme) (BE) (1,4-alpha-D-glucan:1,4-alpha-D-glucan 6-glucosyl-transferase).
 DE GN GLGB OR CE1323.
 OS Corynebacterium efficiens.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacteriaceae; Corynebacteriaceae; Corynebacterium.
 OC NCB1 TaxID=152794;
 RX NCB1 TaxID=152794;
 RP SEQUENCE FROM N.A.
 RP STRAIN=VS-314 / DSM 44549 / JCM 11189;
 RX MEDLINE=22723752; PubMed=12840036;

RA Nishio Y., Nakamura Y., Kawarabayashi Y., Usuda Y., Kimura E.,
 RA Sugimoto S., Matsui K., Yamagishi A., Kinuchi H., Ikeo K.,
 RA Gojobori T.,
 RT "Comparative complete genome sequence analysis of the amino acid
 RT replacements responsible for the thermostability of Corynebacterium
 RT efficiens";
 RU Genome Res. 13:1572-1579 (2003).
 CC -1- FUNCTION: Catalyzes the formation of the alpha-1,6-glucosidic
 CC linkages in glycogen by scission of a 1,4-alpha-linked
 CC oligosaccharide from growing alpha-1,4-glucan chains and the
 CC subsequent attachment of the oligosaccharide to the alpha-1,6
 CC position (By similarity).
 CC -1- CATALYTIC ACTIVITY: Formation of 1,6-glucosidic linkages of
 CC glycogen.
 CC -1- PATHWAY: glycogen biosynthesis; third step.
 CC -1- SUBUNIT: Monomer (By similarity).
 CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
 CC
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 CC or send an email to license@sib-sib.ch).

CC EMBL: AP005218; BAC18133.1; -.
 DR HAMAP: MF_00685; -; 1.
 DR InterPro: IPR006589; Alp_amy1_cat_sub.
 DR InterPro: IPR006047; Alpha_amy1_cat.
 DR InterPro: IPR006407; GLGB.
 DR InterPro: IPR004193; Glyco_hydro_13N.
 DR Pfam: PF00128; alpha-amy1ase; 1.
 DR Pfam: PF02922; isoamy1ase_N; 1.
 DR SMART: SM00642; Amy; 1.
 DR TIGRFAMs: TIGR01515; branching enzym; 1.
 KM glycogen biosynthesis; transferase; Glycosyltransferase;
 KM Complete proteome.
 FT ACT_SITE 303 BY SIMILARITY.
 FT ACT_SITE 338 BY SIMILARITY.
 FT ACT_SITE 343 BY SIMILARITY.
 FT ACT_SITE 406 BY SIMILARITY.
 FT ACT_SITE 408 BY SIMILARITY.
 FT ACT_SITE 461 BY SIMILARITY.
 FT ACT_SITE 461 BY SIMILARITY.
 FT ACT_SITE 528 BY SIMILARITY.
 FT ACT_SITE 529 BY SIMILARITY.
 SQ SEQUENCE 731 AA; 82714 MW; 63B5690B6DBB4E CRC64;

Query Match 13.6%; Score 568.5; DB 1; Length 731;
 Best Local Similarity 26.4%; Pred. No. 4.1e-34;
 Matches 196; Conservative 124; Mismatches 264; Indels 159; Gaps 34;

75 GEKPRVVPKPGDQKIYEIDPTIKDPSRLDVRYSERIRAIIDQHE---GGLEAFSRG 131
 91 GQDPVYVADP-----YIFLPTLIGEMDTYL---ISGR-----HERLMDVLGAIVKT 133
 132 YE-KLGFTRSAEGITTYREMAFGASALVDPENNNPNADTM-TRDDYGVWEIFLPNNAD 189
 134 YETTLGQYR---GTAFAVWAPNAGIYAGVIGFNGMNASGAMSLGSGIWEIIFPN--- 187
 190 GSPALPHGSRVYKIRMDTPSG-VKDSISAMIKESVQAP--GEIFNGIYVYDPPEEKVFPQ 246
 188 ---IGPGEVYKFAIQTRGHRDKADPMARLAELPRPAGSIVY-----ESDQWQ 234
 247 HPO--PKRPE-----SLRIYESHIGMSSPEPKINSYANPDEVLPRIKLGYNAVQIMA 298
 235 DSEWMDKAEIDTATTPMSVYEVHLSGWRG---RYALATATLVLDVYVADLGTVHVEFMP 291
 299 IQEHSYVASFGYHVTNFFAPSSRFGTPEDKSLIDRAHELGVLVMDIVHSHSSNNTLDG 358
 292 VAEHFPGSGWGYQVGYVAPTSRWGSPDELRKLDIDFAHAGIGVITIDWVPAHFPKDW-A 350
 359 LNFPGCTITHYHGSRGHHMMMDLSRLFNYSWVLEFPLSNAMWLEEKYFDPGFRFDGV 418

```
Db 351 LARFDQALYEHDPWRGGEQKDWGTYFNGRSEVNFVANNALYMLSEFHVGLRVDAY 410
QY 419 TSMNTYTHGLQMTFTGNYGEY---FGFATVDVAVYIAMLVNDLIHGLHPDVAISGEDVS 474
Db 411 ASMLY-----LDYSRHEGEMERNVYGGRENLEAVQFLQENNAIVQRYHPGALITAEEST 464
QY 475 GMPTFCIPYEDGVGVEDYRLMAVADKMIELKOSDESWMKGDIVHTLTNRMLKCVTY 534
Db 465 SWPGVTAPFTWDGGIGFSLKNNMGMMNDTLEYFSK-----DPIHRSFHHNELTFSLVY 516
QY 535 A-----ESHQALVGDKTIAFWLMDKMYDPMALDRPSTPRIDRGIALHKMIRLVTM 586
Db 517 AFSERFVLPISHDEVHKGSL-W-----NMPGDTWKKAKGKRTILAYMMA 562
QY 587 GLGGEYLNFMGNEFG-HPEWIDFPRGPQTLPTGKVLPGNNNSYDKCRRRFDLGDADFLR 645
Db 563 HPQKK-LLEWGGELGQDEMSF---AHELPMG-VVEGMOGEYHE-----GISDLVR 608
QY 646 YHGNOEFDQAMQHLBEKYGFTSEHQ-----YVSRGHEE--DKVITFER-GD---LV 691
Db 609 -----ELNSTYKEVTALHQRDPSGEGFTWNRKADDAANNILVFTRRHGDGSGQAL 656
QY 692 FVFRFHMNSFPDVRVCGSRPGKXKVALDSDDALFGFS-----RLDHDVDFYFTT 741
Db 657 CVFNLS-GTSQPEYQIGVSGGSWELVLTNDEQYHGANNPLPETTEAKIDRDGFPYTT 715
QY 742 EHPHDNRPRSFVYTPSRRAVY 764
Db 716 -----TMSPMASAOFY 727
```

Search completed: April 15, 2004, 08:37:03
Job time : 21 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 15, 2004, 08:35:16 ; Search time 52 Seconds
(without alignments)
4659.961 Million cell updates/sec

Title: US-09-508-377-12
Perfect score: 4169
Sequence: 1 MATFAVSGATLVARPPAA.....PRFSVTPSRVAVYALTE 768

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_25: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_organelle: *
9: sp_phase: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_unclassified: *
15: sp_virus: *
16: sp_bacteriaph: *
17: sp_archaeo: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4169	100.0	768	10 Q9ATB5	Q9ATB5 triticum ae
2	4119.5	98.8	823	10 Q9ATU7	Q9ATU7 triticum ae
3	4113.5	98.7	823	10 P93691	P93691 triticum ae
4	4049.5	97.1	819	10 Q9ATB6	Q9ATB6 aegilops ta
5	3937	94.4	734	10 Q9ATB7	Q9ATB7 hordeum vul
6	3915	93.9	729	10 Q24397	Q24397 triticum ae
7	3685	88.4	841	10 Q96X19	Q96X19 cryza sativ
8	3588.5	86.1	814	10 Q24421	Q24421 zea mays (m
9	3362	80.6	825	10 Q40663	Q40663 cryza sativ
10	3351.5	80.4	803	10 Q7XZK7	Q7XZK7 sorghum bic
11	3351	80.4	799	10 Q81387	Q81387 zea mays (m
12	3348.5	80.3	829	10 Q9ZTB6	Q9ZTB6 hordeum vul
13	3346	79.2	922	10 Q41058	Q41058 pisum sativ
14	3307.5	79.3	870	10 Q9XIS5	Q9XIS5 phaseolus v
15	3258	78.1	800	10 Q42531	Q42531 arabidopsis
16	3258	78.1	805	10 Q9L253	Q9L253 arabidopsis

17	3257.5	78.1	868	10 Q948N7	Q948N7 ipomoea bat
18	3219	77.2	696	10 Q9ATV7	Q9ATV7 ipomoea bat
19	3207	76.9	830	10 Q49953	Q49953 solanum tub
20	3194	76.6	836	10 Q9XGA7	Q9XGA7 solanum tub
21	3192	76.6	871	10 Q9XGA5	Q9XGA5 solanum tub
22	3180	76.3	878	10 Q9XGA6	Q9XGA6 solanum tub
23	3155	75.7	858	10 Q23647	Q23647 arabidopsis
24	3135	75.2	854	10 Q42526	Q42526 arabidopsis
25	3135	75.2	882	10 Q9XGA8	Q9XGA8 solanum tub
26	2193.5	52.6	830	10 Q04074	Q04074 triticum ae
27	2189.5	52.5	775	10 Q7XZK6	Q7XZK6 hordeum vul
28	2187	52.5	852	10 Q08131	Q08131 manihot esc
29	2175.5	52.2	833	10 Q9FTU8	Q9FTU8 triticum ae
30	2173.5	52.1	810	10 Q9XGB3	Q9XGB3 triticum ae
31	2173.5	52.1	833	10 Q9XGB1	Q9XGB1 triticum ae
32	2173.5	52.1	865	10 Q9XGB2	Q9XGB2 triticum ae
33	2172.5	52.1	847	10 Q9XIS4	Q9XIS4 phaseolus v
34	2168.5	52.0	830	10 Q04864	Q04864 solanum tub
35	2166.5	52.0	820	10 Q40664	Q40664 oryza sativ
36	2161.5	51.8	820	10 Q7XZP9	Q7XZP9 oryza sativ
37	2156	51.7	832	10 Q9XGP8	Q9XGP8 sorghum bic
38	2146	51.5	823	10 Q41740	Q41740 zea mays (m
39	2138	51.3	823	10 Q84XW7	Q84XW7 zea mays (m
40	2136	51.2	702	4 Q96ENO	Q96ENO homo sapien
41	2134.5	51.2	807	10 Q9XED2	Q9XED2 triticum ae
42	2127	51.0	702	11 Q9D6T9	Q9D6T9 mus musculu
43	2099.5	50.4	826	10 Q41059	Q41059 pisum sativ
44	2059	49.4	689	3 Q96VA4	Q96VA4 aspergillus
45	2049	49.1	686	3 Q9Y8H3	Q9Y8H3 emericella

ALIGNMENTS

RESULT 1

ID Q9ATB5 PRELIMINARY; PRT; 768 AA.

AC Q9ATB5; Q9ATB5; ID Q9ATB5; PRT; 768 AA.
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Starch branching enzyme IIA variant.
OS Triticum aestivum (wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21140316; PubMed=11244112;
RA Rahman S., Regina A., Li Z., Mukai Y., Yamamoto M., Kosar-Hashemi B.,
RA Abraham S., Morell M.K.,
RT "Comparison of Starch-Branched Enzyme Genes Reveals Evolutionary
RT Relationships Among Isoforms. Characterization of a Gene for Starch-
RT Branching Enzyme IIA from the wheat D Genome Donor Aegilops
RT tauschii.";
RL Plant Physiol. 125:1314-1324(2001).
DR EMBL; AF384332; AAK26822.1; -
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0004553; F:hydrolyase activity; hydrolyzing O-glycosyl . . . ; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha-amyl_cat.
DR InterPro; IPR004193; Glyco_hydro_13N.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00128; alpha-amylase; 1.
DR Pfam; PF02922; isomylase N; 1.
SQ SEQUENCE 768 AA; 87430 MW; E0E4037755084A8F CRC64;

Query Match 100.0%; Score 4169; DB 10; Length 768;
Best Local Similarity 100.0%; Pred. No. 2e-303;
Matches 768; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 MATFAVSGATLVARPPAAQPEELQIPEDIEBQTAENVMTGCTAETLESSEPTGIVET 60

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Db      1 MATFAVSGATLGVARRPAAQPELQIPEDIEBQTAENMTGTAELDESEPTQGIIVET 60
QY      61 IIDGVTGKVELVGEKPRVVPKPGDQKIYEIDPTLKDFRSHLDYRSEYRIRAAIDQ 120
Db      61 IIDGVTGKVELVGEKPRVVPKPGDQKIYEIDPTLKDFRSHLDYRSEYRIRAAIDQ 120
QY      121 HEGGLEAFSRGYEKLGFTRSAEGITTYEWAPGAHSALVGDENNANADMTDIDYGVW 180
Db      121 HEGGLEAFSRGYEKLGFTRSAEGITTYEWAPGAHSALVGDENNANADMTDIDYGVW 180
QY      181 EITFLPNNAGSPALPHGSRVKIRMDTPSGVDSISAMIKSVQAPGEIPNGIYYDPPEE 240
Db      181 EITFLPNNAGSPALPHGSRVKIRMDTPSGVDSISAMIKSVQAPGEIPNGIYYDPPEE 240
QY      241 EKXVFGHPQPKRPESLRIYESHIGMSPEPKINSYANFRDEVLPRIKLGYNAVQIMAIQ 300
Db      241 EKXVFGHPQPKRPESLRIYESHIGMSPEPKINSYANFRDEVLPRIKLGYNAVQIMAIQ 300
QY      301 EHSYVAFGYHVTNFPAPSSRFPTBEDLKSILIDRAHELGLVMDIYHSHSNNTLDGLN 360
Db      301 EHSYVAFGYHVTNFPAPSSRFPTBEDLKSILIDRAHELGLVMDIYHSHSNNTLDGLN 360
QY      361 GPDGTTHYHGGPRGHHMMWDSLENYGSWEVLRFILSNARWMLEEYKFGFDFGVTS 420
Db      361 GPDGTTHYHGGPRGHHMMWDSLENYGSWEVLRFILSNARWMLEEYKFGFDFGVTS 420
QY      421 NMVTHGLQMTFTGNVGEYGFATDVAVVYLMVNDLIHGLHPDAYSIGEDVSGMPTFC 480
Db      421 NMVTHGLQMTFTGNVGEYGFATDVAVVYLMVNDLIHGLHPDAYSIGEDVSGMPTFC 480
QY      481 IVPDGGVGFDFRLHMAVADKMIELKQSDSWKMGDIVHTLTNRWLEKCVTYAESHDQ 540
Db      481 IVPDGGVGFDFRLHMAVADKMIELKQSDSWKMGDIVHTLTNRWLEKCVTYAESHDQ 540
QY      541 ALVGDKTIAWMDKMDYDPMALDRPSTPRIDRGIALHKMRLVTMGSGEGYLMFMGNE 600
Db      541 ALVGDKTIAWMDKMDYDPMALDRPSTPRIDRGIALHKMRLVTMGSGEGYLMFMGNE 600
QY      601 FGHPEWIDFRGPOTLPFGKVLPGNNNSYDKCRRRFDLGADFLRYHGOEFDQMOHLE 660
Db      601 FGHPEWIDFRGPOTLPFGKVLPGNNNSYDKCRRRFDLGADFLRYHGOEFDQMOHLE 660
QY      661 EKYGFMTSEHQYVSRKHEDEKVIIFERGDIVFVFNFMHNSFFDYRVGCSRGKXKVALD 720
Db      661 EKYGFMTSEHQYVSRKHEDEKVIIFERGDIVFVFNFMHNSFFDYRVGCSRGKXKVALD 720
QY      721 SDDALFGGFSRLDHDVDVFTTEHPHDNRPRSFSVYTPSRITAVVYALTE 768
Db      721 SDDALFGGFSRLDHDVDVFTTEHPHDNRPRSFSVYTPSRITAVVYALTE 768

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RESULT 2

Q9FUT7 PRELIMINARY; PRT; 823 AA.

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ID Q9FUT7 AC Q9FUT7;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Search branching enzyme 2 (EC 2.4.1.81).
GN SBE2.
OS Triticum aestivum (wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticaceae; Triticum.
OC Triticaceae; Triticum.
OC NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Cheyenne, TISSUE=Endosperm;
RA McCue K.F., Huirnan W.J., Tanaka C.K., Anderson O.D.;
RT "Search Branching Enzymes Sbel and Sbe2 from Wheat (Triticum aestivum cv. Cheyenne): Molecular Characterization, Developmental Expression, and Homolog Assignment by Differential PCR.";

```

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BL Submitted (JUL-2000) to the EMBL/Genbank/DDBJ databases.
DR EMBL; AF286319; AAC27623.1; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0004553; F:hydrolyase activity; hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0016757; F:transferase activity; transferring glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_ami1_cat.
DR InterPro; IPR004193; Glyco_hydro_13N.
DR InterPro; IPR007110; Ig_1like.
DR Pfam; PF00128; alpha-amylase; 1.
DR Pfam; PF02922; isoamylase N; 1.
KW Glycosyltransferase; Transferase.
SQ
SEQUENCE 823 AA; 92970 MW; 58915B0B65A462A CRC64;

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Query Match 98.8%; Score 4119.5; DB 10; Length 823;
Best Local Similarity 93.1%; Pred. No. 12e-299;
Matches 766; Conservative 0; Mismatches 2; Indels 55; Gaps 1;

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QY      1 MATFAVSGATLGVARRPAA----- 19
Db      1 MATFAVSGATLGVARRPAGGGLPRSSSERGGVDLPULLRKXDSRAVLSPAAPGK 60
QY      20 -----AQPFLQIPEDIEBQTAENMTGTAELDESEPTQGIIVETIDGV 65
Db      61 VLPDGSDDLSPAQPELQIPEDIEBQTAENMTGTAELDESEPTQGIIVETIDGV 120
QY      66 TKGVLELVGEKPRVVPKPGDQKIYEIDPTLKDFRSHLDYRSEYRIRAAIDQHEGGL 125
Db      121 TKGVLELVGEKPRVVPKPGDQKIYEIDPTLKDFRSHLDYRSEYRIRAAIDQHEGGL 180
QY      126 EAFSRGYEKLGFTRSAEGITTYEWAPGAHSALVGDENNANADMTDIDYGVWIEFLP 185
Db      181 EAFSRGYEKLGFTRSAEGITTYEWAPGAHSALVGDENNANADMTDIDYGVWIEFLP 240
QY      186 NNADGSPALPHGSRVKIRMDTPSGVDSISAMIKSVQAPGEIPNGIYYDPPEEKKYF 245
Db      241 NNADGSPALPHGSRVKIRMDTPSGVDSISAMIKSVQAPGEIPNGIYYDPPEEKKYF 300
QY      246 QHPQRPPESLRIYESHIGMSPEPKINSYANFRDEVLPRIKLGYNAVQIMAIQESHY 305
Db      301 QHPQRPPESLRIYESHIGMSPEPKINSYANFRDEVLPRIKLGYNAVQIMAIQESHY 360
QY      306 ASFGYHVTNFPAPSSRFPTBEDLKSILIDRAHELGLVMDIYHSHSNNTLDGLNGPDT 365
Db      361 ASFGYHVTNFPAPSSRFPTBEDLKSILIDRAHELGLVMDIYHSHSNNTLDGLNGPDT 420
QY      366 DTHYFHGPRGHHMMWDSLENYGSWEVLRFILSNARWMLEEYKFGFDFGVTSMMYTH 425
Db      421 DTHYFHGPRGHHMMWDSLENYGSWEVLRFILSNARWMLEEYKFGFDFGVTSMMYTH 480
QY      426 HGLQMTFTGNVGEYGFATDVAVVYLMVNDLIHGLHPDAYSIGEDVSGMPTFCIPVD 485
Db      481 HGLQMTFTGNVGEYGFATDVAVVYLMVNDLIHGLHPDAYSIGEDVSGMPTFCIPVD 540
QY      486 GGVGFDYRLHMAVADKMIELKQSDSWKMGDIVHTLTNRWLEKCVTYAESHDQALYGD 545
Db      541 GGVGFDYRLHMAVADKMIELKQSDSWKMGDIVHTLTNRWLEKCVTYAESHDQALYGD 600
QY      546 KTIAPWMDKMDYDPMALDRPSTPRIDRGIALHKMRLVTMGSGEGYLMFMGNEFGHPE 605
Db      601 KTIAPWMDKMDYDPMALDRPSTPRIDRGIALHKMRLVTMGSGEGYLMFMGNEFGHPE 660
QY      606 WIDPFGPOTLPFGKVLPGNNNSYDKCRRRFDLGADFLRYHGOEFDQMOHLEEKYGF 665
Db      661 WIDPFGPOTLPFGKVLPGNNNSYDKCRRRFDLGADFLRYHGOEFDQMOHLEEKYGF 720
QY      666 MTSEHQYVSRKHEDEKVIIFERGDIVFVFNFMHNSFFDYRVGCSRGKXKVALDSDAL 725
Db      721 MTSEHQYVSRKHEDEKVIIFERGDIVFVFNFMHNSFFDYRVGCSRGKXKVALDSDAL 780
QY      726 FGGFSRLDHDVDVFTTEHPHDNRPRSFSVYTPSRITAVVYALTE 768
Db      781 FGGFSRLDHDVDVFTTEHPHDNRPRSFSVYTPSRITAVVYALTE 823

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RESULT 3

P93691 PRELIMINARY; PRT; 823 AA.
 ID P93691
 AC P93691
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE 1,4-alpha-glucan branching enzyme II precursor (EC 2.4.1.18).
 GN SBE2.
 OS Triticum aestivum (Wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Triticum.
 OC NCBI_taxid=4565;
 RX STRAIN=cv. Fielder;
 RA Nair R.B., Baga M., Scoles G.J., Kartha K.K., Chibbar R.N.;
 RT "Isolation, characterization and expression analysis of a starch
 branching enzyme II cDNA from wheat.";
 RL Plant Sci. 0:0-0(0).
 DR EMBL; Y11282; CAA72154.1; -.
 DR PIR; T06574; T06574.
 DR GO; GO:0003844; F.1.4-alpha-glucan branching enzyme activity; IEA.
 DR GO; GO:0004556; F.alpha-amylose activity; IEA.
 DR GO; GO:0004553; F.hydrolyase activity, hydrolyzing O-glycosyl. . .; IEA.
 DR GO; GO:0016757; F.transferase activity, transferring glycosyl. . .; IEA.
 DR GO; GO:0005975; P.carbohydrate metabolism; IEA.
 DR InterPro; IPR006047; Alpha amyl cat.
 DR InterPro; IPR004193; Glyco_hydro_13N.
 DR InterPro; IPR007110; Ig-1like.
 DR Pfam; PF00128; alpha-amylose; 1.
 DR Pfam; PF02922; isoamylase N; 1.
 DR KX GlycoSignal; signal; Transferase.
 FT SIGNAL 1 54 POTENTIAL.
 FT CHAIN 55 823 1,4-ALPHA-GLUCAN BRANCHING ENZYME II.
 SQ SEQUENCE 823 AA; 92936 MW; 80135FA52CBA4549 CRC64;

Query Match

Best Local Similarity 98.7%; Score 4113.5; DB 10; Length 823;
 Matches 765; Conservative 0; Mismatches 3; Indels 55; Gaps 1;

QY 1 MATFAVSGATLGVARPPAA----- 19
 DB 1 MATFAVSGATLGVARPPAGAGGGLPRSGSRRGGVDDPSLLRKDSSRAVLSRAASPGK 60
 QY 20 -----AOPEELQIPEDIEQTAEVNMTGTAELKLESSSEPTQIVETITDGV 65
 DB 61 VLVPPDESDDLAPAPPEELQIPEDIEQTAEVNMTGTAELKLESSSEPTQIVETITDGV 120
 QY 66 TKGVELVVEGKERVPYKPGDGOKIYIDPTLKDPSHLDVRYSEYRIRRAIDQHEGGL 125
 DB 121 TKGVELVVEGKERVPYKPGDGOKIYIDPTLKDPSHLDVRYSEYRIRRAIDQHEGGL 180
 QY 126 EAFSRGVEKLGFRSAAGITTYRENAFAHSAALVGDNNMNPNDTMTTRDYGWEIFLP 185
 DB 181 EAFSRGVEKLGFRSAAGITTYRENAFAHSAALVGDNNMNPNDTMTTRDYGWEIFLP 240
 QY 186 NNADGSPAIHGSRYKRMPTSGVKDSISAMIKFSVOAPEIFNGIYVPPREEKVF 245
 DB 241 NNADGSPAIHGSRYKRMPTSGVKDSISAMIKFSVOAPEIFNGIYVPPREEKVF 300
 QY 246 QHPQKRPESRLIYESHIGSSPEPKINSYANFDEVLPRIKLGYNVAVOIMAIQESHY 305
 DB 301 QHPQKRPESRLIYESHIGSSPEPKINSYANFDEVLPRIKLGYNVAVOIMAIQESHY 360
 QY 306 ASGGYVNTNFASSSRGTEDLKSLLDRAHEGLVLMQIVHSHSSNNTLDGLNGPCT 365
 DB 361 ASGGYVNTNFASSSRGTEDLKSLLDRAHEGLVLMQIVHSHSSNNTLDGLNGPCT 420
 QY 366 DTHYFHGGPRGHHMMWDSRLFNYSGWELRFLSNARWMLSEYKFDGFRFGVTSMMYTH 425

RESULT 4

Q9ATB6 PRELIMINARY; PRT; 819 AA.
 ID Q9ATB6
 AC Q9ATB6
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Starch branching enzyme IIa.
 OS Aegilops tauschii (Tausch's goatgrass) (Aegilops squarrosa).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Aegilops.
 OC NCBI_taxid=37682;
 RX MEDLINE=21140316; PubMed=11244112;
 RA Rahman S., Regina A., Li Z., Mukai Y., Yamamoto M., Kosar-Hashemi B.,
 RA Abraham S., Korell M.K.;
 RT "Comparison of Starch-Branching Enzyme Genes Reveals Evolutionary
 RT Relationships Among Isoforms. Characterization of a Gene for Starch-
 RT Branching Enzyme IIa from the Wheat D Genome Donor Aegilops
 RT tauschii.";
 RL Plant Physiol. 125:1314-1324(2001).
 DR EMBL; AP338431; AA26821.1; -.
 DR GO; GO:0004556; F.alpha-amylose activity; IEA.
 DR GO; GO:0004553; F.hydrolyase activity, hydrolyzing O-glycosyl. . .; IEA.
 DR GO; GO:0005975; P.carbohydrate metabolism; IEA.
 DR InterPro; IPR006047; Alpha amyl cat.
 DR InterPro; IPR004193; Glyco_hydro_13N.
 DR InterPro; IPR007110; Ig-1like.
 DR Pfam; PF00128; alpha-amylose; 1.
 DR Pfam; PF02922; isoamylase N; 1.
 SQ SEQUENCE 819 AA; 92607 MW; E41F63050E501AA4 CRC64;

Query Match

Best Local Similarity 97.1%; Score 4049.5; DB 10; Length 819;
 Matches 754; Conservative 6; Mismatches 8; Indels 51; Gaps 1;

QY 1 MATFAVSGATLGVARPPAA----- 16
 DB 1 MATFAVSGATLGVARPPAGAGGGLPRSGSRRGGVDDPSLLRKDSSRAVLSRAASPGKVLVP 60
 QY 17 -----PAAAPPEELQIPEDIEQTAEVNMTGTAELKLESSSEPTQIVETITDGVTKGV 69
 DB 61 DDESDDLAPAPPEELQIPEDIEQTAEVNMTGTAELKLESSSEPTQIVETITDGVTKGV 120

QY 70 KELVGEKPRVVPKPDGQKIYEIDPLKDFRSHLDYRYSRRIIRAIDHGGLEAFS 129
 Db 121 KELVGEKPRVVPKPDGQKIYEIDPLKDFRSHLDYRYSRRIIRAIDHGGLEAFS 180
 QY 130 RGEXKGFRTSAGGITREMAFGAHSALVGFNNMNPADMTMRDVGWEIPLFNAD 189
 Db 181 RGEXKGFRTSAGGITREMAFGAHSALVGFNNMNPADMTMRDVGWEIPLFNAD 240
 QY 190 GSPAIPIHGSIVKIRMDTPSGVKOSISAMIKFSVQAPGEIPNGIYYDPPEEKYVFOHPQ 249
 Db 241 GSPAIPIHGSIVKIRMDTPSGVKOSISAMIKFSVQAPGEIPNGIYYDPPEEKYVFOHPQ 300
 QY 250 PKRPESLRIESHIGMSPEPKINSYANFDEVLPRIKRGYMAVQMAIOHGYVYASFG 309
 Db 301 PKRPESLRIESHIGMSPEPKINSYANFDEVLPRIKRGYMAVQMAIOHGYVYASFG 360
 QY 310 YHVTNFPAPSSRGTPEDLSLIDRAHELGILVMDIVSHSSNNITLDGLNGFGDTTHY 369
 Db 361 YHVTNFPAPSSRGTPEDLSLIDRAHELGILVMDIVSHSSNNITLDGLNGFGDTTHY 420
 QY 370 FHGGPRGHMMWMDSRLEFNYSWEVLRLSNARWLEBYKFDGFRPDGVTSMYTHGLQ 429
 Db 421 FHGGPRGHMMWMDSRLEFNYSWEVLRLSNARWLEBYKFDGFRPDGVTSMYTHGLQ 480
 QY 430 MFTTGNGEYFGPATVDVAVYIYMLVNDLIHGLHPDAVISEDVSGMPTFCIPVDDGVG 489
 Db 481 MFTTGNGEYFGPATVDVAVYIYMLVNDLIHGLHPDAVISEDVSGMPTFCIPVDDGVG 540
 QY 490 FDRLEHAAVADKMTIELKQSDSKMGDIYHTLTNRRALEKCVTAESHDQALVADKITA 549
 Db 541 FDRLEHAAVADKMTIELKQSDSKMGDIYHTLTNRRALEKCVTAESHDQALVADKITA 600
 QY 550 FWLMDKMDYFMAIDRSTPRIDRGIALHKMIRLVTMGLGEGYLNFNGNEFGHEWIDF 609
 Db 601 FWLMDKMDYFMAIDRSTPRIDRGIALHKMIRLVTMGLGEGYLNFNGNEFGHEWIDF 660
 QY 610 PRGPQTLPTGKVLPGNNNSYDKCRRRPDLGADFLRYHGMQEPQAMHLEKYGEMTSE 669
 Db 661 PRGPQTLPTGKVLPGNNNSYDKCRRRPDLGADFLRYHGMQEPQAMHLEKYGEMTSE 720
 QY 670 HOVSRRGHEEDKVIIFERGDVLFVFNFMWSNFEDYRGCSRPKGYKALDSDDALFGGF 729
 Db 721 HOVSRRGHEEDKVIIFERGDVLFVFNFMWSNFEDYRGCSRPKGYKALDSDDALFGGF 780
 QY 730 SRLDHDVYFTTEHPHNDNRRSFSVYTPSRATVAYALTE 768
 Db 781 SRLDHDVYFTTEHPHNDNRRSFSVYTPSRATVAYALTE 819

RESULT 5
 Q9ZTB7 PRELIMINARY; PRT; 734 AA.
 AC Q9ZTB7;
 DT 01-MAY-1999 (Tremblrel. 10. Created)
 DT 01-MAY-1999 (Tremblrel. 10. Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25. Last annotation update)
 DE Starch branching enzyme IIA (EC 2.4.1.18).
 GN SBE1 OR SBE1A.
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae;
 OC Triticaceae; Hordeum.
 OC Triticaceae; Hordeum.
 OC NCBI_TaxID=4513;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. BOMI;
 RX MEDLINE=98404232; PubMed=9733524;
 RA Sun C., Sathish P., Ahlstrandberg S., Jansson C.;
 RT "The two genes encoding starch-branching enzymes IIA and IIB are
 differentially expressed in barley.";
 RT Plant Physiol. 118:37-49 (1998).
 RL
 RMBL: AF064560; AAC69753 1; -

DR EMBL: AF064562; AAC72335.1; -;
 DR GO: GO:0003844; F:1.4-alpha-glucan branching enzyme activity; IEA.
 DR GO: GO:0004556; F:alpha-amylase activity; IEA.
 DR GO: GO:0004555; F:hydrolyase activity, hydrolyzing O-glycosyl. . .; IEA.
 DR GO: GO:0016757; F:transesterase activity, transferring glycosyl. . .; IEA.
 DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro: IPR004193; Glyco_hydro_13N.
 DR InterPro: IPR007110; Ig-like.
 DR Pfam: PF00128; alpha-amylase; 1.
 DR Pfam: PF02922; isoamylase; 1.
 DR GlycoSy:transesterase; Transfesterase.
 SQ SEQUENCE 734 AA; 83832 MW; DE4F0EBD30ACAF93 CRC64;

Query Match 94.4%; Score 3937; DB 10; Length 724;
 Best Local Similarity 98.5%; Pred. No. 4.6e-286;
 Matches 722; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

36 AEVNTGGAETKLESSEPTQGIYETITDGTGKELVWGEKPRVVPKPDGQKIYEIDP 95
 2 AEVNTGGAETKLESSEPTQGIYETITDGTGKELVWGEKPRVVPKPDGQKIYEIDP 61
 96 TKDFRSHLDYRYSRRIIRAIDHGGLEAFSRGYKLGFTRSAGITREMAFGAHS 155
 62 TKDFRSHLDYRYSRRIIRAIDHGGLEAFSRYKLGFTRSAGITREMAFGAHS 121
 156 AALVGDFFNNMNPADMTMRDVGWEIPLFNNDGSPAIPIHGSIVKIRMDTPSGVKOSIS 215
 122 AALVGDFFNNMNPADMTMRDVGWEIPLFNNDGSPAIPIHGSIVKIRMDTPSGVKOSIS 181
 216 AMIKFSVQAPGEIPNGIYYDPPEEKYVFOHPQPKRPESLRIESHIGMSPEPKINSY 275
 182 AMIKFSVQAPGEIPNGIYYDPPEEKYVFOHPQPKRPESLRIESHIGMSPEPKINSY 241
 276 ANFRDEVLPRIKRGYMAVQMAIOHGYVYASGCHYTNFPASSRGTPEDLSLIDRA 335
 242 ANFRDEVLPRIKRGYMAVQMAIOHGYVYASGCHYTNFPASSRGTPEDLSLIDRA 301
 336 HELGLVMDIVSHSSNNITLDGLNGFGDTTHYFHGGPRGHMMWMDSRLEFNYSWEVL 395
 302 HELGLVMDIVSHSSNNITLDGLNGFGDTTHYFHGGPRGHMMWMDSRLEFNYSWEVL 361
 396 FFLSNARWLEBYKFDGFRPDGVTSMYTHGLQMTFTGNGEYFGPATVDVAVYIYMLV 455
 362 FFLSNARWLEBYKFDGFRPDGVTSMYTHGLQMTFTGNGEYFGPATVDVAVYIYMLV 421
 456 NDLIHGLHPDAVISEDVSGMPTFCIPVDDGVGFRDRLMAVAADKIELLKQSDSKM 515
 422 NDLIHGLHPDAVISEDVSGMPTFCIPVDDGVGFRDRLMAVAADKIELLKQSDSKM 481
 516 GDIVHTLTNRRALEKCVTAESHDQALVGDKITAFLMDKMDYFMAIDRSTPRIDRG 575
 482 GDIVHTLTNRRALEKCVTAESHDQALVGDKITAFLMDKMDYFMAIDRSTPRIDRG 541
 576 ALHKMIRLVTMGLGEGYLNFNGNEFGHEWIDFPRGPQTLPTGKVLPGNNNSYDKCRR 635
 542 ALHKMIRLVTMGLGEGYLNFNGNEFGHEWIDFPRGPQTLPTGKVLPGNNNSYDKCRR 601
 636 FDIADGDFLRHYGMQEPQAMHLEKYGEMTSEHQVSRRGHEEDKVIIFERGDVLFVN 695
 602 FDIADGDFLRHYGMQEPQAMHLEKYGEMTSEHQVSRRGHEEDKVIIFERGDVLFVN 661
 696 FHMNSKDYRYGCSRPKGYKALDSDDALFGGFSRLDHDVYFTTEHPHNDNRRSFSVY 755
 662 FHMNSKDYRYGCSRPKGYKALDSDDALFGGFSRLDHDVYFTTEHPHNDNRRSFSVY 721
 756 TPSTATVAYALTE 768
 722 TPSTATVAYALTE 734

RESULT 6
 Q24397

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ID 024397 PRELIMINARY; PRT; 729 AA.
AC 024397;
DT 01-JAN-1998 (TRENBLREL. 05, Created)
DT 01-JAN-1998 (TRENBLREL. 05, Last sequence update)
DT 01-OCT-2003 (TRENBLREL. 25, Last annotation update)
DE 1,4-alpha-glucan branching enzyme (EC 2.4.1.18).
DE Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae;
OC Triticaceae; Triticum.
OC NCB1_Taxid=4565;
OK NCB1_Taxid=4565;
RN SEQUENCE FROM N.A.
RC STRAIN=cv. T.A. Florida; TISSUE=kernel 21 DAP;
RA Kroeger C., Ioez H., Luetticke S.;
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U66376; AAB17086.1; -.
DR PIR; T06797; T06797.
DR GO; GO:0003844; F:1,4-alpha-glucan branching enzyme activity; IEA.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl. . .; IEA.
DR GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_Amy1_cat.
DR InterPro; IPR004193; Glyco_hydro_13N.
DR InterPro; IPR007110; Ig-1ike.
DR Pfam; PF00128; alpha-amylase; 1.
DR Pfam; PF02922; isoamylase_N; 1.
DR GlycoStyltransferase; Transferase.
SQ SEQUENCE 729 AA; 83441 MW; 01AB2F8AC1536BCF CRC64;

Query Match 93.9%; Score 3915; DB 10; Length 729;
Best Local Similarity 98.2%; Pred. No. 2e-284;
Matches 746; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 40 MTGTAETKLESSPPTQIGVETITTDGVTKGKVELVGEKRPVVPKPGDQKIYEIDPTLKD 99
DB 1 MTGTAETKLESSPPTQIGVETITTDGVTKGKVELVGEKRPVVPKPGDQKIYEIDPTLKD 60

QY 100 FRSHLDVRYSEYRIRRAIDQHEGGLAFSGYKLGTRRAAGITTYEMPGASALV 159
DB 61 FRSHLDVRYSEYRIRRAIDQHEGGLAFSGYKLGTRRAAGITTYEMPGASALV 120

QY 160 GDMNNMNNADMTTRDDYGVWEIFLPNNADSPAIPIHRSRKIRMDTSGVDSISAMIK 219
DB 121 GDMNNMNNADMTTRDDYGVWEIFLPNNADSPAIPIHRSRKIRMDTSGVDSISAMIK 180

QY 220 FSYVAPGEIIPFNGIYYDPPEBEKTVFOHPQKPEESLRITYSHIGMSSPEPKINSYANR 279
DB 181 FSYVAPGEIIPFNGIYYDPPEBEKTVFOHPQKPEESLRITYSHIGMSSPEPKINSYANR 240

QY 280 DEVLPRIKRIGYNAVOIMAIQESHYASFGYHNTNFPAPSSRFQIPEDLKSIDRAHBLG 339
DB 241 DEVLPRIKRIGYNAVOIMAIQESHYASFGYHNTNFPAPSSRFQIPEDLKSIDRAHBLG 300

QY 340 LVLVMDLVHSHSNNTLDGLNGFDGTDTHYFHGGPRGHMMMDSLFVYSGWEVLRFLLS 399
DB 301 LVLVMDLVHSHSNNTLDGLNGFDGTDTHYFHGGPRGHMMMDSLFVYSGWEVLRFLLS 360

QY 400 NAAMWLEEKYFQDFRPGDVTSMYTHHGLQMTFTGNYSYGFATDVAVVYLMVNDLI 459
DB 361 NAAMWLEEKYFQDFRPGDVTSMYTHHGLQMTFTGNYSYGFATDVAVVYLMVNDLI 420

QY 460 HGLHPDAVSGEDVSGMPTFCIPYPDGSGFDYRLHMAVADKWITLLQSDSSMWGDIY 519
DB 421 HGLHPDAVSGEDVSGMPTFCIPYPDGSGFDYRLHMAVADKWITLLQSDSSMWGDIY 480

QY 520 HTLTNRWLEKCVYVASHDQALVQDKTIAFWLMDKMDYDFMALDRPSTPRIDRGIATLK 579
DB 481 HTLTNRWLEKCVYVASHDQALVQDKTIAFWLMDKMDYDFMALDRPSTPRIDRGIATLK 540

QY 580 MIRLVNGLGEGYLVNFMNGFHPHPIWIDFRPGQTLTGKVLPGNNNSYDKCRPRFDLG 639
DB 541 MIRLVNGLGEGSYLVNFMNGFHPHPIWIDFRPGQTLTGKVLPGNNNSYDKCRPRFDLG 600

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DB 541 MIRLVNGLGEGSYLVNFMNGFHPHPIWIDFRPGQTLTGKVLPGNNNSYDKCRPRFDLG 600
QY 640 DADFLRYHGMQEPDQAMQHLBEKRYGFMISEHQYVSRKHEBKVIIIERGDLVVFVNFHMS 699
DB 601 DAEFLRYHGMQEPDQAMQHLBEKRYGFMISEHQYVSRKHEBKVIIIERGDLVVFVNFHMS 660

QY 700 NSFEDRYVGCSPKRYKVALDSDDALFGGFSRLDHDVYDTTTHPHNRRSPSVYTPSR 759
DB 661 NSFEDRYVGCSPKRYKVALDSDDALFGGFSRLDHDVYDTTTHPHNRRSPSVYTPSR 720

QY 760 TAVVYALTE 768
DB 721 TAVVYALTE 729

RESULT 7
ID 09SX19 PRELIMINARY; PRT; 841 AA.
AC 09SX19;
DT 01-MAY-2000 (TRENBLREL. 13, Created)
DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
DT 01-OCT-2003 (TRENBLREL. 25, Last annotation update)
DE Starch branching enzyme rbe4.
DE RBE4.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OK NCB1_Taxid=4530;
RN SEQUENCE FROM N.A.
RA Mizuno K., Tachibana M., Kobayashi E., Kawasaki T., Funane K.,
RA Kobayashi M., Baba T.;
RT Molecular cloning and expression analysis of a novel member of starch
RT branching enzyme isoform in developing rice seeds.
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB023498; BAA8282.1; -.
DR Gramene; 09SX19; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl. . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_Amy1_cat.
DR InterPro; IPR004193; Glyco_hydro_13N.
DR InterPro; IPR007110; Ig-1like.
DR Pfam; PF00128; alpha-amylase; 1.
DR Pfam; PF02922; isoamylase_N; 1.
SQ SEQUENCE 841 AA; 94547A52A6216215 CRC64;

Query Match 88.4%; Score 3685; DB 10; Length 841;
Best Local Similarity 88.1%; Pred. No. 4.4e-267;
Matches 668; Conservative 37; Mismatches 43; Indels 10; Gaps 2;

QY 21 QBEHLQIPDD-----IEEQ-----TAEVNMGTGAELKLESSPPTQIGVETITTDGVTKVK 70
DB 83 QBEHLQIPDDKKYKPEEKEEIPAVLAESIKVVAEDLKLESSPPTQIGVETITTDGVTKVKAD 142

QY 71 ELVVGKRPVVPKPGDQKIYEIDPTLKDPRSHLDVRYSEYRIRRAIDQHEGGLAFSR 130
DB 143 ELVVGKRPVVPKPGDQKIYEIDPTLKDPRSHLDVRYSEYRIRRAIDQHEGGLAFSR 202

QY 131 GYEKLGFTSAGGITYREMAPGAASALVDENNNWPNADTMTDDYGVWEIFLPNADG 190
DB 203 GYEKLGFTSAGGITYREMAPGAASALVDENNNWPNADTMTDDYGVWEIFLPNADG 262

QY 191 SPAPHSGSVKIRMDPSPGVKDSISAMIKFSVAPGGEIIPFNGIYYDPPEBEKTVFOHPQ 250
DB 263 SPAPHSGSVKIRMDPSPGVKDSISAMIKFSVAPGGEIIPFNGIYYDPPEBEKTVFOHPQ 322

QY 251 KRPEESLRITYSHIGMSSPEPKINSYANFRDEVLPRIKRIGYNAVOIMAIQESHYASFGY 310
DB 323 KRPEESLRITYSHIGMSSPEPKINSYANFRDEVLPRIKRIGYNAVOIMAIQESHYASFGY 382

QY 311 HTTNFPAPSSRFQIPEDLKSIDRAHBLGLLVYLMVHSHSNNTLDGLNGFDGTDTHYF 370
DB 311 HTTNFPAPSSRFQIPEDLKSIDRAHBLGLLVYLMVHSHSNNTLDGLNGFDGTDTHYF 370

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DB 383 HTNFPAPSSRFPTEDLSKLIDKAHELGLLVLMIDVSHSHSNNTLDGNGFDGTDTHYF 442
QY 371 HGGPRHHMMWDRSLFNYGSMEVLRFLLSNARWMLLESEYKEDGFRFDGVTSMYTHHGLQM 430
DB 443 HGGPRHHMMWDRSLFNYGSMEVLRFLLSNARWMLLESEYKEDGFRFDGVTSMYTHHGLQV 502
QY 431 TPTGNYGEYGFATDVAVVYLMVNDLHGLHDAVSIGEDVGMPFICLPYDDGCVGF 490
DB 503 AFTGNYGEYGFATDVAVVYLMVNDLHGLHDAVSIGEDVGMPFICLPYDDGCVGF 562
QY 491 DYRLHAAVADKWIELKQSDSESMWKGDIIVHTLTNRRLMEKCVTAESHDQALVGDKTIAF 550
DB 563 DYRLHAAVADKWIELKQSDSESMWKGDIIVHTLTNRRLMEKCVTAESHDQALVGDKTIAF 622
QY 551 WLMDCXMYDPMALDRPSTPRIDRGIALHKMIRLVTMGVGGEGYINFMGNEFGHEMIDFP 610
DB 623 WLMDCXMYDPMALDRPSTPRIDRGIALHKMIRLVTMGVGGEGYINFMGNEFGHEMIDFP 682
QY 611 RGPQTLPTGKVLPGNNNSYDKCRPRFDLGDADFLRYHGMQSPDQAMQHLSEKYGMTSEH 670
DB 683 RGPQSLPNSGVLPNNNSYDKCRPRFDLGDADFLRYHGMQSPDQAMQHLSEKYGMTSEH 742
QY 671 QYLSRKHEEKVLIIFERGDVLFVFNFMHNSFPDYRVGCSRPGKYKVALDSDALFGGFS 730
DB 743 QYLSRKHEEKVLIIFERGDVLFVFNFMHNSFPDYRVGCLRPGKYKVALDSDALFGGFS 802
QY 731 RLDDVDVFTTEHPDNRPRSFVYTPSRITAVVYALTE 768
DB 803 RLDDVDVFTTEHPDNRPRSFVYTPSRITAVVYALTE 840

RESULT 8
024421 PRELIMINARY; PRT: 814 AA.
AC 024421;
DT 01-JAN-1998 (TRENBLrel. 05, Created)
DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Search branching enzyme Ila (EC 2.4.1.18) (Fragment).
GN SBE2A.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoidae; Andropogoneae; Zea.
CX NCBI_Taxid=4577;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=B73;
RX MEDLINE=97303618; PubMed=9159942;
RA Gao M., Fisher D.K., Kim K.N., Shannon J.C., Gultinan M.J.;
RT "Independent genetic control of maize starch-branching enzymes Ila and
RT I1b. Isolation and characterization of a Sbe2a cDNA."
RL Plant Physiol. 114:67-78(1997).
DR EMBL: U65948; AAC67316.1; -.
DR PIR: T02041; T02041.
DR GO: GO:0003844; F.1.4-alpha-glucan branching enzyme activity; IEA.
DR GO: GO:0004556; F.alpha-amylose activity; IEA.
DR GO: GO:0004553; F.hydrolyase activity; hydrolyzing O-glycosyl. . .; IEA.
DR GO: GO:0016757; F.transferase activity; transferring glycosyl. . .; IEA.
DR InterPro: IPR006047; Alpha_amy1_cat.
DR InterPro: IPR004193; Glyco_hydro_13N.
DR Pfam: PF00128; alpha-amyase; 1.
DR Pfam: PF02922; isoamyase N; 1.
DR GlycoSite: transferase; Transferase.
KM NON_TER
FT SEQUENCE 814 AA; 91866 MW; 0C88B78127511938 CRC64;

Query Match 86.1%; Score 3588.5; DB 10; Length 814;
Best Local Similarity 84.7%; Pred. No. 7e-260;
Matches 662; Conservative 32; Mismatches 49; Indels 39; Gaps 4;

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QY 11 LGVAPPAAPPEELQIPEDEIEQTAEVNMTGTAIEKLESSEPTQ----- 55
DB 38 LSSAFPVDTQPEELQIPE-----AEL-----TYEK-TSSSEPTQTTSAVAEASGVAE 85
QY 56 -----GIYETTTDGYTKVKVELVGEKPRVVPKPGGQKTYEIDPLKDRSH 103
DB 86 ERPELSEYVIGVGTGTGIXIDGAGIRAKAPLVEKEPVVIPPGGQRIYELIDMLEGRGH 145
QY 104 LDYRSEYRIRRAAIDQHEGGLAEPFRGYEKGTFTSAEGITRYENAPGAHSAALVDFN 163
DB 146 LDYRSEYRIRRAAIDQHEGGLAEPFRGYEKGTFTSAEGITRYENAPGAHSAALVDFN 205
QY 164 MNPNPADTWTBDYGVWEIIFLPNNADGSPAIPHGSFVKIRMDTPSGYKOSISAWIKSVQ 223
DB 206 MNPNPADTWTBDYGVWEIIFLPNNADGSPAIPHGSFVKIRMDTPSGYKOSISAWIKSVQ 265
QY 224 APGEIIPNGIYYDPPEEEKYVQHPQKPEESIRITESHIGMSPEPKINSYANFREVL 283
DB 266 APGEIIPNGIYYDPPEEEKYVQHPQKPEESIRITESHIGMSPEPKINSYANFREVL 325
QY 284 PRKXELGVNAVOIMAIQESHYSYASFGYHTNFPAPSSRFPTEDLSKLIDRAHELGLVL 343
DB 326 PRKXELGVNAVOIMAIQESHYSYASFGYHTNFPAPSSRFPTEDLSKLIDRAHELGLVL 385
QY 344 MDIVSHSSNNTLDGNGFDGTDTHYFHGGPRGHMMWDRSLFNYGSMEVLRFLLSNARW 403
DB 386 MDIVSHSSNNTLDGNGFDGTDTHYFHGGPRGHMMWDRSLFNYGSMEVLRFLLSNARW 445
QY 404 WLESEYKEDGFRFDGVTSMYTHHGLQMTFTGNYGEYGFATDVAVVYLMVNDLHGLH 463
DB 446 WLESEYKEDGFRFDGVTSMYTHHGLQMTFTGNYGEYGFATDVAVVYLMVNDLHGLH 505
QY 464 PDAVSIAGEDVSGMPTCIPYDDGCVGFYRLHAAVADKWIELKQSDSESMWKGDIIVHTLT 523
DB 506 PDAVSIAGEDVSGMPTCIPYDDGCVGFYRLHAAVADKWIELKQSDSESMWKGDIIVHTLT 565
QY 524 NREMLEKCVTAESHDQALVGDKTIAFWLMDCXMYDPMALDRPSTPRIDRGIALHKMIRL 583
DB 566 NREMLEKCVTAESHDQALVGDKTIAFWLMDCXMYDPMALDRPSTPRIDRGIALHKMIRL 625
QY 584 VTMGLGEGEYINFMGNEFGHEMIDFPDPRGQTLPTGKVLPGNNNSYDKCRPRFDLGDADY 643
DB 626 VTMGLGEGEYINFMGNEFGHEMIDFPDPRGQTLPTGKVLPGNNNSYDKCRPRFDLGDADY 685
QY 644 LRHGMQEPQAOHQHLEKYGMTSEHQYYSRKHEEDKVIIFERGDVLFVFNFMHNSFF 703
DB 686 LRHGMQEPQAOHQHLEKYGMTSEHQYYSRKHEEDKVIIFERGDVLFVFNFMHNSFF 745
QY 704 DYRVGCSRPGKYKVALDSDDALFGGFSRLDDVDVFTTEHPDNRPRSFVYTPSRITAVV 763
DB 746 DYRVGCSRPGKYKVALDSDDALFGGFSRLDDVDVFTTEHPDNRPRSFVYTPSRITAVV 805
QY 764 YA 765
DB 806 YA 807

RESULT 9
040663 PRELIMINARY; PRT: 825 AA.
AC 040663;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Branching enzyme-3 precursor.
GN Oryza sativa (Rice).
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Eukaryota; Viridiplantae; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Euphorbiaceae; Oryzae; Oryza.
CX NCBI_Taxid=4530;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=93366833; PubMed=8360192;

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RA Mizuno K., Kawasaki T., Shimada H., Satoh H., Kobayashi E.,
 RA Okumura S., Arai Y., Baba T.,
 RT "Alteration of the structural properties of starch components by the
 RT lack of an isoform of starch branching enzyme in rice seeds.",
 RL J. Biol. Chem. 268:19084-19091(1993).
 DR EMBL: D16201; BAA03738.1; -.
 DR PIR: A48537; A48537.
 DR Gramene; Q40653; F:alpha-amylase activity; IEA.
 DR GO; GO:0004556; F:hydrolyzing O-glycosyl . . .; IEA.
 DR GO; GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . .; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR006047; Alpha amyl cat.
 DR InterPro; IPR004193; Glyco_hydro_13N.
 DR Pfam; PF00128; alpha-amylase; 1.
 DR Pfam; PF02922; isoamylase_N; 1.
 DR Transit peptide.
 KW TRANSIT 1 65 POTENTIAL.
 FT CHAIN 66 825 BRANCHING ENZYME-3.
 FT SEQUENCE 825 AA; 92757 MW; 10B6B57B3DDE71D CRC64;
 SQ
 Query Match 80.6%; Score 3362; DB 10; Length 825;
 Best Local Similarity 80.1%; Pred. No. 6.8e-243;
 Matches 602; Conservative 68; Mismatches 72; Indels 10; Gaps 2;
 QY 17 PAAAPDEEIQIPEDIEQTAENVTGTAETKSSSEPTGIVETITDGTGKVELVYGE 76
 DB 84 PVSAGSDDLQPLMDLDELSTEV---GAEEVEISSGASD-----VEGVKRVLELAAEQ 133
 QY 77 KPRVVPKPDGQKIYEIDPTLKDFRSHLDYRSEYRIRARAIQDHEGGLAENFSGYEKL 136
 DB 134 KRRVVPPTDGGQKIFQMDSLNGKYHLEYRYSLYRRLRSIDIDYEGGLETFSGYEKFG 193
 QY 137 FTRSAEGITTYREMAFGAHSAAALVGDENNMPNADTWTTRDYGVEITFLPNNADGSPALPH 196
 DB 194 FHSAGVITYREMAFGAHSAAALVGDENNMPNADTWTTRDYGVEITFLPNNADGSSPLPH 253
 QY 197 GSRVKTIRMTDPSGVNDSISMIKFSVQAPGEIPNGIYDPEEEKVYFQHPKRPESL 256
 DB 254 GSRVKTIRMTDPSGVNDSISMIKFSVQAPGEIPNGIYDPEEEKVYFQHPKRPESL 313
 QY 257 RIYESHIGSSPEPKINSYANFRDEVLPRIKLGYNVAOIMAIQESHYSYASFGYHVTNF 316
 DB 314 RIYETHVGNSTPEPKINTYANFRDEVLPRIKLGYNVAOIMAIQEHAYVSGFYHVTNF 373
 QY 317 APSRSFGTPEDLKSLIDRAHELGLLVMDIVSHSSNNNTLDGLNGFGDTTHYHGGPRG 376
 DB 374 APSRSFGTPEDLKSLIDRAHELGLLVMDIVSHSSNNNTLDGLNGFGDTTHYHGGPRG 433
 QY 377 HHMMMSRLFNYSWEYLRFLLSNARWLEBYKDFGRPDGVTSMYTHHGLQMTFGNY 436
 DB 434 HHMMMSRLFNYSWEYLRFLLSNARWLEBYKDFGRPDGVTSMYTHHGLQMTFGNY 493
 QY 437 GEYFGPATDVAVYVLMVNDLIHGHPDAVSIGEDYSGMPTFCIPYDGGVGEDYRLHM 496
 DB 494 SEYFGPATDVAVYVLMVNDLIHGHPDAVSIGEDYSGMPTFCIPYDGGVGEDYRLHM 553
 QY 497 AVADKMIELIKQSDSWKMGDIYHTLTNRNMLEKCVTYAESHDOALVGDKTIAFWLMDX 556
 DB 554 AVADKMIELIKQSDSWKMGDIYHTLTNRNMLEKCVTYAESHDOALVGDKTIAFWLMDX 613
 QY 557 MDPFMLDPRSTRIDGIALHKMIRLVMTGLGEGYLNFENSGFHEMTDFPRGPOTL 616
 DB 614 MDPFMLDPRSTRIDGIALHKMIRLVMTGLGEGYLNFENSGFHEMTDFPRGPOTL 673
 QY 617 PTGKVLPGNNNSYDKCRRREFLDGADFLRYHGOEFDQAMQHEKTYGFMTEHQYVSRK 676
 DB 674 PTKGVLPGNNNSYDKCRRREFLDGADFLRYHGOEFDQAMQHEKTYGFMTEHQYVSRK 733
 QY 677 HEEDKVIIFERRGDLVYVFNTHMSNFPDYRVCGRPGKYKALSDDALPFGFSRLDDV 736
 DB 734 HEEDKVIIFERRGDLVYVFNTHMSNFPDYRVCGRPGKYKALSDDALPFGFSRLDDV 793
 QY 737 DYETTEHPHNRPSFSVTPSPRAVYVYALTE 768

DB 794 EHFADGSHDNRPFYSFYSVSPSRTCVVYAPAE 825
 RESULT 10
 QYXZK7 PRELIMINARY; PRT; 803 AA.
 ID QYXZK7
 AC QYXZK7
 DT 01-OCT-2003 (TREMBlrel. 25, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Starch branching enzyme IIb (EC 2.4.1.18).
 GN SBE11B.
 OS Sorghum bicolor (Sorghum) (Sorghum vulgare).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Panicoideae; Andropogoneae; Sorghum.
 OC NCBI_TaxId=4558;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Kari-Williams;
 RA Mutista J., Satish P., Sun C., Anderson L., Ahlandsberg S.,
 RA Baguma Y., Palmqvist S., Odhiambo B., Aman P., Jansson C.;
 RT "Starch branching enzymes in sorghum (Sorghum bicolor) and barley
 RT (Hordeum vulgare): Comparative analyses of enzyme structure and gene
 RT expression.";
 RL J. Plant Physiol. 0:0-0(2003).
 DR EMBL; AY304540; AAP72267.1; -.
 KW Glycosyltransferase; Transferase.
 SQ SEQUENCE 803 AA; 90757 MW; C5CD321D2C8F7E1 CRC64;
 Query Match 80.4%; Score 3351.5; DB 10; Length 803;
 Best Local Similarity 75.3%; Pred. No. 4e-242;
 Matches 609; Conservative 78; Mismatches 75; Indels 47; Gaps 4;
 QY 1 MATFAVSGATLGA-----RPPAA 20
 DB 1 MAFAVSGALGAVARAPLTGEEGLSVRRTPFLTRAGARVGGSTGHAMRAAAS 60
 QY 21 QPEEIQIPEDIEQTAENVTGTAETKSSSEPTGIVETITDGTGKVELVGEKPR 79
 DB 61 SRKAVVAEDENDGLASKDSAQFQSDLEVPVTE---ETMKDA---GVADQALNRVR 114
 QY 80 VYKPDGQGIYEIDPTLKDFRSHLDYRSEYRIRARAIQDHEGGLAENFSGYEKLGFTR 139
 DB 115 VYKPDGQGIYEIDPTLKDFRSHLDYRSEYRIRARAIQDHEGGLAENFSGYEKLGFTR 174
 QY 140 SAEGITTYREMAFGAHSAAALVGDENNMPNADTWTTRDYGVEITFLPNNADGSPALPH 199
 DB 175 SAEGITTYREMAFGAHSAAALVGDENNMPNADTWTTRDYGVEITFLPNNADGSPALPH 234
 QY 200 VKIRMDTPSGVNDISAMTKFSVQAPGEIPNGIYDPEEEKVYFQHPKRPESLRIY 259
 DB 225 VYKMDTPSGVNDISAMTKFSVQAPGEIPNGIYDPEEEKVYFQHPKRPESLRIY 294
 QY 260 ESHIGSSPEPKINSYANFRDEVLPRIKLGYNVAOIMAIQESHYSYASFGYHVTNF 319
 DB 295 ESHIGSSPEPKINSYANFRDEVLPRIKLGYNVAOIMAIQESHYSYASFGYHVTNF 354
 QY 320 SRFGTPEDLKSLIDRAHELGLLVMDIVSHSSNNNTLDGLNGFGDTTHYHGGPRGHW 379
 DB 355 SRFGTPEDLKSLIDRAHELGLLVMDIVSHSSNNNTLDGLNGFGDTTHYHGGPRGHW 414
 QY 380 MDSLFLNYSWEYLRFLLSNARWLEBYKDFGRPDGVTSMYTHHGLQMTFGNYGEY 439
 DB 415 MDSLFLNYSWEYLRFLLSNARWLEBYKDFGRPDGVTSMYTHHGLQMTFGNYGEY 474
 QY 440 PFGATDVAVYVLMVNDLIHGHPDAVSIGEDYSGMPTFCIPYDGGVGEDYRLHNAVA 499
 DB 475 PFGATDVAVYVLMVNDLIHGHPDAVSIGEDYSGMPTFCIPYDGGVGEDYRLHNAVA 534
 QY 500 DKMIELIKQSDSWKMGDIYHTLTNRNMLEKCVTYAESHDOALVGDKTIAFWLMDKMYD 559

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Db 535 DKMIEFLKSDKDEAKMGDIHTLTNRRLKCVTAESHQALVGDKTIAFWLMDKMD 594
Qy 560 FMAIDPSTPRIDRGIALHNMIRLVTVGLGEGYALNFMNGEFGHPREWIDPRGQTLPTG 619
Db 595 FMAIDPSTPRIDRGIALHNMIRLVTVGLGEGYALNFMNGEFGHPREWIDPRGQTLPTG 654
Qy 620 KYLPNNNSYDKCRRRFDLGDADLRYHGMQEFQAMQHEBKXGFMISEHQYVSRKHE 679
Db 655 KFIPIKNNNSYDKCRRRFDLGDADLRYHGMQEFQAMQHEBKXGFMISEHQYVSRKHE 714
Qy 680 DKIIIFERGLVVFENFMHNSFEFDYVGSRGPKYKVALDSDALFGSGFRLDHDVDF 739
Db 715 DKMIEFLKSDKDEAKMGDIHTLTNRRLKCVTAESHQALVGDKTIAFWLMDKMD 774
Qy 740 TTEPHDNRPSFVSPTPSRTAVVYALTE 768
Db 775 TTDSHNRPSFVSPTPSRTAVVYALTE 803

RESULT 11
ID 081387 PRELIMINARY; PRT; 799 AA.
AC 081387;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Search branching enzyme IIB.
GN Zea mays (Maize).
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxId=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. B73;
RA Kim K.-N., Fisher D.K., Gao M., Guitman M.J.,
RT Molecular cloning and characterization of the amylose-extender gene
RT encoding starch branching enzyme IIB in maize.
RT Submitted (JUN-1998) to the EMBL/Genbank/DBD databases.
RL EMBL; AF072725; AAC33764.1; -.
DR DR EMBL; AF072725; AAC33764.1; -.
DR GO; GO:0004556; F:alpha-amylose activity; IEA.
DR GO; GO:000507; F:copper ion binding; IEA.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0005453; F:hydrolyase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006047; AlphaAmy1_cat.
DR InterPro; IPR000923; AlphaAmy1.
DR InterPro; IPR004193; Glyco_hydro_13N.
DR Pfam; PF00128; alpha-amylose; 1.
DR Pfam; PF02922; isoamylose_N; 1.
DR PROSITE; PS00196; COPPER_BLUE; 1.
SQ SEQUENCE 799 AA; 90665 MW; 4FD7B1EBC3B759F0 CRC64;

Query Match 80.4%; Score 3351; DB 10; Length 799;
Best Local Similarity 78.5%; Pred. No. 4,3e-242;
Matches 609; Conservative 68; Mismatches 77; Indels 22; Gaps 4;
4 FAVSGATIGV-----ARPAQAQPEELQIPEDIEQTAENVMTGTAKLESSE----- 52
35 FLTRGARVCSGTHGMRAAAARAKAVMVEGEND-----GLASRADSQFOSDEL 85
53 PNOGIVETITDGVTKVKELVGEKRVVKKPKDGQKIVIEDPLTKDFRSHLDVRYSEYR 112
86 EYVDISEETTCGA--GVADAQALNRRVVPSPDGGQIFQIDPVLQGYKTHLEIRYSLIR 143
113 RTAAIDQEGGEGEASRGYKLGTRRSAGITRYEWAFAHSAALVGDENNMMNPNADTM 172
144 RIRSDIDHEGGLEASRSYKKGFRNSAGITRYEWAFAHSAALVGDENNMMNPNADTM 203

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Qy 173 TRDQYWEIFLNNADGSPALPHGSRYKIRMDTSGVSDISAMWIKFSVQABGEIIFNG 232
Db 204 SKNEGWEIFLNNADGSPALPHGSRYKIRMDTSGVSDISAMWIKFSVQABGEIIFNG 263
Qy 223 IYDPEEKEKYVFOHPPKRPESLRITYESHIGNSPEPKINSYANRDEYLPRIKRGYN 292
Db 264 IYDPEEKEKYVFOHPPKRPESLRITYESHIGNSPEPKINSYANRDEYLPRIKRGYN 323
Qy 293 AVQIALIGHSYYASFGYVTVTFPAASSRFGPEDEKSLIDRAHEGLVLMIVHSSS 352
Db 324 AVQIALIGHSYYASFGYVTVTFPAASSRFGPEDEKSLIDRAHEGLVLMIVHSSS 383
Qy 353 NNTLDGLNGFDGTDTHYFHGPRGHMMDSRLFNYSMEVLRFLSNARWMLBEYKFDG 412
Db 384 NNTLDGLNGFDGTDTHYFHGPRGHMMDSRLFNYSMEVLRFLSNARWMLBEYKFDG 443
Qy 413 PRFDGVTSMYTHHGLQMTFTGNYGEYFGFADVDVAVYMLVNDLHGHHPDAVSGED 472
Db 444 PRFDGVTSMYTHHGLQMTFTGNYGEYFGFADVDVAVYMLVNDLHGHHPDAVSGED 503
Qy 473 VSGMPFPCIPVDPGGVGPDPYRLMAVADKIELLKOSDESQKMGDIHTLTNRRLKCV 532
Db 504 VSGMPFPCIPVDPGGVGPDPYRLMAVADKIELLKOSDESQKMGDIHTLTNRRLKCV 563
Qy 533 TYAESHQALVGDKTIAFWLMDKMDYFMAIDPSTPRIDRGIALHNMIRLVTVGLGEG 592
Db 564 TYAESHQALVGDKTIAFWLMDKMDYFMAIDPSTPRIDRGIALHNMIRLVTVGLGEG 623
Qy 593 YLNFMGNEGHPMIDFPRGQTLPTGKVLPGNNNSYDKCRRRFDLGDADLRYHGMQEF 652
Db 624 YLNFMGNEGHPMIDFPRGQTLPTGKVLPGNNNSYDKCRRRFDLGDADLRYHGMQEF 683
Qy 653 DQAMQHEBKXGFMISEHQYVSRKHEBKXIIIFERGLVVFENFMHNSFEFDYVGSRG 712
Db 684 DQAMQHEBKXGFMISEHQYVSRKHEBKXIIIFERGLVVFENFMHNSFEFDYVGSRG 743
713 GYKVALDSDALFGSGFRLDHDVDFTEPHDNRPSFVSPTPSRTAVVYALTE 768
744 GYKVALDSDALFGSGFRLDHDVDFTEPHDNRPSFVSPTPSRTAVVYALTE 803

RESULT 12
ID 092786 PRELIMINARY; PRT; 829 AA.
AC 092786;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Search branching enzyme IIB.
GN SBE1 OR SBE1B.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Hordeum.
OX NCBI_TaxId=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. BOMI;
RA Sun C., Sachish P., Ahlstrandberg S., Jansson C.,
RT "The two genes encoding starch-branching enzymes IIA and IIB are
RT differentially expressed in barley."
RL Plant Physiol. 118:37-49 (1998).
DR EMBL; AF064561; AAC69754.1; -.
DR EMBL; AF064563; AAC72336.1; -.
DR GO; GO:0004556; F:alpha-amylose activity; IEA.
DR GO; GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; AlphaAmy1_cat.
DR InterPro; IPR004193; Glyco_hydro_13N.
DR Pfam; PF00128; alpha-amylose; 1.
DR Pfam; PF02922; isoamylose_N; 1.

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KM	Glycosyltransferase; Transferase.	
8Q	SEQUENCE 829 AA; 93602 MW; E915BDEFB3E0604 CRC64;	
Query Match	80.3%; Score 3348.5; DB 10; Length 829;	
Best Local Similarity	79.1%; Pred. No. 7e-242;	
Matches 605; Conservative	72; Mismatches 75; Indels 13; Gaps 3;	
QY	8 GATLGVARPPAAA-----OPEELQIP--EDIEBQTAVNNMTGGFAEKLESSEPTQGIYET 60	
DB	68 GSSGSGSCTPPSITBSGVQFESDDLEVPFID-----PSLHDDGEEDITRSSETQVTEI 121	
QY	61 ITDGVTKGVKELVNGEKPRVVPKPGDGQKIYEIDPTLKDRSHLDYRSEYRIRRAIDQ 120	
DB	122 DAGVSRMDKESTVAKIRIVPQPGNQQIYDIDPMLDRPKYHLEHYSLYRIRRSIDE 181	
QY	121 HEGGLEAFSRGYEKLQFTRSABGITTREMAPGAASALVGDENNMMNADTMTEDYGVW 180	
DB	182 YDGMADVFSRGYEKFGFVVSABGITYREMAPGADSAALVDEFNWMDPTADHMSKNDLGITW 241	
QY	181 EFLFPNNADGSPAIPHGSRYKIRMDIPSGVCDISAMIKFSVOAGRIPIENGIIYDDPEE 240	
DB	242 EFLFPNNADGSPPIPHGSRYKVRMDIPSGTKDSIPAWIKTSVQTPGDIPIYNGIIYDDPEE 301	
QY	241 EKYVFOHPQPKRPESLRIYESHIGMSSPEPKINSYANFRDEVLPRIKLGYNVQVAINAQ 300	
DB	302 EKYVFOHPQPKRPSKIRIYETHYGMSSPEPKINTYANFRDEVLPRIKLGYNVQVAINAQ 361	
QY	301 EHSYIASFGIHYNTNFPAPSGRFGTPEDDKSLIDRAHELGLLVMDIYHSSSNNTLDGLN 360	
DB	362 EHSYISFGIHYNTNFPAPSGRFGSPEDLKSLIDRAHELGLLVMDIYHSSSNNTLDGLN 421	
QY	361 GPDGDTHTFHGGSPRGHMMWMSRLFNYSWEYLRLISNARWLEBYKXPDGFEFGDVS 420	
DB	422 GPDGDTHTFHGGSRGHMMWMSRVFNYSKEVIRFLISNARWLEBYKXPDGFEFGDVS 481	
QY	421 NMYTHGLQMTFTGNYGEGYGFATDYDAVYVLYMLVNDLIGHLPDAVSIQEDVSGMPTFC 480	
DB	482 NMYTHGLQVTFPGSYHEFYGFATDYDAVYVLYMLVNDLIGHLPDAVSIQEDVSGMPTFC 541	
QY	481 IVPDGGVGFDRILHMAVADKMIELIKQSDPSWKMGIYHTLTNRRLKCVTYAESHDQ 540	
DB	542 IVPQVGVGFDRILHMAVADKMIELIKQSDPSWKMGIYHTLTNRRLKCVTYAESHDQ 601	
QY	541 ALVGRKTIAPWMDKMYDPMALDRPSTPRIDRGILAHKMIRLVTMGLGEGYINFMGNE 600	
DB	602 ALVGRKTIAPWMDKMYDPMALDRPSTPRIDRGILAHKMIRLVTMGLGEGYINFMGNE 661	
QY	601 FGHPEWIDPRPGQVLPPTGKVLTPGNNSYDKCRRRPFGLDADFLRYHGMQFDDAMQLE 660	
DB	662 FGHPEWIDPRPGQVLPPTGKVLTPGNNSYDKCRRRPFGLDADFLRYHGMQFDDAMQLE 721	
QY	661 EKYGMTSCHOYVSRKHEEDKVIIPERGLIVYVFNFMWSNFPDYRVGCRPPKRYKALD 720	
DB	722 EKYGMTSCHOYVSRKHEEDKVIIPERGLIVYVFNFMWSNFPDYRVGCRPPKRYKALD 781	
QY	721 SDDALFGFSPRLDHDVDYFTTEHPHNDNRPSPSVYVPTSTAVVYA 765	
DB	782 SDAGLFGFGRIHHTGEHFTNGCQHDNRPHSFSVYIPTSRTCVYA 826	

QY	20 APEELQIPED-----IEBQTAVNNMTGGFAEKLE----- 49	
DB	62 AESDVLIIPEDQDNSVSLADQLENPDITSEDAQNEDLTMTKQGNKYINDESTSYEVDG 121	
QY	50 --SSEPFGIYETITDGYTKGVK---ELVVEKPRVVPKPGDGQKIYEIDPTLKDRSH 103	
DB	122 EKGSTSSLDVNDVTQAKTQSVSHDKVKVKKPIIPPFGGQKIYEIDPTLQARQH 181	
QY	104 LDYRSEYRIRRAAIDQHEGLEAFSRGYEKLQFTRSABGITYREMAPGAHSAALVGFEN 163	
DB	182 LDFRGGQKRIREIDKXEGGLDASRGYEKGFTRSAIGITYREMAPGAKSAALVGFEN 241	
QY	164 NNNPNADTMTEDYGVWEIIFLNNADGSPAIPHGSRVKIRMDTPSGVKDSISAMIKFSVQ 223	
DB	242 NNNPNADTMTEDYGVWEIIFLNNADGSPAIPHGSRVKIRMDTPSGVKDSISAMIKFSVQ 301	
QY	224 APGEIPIYNGIYDDPEEEKYVQHOPKRPBSLRIYESHIGMSSPEPKINSYANFRDEV 283	
DB	302 APGEIPIYNGIYDDPEEEKYVQHOPKRPBSLRIYESHIGMSSPEPKINTYANFRDEV 361	
QY	284 PRIKLGYNVQVAINAQIHSYASFGYHTNFPAPSGRFGTPEDDKSLIDRAHELGLLV 343	
DB	362 PRIKLGYNVQVAINAQIHSYASFGYHTNFPAPSGRFGTPEDDKSLIDRAHELGLLV 421	
QY	344 MDIYHSSSNNTLDGANGFDGDTHTYFHGPGRGHMMWMSRLFNYSWEYLRLISNARW 403	
DB	422 MDIYHSSSNNTLDGANGFDGDTHTYFHGPGRGHMMWMSRLFNYSWEYLRLISNARW 481	
QY	404 MLEBYKPGFRFDGYTSMYTHHGLQMTFTGNYGEGYGFATDYDAVYVLYMLVNDLIGHL 463	
DB	482 MLEBYKPGFRFDGYTSMYTHHGLQMTFTGNYGEGYGFATDYDAVYVLYMLVNDLIGHL 541	
QY	464 PDVASIGDVGMPFTCIIPVDGGVGFDRILHMAVADKMIELIKQSDPSWKMGIYHTLT 523	
DB	542 PDVASIGDVGMPFTCIIPVDGGVGFDRILHMAVADKMIELIKQSDPSWKMGIYHTLT 601	
QY	524 NRRWLEKCVTYAESHDQALVGDXTIAFWLMDXMDTDMALDRPSTPRIDRGILAHKMIRL 583	
DB	602 NRRWLEKCVTYAESHDQALVGDXTIAFWLMDXMDTDMALDRPSTPRIDRGILAHKMIRL 661	
QY	584 VTMGLGEGYINFMGNEGRHPWIDPRPGQVLPPTGKVLTPGNNSYDKCRRRPFGLDADF 643	
DB	662 ITMGIGGGYINFMGNEGRHPWIDPRPGQVLPPTGKVLTPGNNSYDKCRRRPFGLDADF 721	
QY	644 LRYHGMQFDDAMQLEBYKXGFMTSCHOYVSRKHEEDKVIIPERGLIVYVFNFMWSNFP 703	

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Db 722 LRYHGMQEPFRAMQHLERXYGFMTESEHQYISRKNEGDRVILFERDNLVFVFNFMNTNSYS 781
QY 704 DYKXGCRSPGKRYKVALDSDDLFGGFSRLDHDVDYFTTEHPHNDNPRPSVYTPBRTAVY 763
Db 782 DYKXGCRSPGKRYKVALDSDDLFGGFSRLDHDVDYFTTEHPHNDNPRPSVYTPBRTAVY 841
QY 764 YALTE 768
Db 842 YALAD 846

RESULT 14
QX15S PRELIMINARY; PRT; 870 AA.
ID 09X15S
AC 09X15S;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Branching enzyme 1 precursor (EC 2.4.1.18).
KBEL.
OS Phaseolus vulgaris (Kidney bean) (French bean).
OC Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.
NCBI_Taxid=3885;
RN [1]
RP SEQUENCE FROM N.A.
RA Nozaki K., Ito H., Matsui H., Honma M.,
RT "Phaseolus vulgaris L. mRNA for starch branching enzyme 1.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB029548; BAA82348.1; -
DR GO; GO:0003844; F:1.4-alpha-glucan branching enzyme activity; IEA.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0004553; F:hydrolase activity; hydrolyzing O-glycosyl. . .; IEA.
DR GO; GO:0016757; F:transferase activity; transferring glycosyl. . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro: IPR006047; Alpha amyl cat.
DR InterPro: IPR004193; Glyco_hydro_13N.
DR Pfam: PF00128; alpha-amylase; 1.
DR Pfam: PF02922; isoamylase_N; 1.
DR GlycoStL:transferrase; Transferrase; Transferrase.
KW TRANSIT 1 156 POTENTIAL.
SQ SEQUENCE 870 AA; 98891 MW; BDB5C028B6694EC CRC64;

Query Match 79.3%; Score 3307.5; DB 10; Length 870;
Best Local Similarity 76.3%; Pred. No. 8.9e-235;
Matches 601; Conservative 72; Mismatches 78; Indels 37; Gaps 4;

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QY 341 LVLMDIVSHSSNNNTLDGNGFDGDTIDHYFHGGRGHMMWDSRLFYNGSWELRFLSN 400
Db 418 LVLMDIVSHSSNNNTLDGNGFDGDTIDHYFHGGRGHMMWDSRLFYNGSWELRFLSN 477
QY 401 ARWLEERYKFDGFRPGVTSMTTHGLQMTFTGNICEYGFATDVDAVYVLMVNDLIH 460
Db 478 ARWLEERYKFDGFRPGVTSMTTHGLQMTFTGNICEYGFATDVDAVYVLMVNDLIH 537
QY 461 GLHPDAVSIQEDVSGMPTFCIPVDDGVGFDYRLHMAVAWKIILLKQSDSMWKGDIYH 520
Db 538 GLFPEAVITIGEDVSGMPTFCIPVDDGVGFDYRLHMAVAWKIILLKQSDSMWKGDIYH 597
QY 521 TLNRRMLEKCVTYAASHDQALVGDKTIAFMWDKMDYDPMALDRPSTPRIDRIGIALHKM 580
Db 598 TLNRRMLEKCVTYAASHDQALVGDKTIAFMWDKMDYDPMALDRPSTPRIDRIGIALHKM 657
QY 581 IRLVTMGLGEGYGLANNGNEFGHPENIDFPRGQTLPTGKYLPGNNNSYDCRRRFDLGD 640
Db 658 IRLVTMGLGEGYGLANNGNEFGHPENIDFPRGQTLPTGKYLPGNNNSYDCRRRFDLGD 717
QY 641 ADFLRXHGQEPDQANQHLERXYGFMTESEHQYISRKNEGDRVILFERDNLVFVFNFMNSN 700
Db 718 ADFLRXHGQEPDQANQHLERXYGFMTESEHQYISRKNEGDRVILFERDNLVFVFNFMNSN 777
QY 701 SFEDYVVGSRPGKRYKVALDSDDLFGGFSRLDHDVDYFTTEHPHNDNPRPSVYTPBRT 760
Db 778 SFEDYVVGSRPGKRYKVALDSDDLFGGFSRLDHDVDYFTTEHPHNDNPRPSVYTPBRT 837
QY 761 YALTE 768
Db 838 YALAD 845

RESULT 15
ID 042531 PRELIMINARY; PRT; 800 AA.
AC 042531;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Starch branching enzyme class II (EC 2.4.1.18) (fragment).
DE SBE2-2.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Arabidopsia; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsia.
NCBI_Taxid=702;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=ecotype Columbia; TISSUE=Hypocotyl;
RX MEDLINE=96197401; PubMed=8616246;
RA Fisher D.K., Gao M., Kim K.N., Boyer C.D., Guiltinan M.J.;
RT "Two closely related cDNAs encoding starch branching enzyme from
RT Arabidopsis thaliana."
RL Plant Mol. Biol. 30:97-108 (1996).
DR EMBL; U22428; AAB03100.1; -
DR PIR; S65046; S65046.
DR GO; GO:0003844; F:1.4-alpha-glucan branching enzyme activity; IEA.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0004553; F:hydrolase activity; hydrolyzing O-glycosyl. . .; IEA.
DR GO; GO:0016757; F:transferase activity; transferring glycosyl. . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro: IPR006047; Alpha amyl cat.
DR InterPro: IPR004193; Glyco_hydro_13N.
DR Pfam: PF00128; alpha-amylase; 1.
DR Pfam: PF02922; isoamylase_N; 1.
DR GlycoStL:transferrase; Transferrase.
KW NON TER 1
SQ SEQUENCE 800 AA; 92098 MW; 8D47E940B403258 CRC64;

Query Match 78.1%; Score 3258; DB 10; Length 800;
Best Local Similarity 76.6%; Pred. No. 4e-235;
Matches 584; Conservative 75; Mismatches 71; Indels 32; Gaps 4;

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QY 18 AAAQPELQIP-----DIEQTAENVMTGGTAEKLESSEPTQGIIVETITDG 64
DB 54 AISAQKVLVPMNDLDDPPGFSQJFLESQTMEX-----TEAVRTEDQTMNV----- 100
QY 65 VIKGVKELVVGKPRVYKPGDGGOKIYEIDPTLKDFRSHLDYRSEYRIRRAIDQHEGG 124
DB 101 ---VKER--GVKPRIVPPGDKKIYEIDPMLRTYNNHLDYRQYQYKRLREEDKYEKG 154
QY 125 LEAFSGYKELGFTSRASAGITTYREMAPASALVGDENNPNPNADITWTRDDYGVWEIFL 184
DB 155 LEAFSGYKELGFTSRASAGITTYREMAPAKAASLIGDPNNNSNADINTREBFQWWEIFL 214
QY 185 PNNADSPALPHGSRVYKIRMDTPSGVDSISAWIKFSVQAPGEIPNGIYYDPPEEKYV 244
DB 215 PNNTPDSPALPHGSRVYKIRMDTPSGIKDSIPAWIKFSVQAPGEIPNGIYYDPPEEKYV 274
QY 245 PQHPQKRPESLAIYESHIGMSPEPKINSYANRDEVLPRIKLGYNVQIMAIQESHY 304
DB 275 PQHPQKRPESLAIYESHIGMSPEPKINSYANRDEVLPRIKLGYNVQIMAIQESHY 334
QY 305 YASFGYHVTTFPAPSSRFGTPEDLKSLIDRAHEGLVLMIDIVHSHSSNNTLDGLNGFDG 364
DB 335 YASFGYHVTTFPAPSSRFGTPEDLKSLIDRAHEGLVLMIDIVHSHSKNTLDGLNGFDG 394
QY 365 TDTHYFHGGRGHMMWMSRLFNYSWEVLRFLLSNARWMLBXYKFDGFRPDGYTSMYT 424
DB 395 TDAHVFHSGRGVHMMWMSRLFNYSWEVLRYLLSNARWMLBXYKFDGFRPDGYTSMYT 454
QY 425 HHGLQMTFTGNIGEYGFATDVAVYVLMVNDLHGLHPDAVSGEDVSGMPTFCIYPV 484
DB 455 HHGLSYGFTGNYTEYFGLTVDVAVNYLMLVNDMIGHLYPEALITVGEDVSGMPTFCIYPVQ 514
QY 485 DGGVGFYRLHMAVADKMIELLKQSDSWMKGDIVHTLTNRMTLEKCYTAESHDAQLVG 544
DB 515 DGGVGFYRLHMAVADKMIELLKQSDSWMKGDIVHTLTNRMTLEKCIYTAESHDAQLVG 574
QY 545 DKTIAFWLMDKMDYDFPMALDRPSTPRIIDRGIALHKMIRLVMTGLGEGYINFMGNFQHP 604
DB 575 DKTIAFWLMDKMDYDFPMALDRPSTPRIIDRGIALHKMIRLVMTGLGEGYINFMGNFQHP 634
QY 605 EMTDPRGPOTLETKYLPENNNNSYDKCRRRFDLGDADFLRYHGOEFDOAMOHLEEKY 664
DB 635 EMTDPRGPOTLETKYLPENNNNSYDKCRRRFDLGDADFLRYHGOEFDOAMOHLEEKY 694
QY 665 FMTSEHQYVSRKAEEDKVIIFERGDVLFVFNFMHNSFPDYRVGCSRPGKYKVALDSDDA 724
DB 695 FMTSEHQYVSRKAEEDKVIIFERGDVLFVFNFMHNSFPDYRVGCSRPGKYKVALDSDDA 754
QY 725 LFGGFSRLDHDVDYFTTEHPHDKRPRSPSYTTSBRTAVVYAL 766
DB 755 LFGGFSRLDHDVDYFTTEHPHDKRPRSPSYTTSBRTAVVYAL 796
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